

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:12:47 ; Search time 6749.08 Seconds
(without alignments)
11409.857 Million cell updates/sec

Title: US-10-056-454a-14_COPY_145_2790

Perfect score: 2646
Sequence: 1 ATGGTATACACTCTCTGG.....AGCTAGTAGAAGAGAA 2646

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sy:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2646	100.0	2992	8	STU011890
2	2646	100.0	3033	6	A58164
3	2581	97.5	3074	6	AR123355
4	2563.6	96.9	2982	8	STU011888
5	2558.2	96.7	3231	6	A58168
6	2551	96.4	3003	6	A58162
7	2538	95.9	2955	8	STU011885
8	2514	95.0	2975	6	A58163
9	2486.8	94.0	2563	6	AX256072
10	2471.6	93.4	2529	6	A58167
11	2470.6	93.4	2523	8	STU011889
12	2465.8	93.2	2578	6	A58169
13	2455	92.8	2576	6	A58166
14	2435.6	92.0	2493	8	STSBEII
15	1708.6	64.6	3123	8	AB071286
16	1509	57.0	2517	8	AB042937
17	1429.4	54.0	3090	6	A92164
18	1414.6	53.5	3360	8	AB029548
19	1370.4	51.8	3549	8	PSSBEIGEN
20	1369.8	51.8	1393	6	AR123356
21	1362	51.5	2913	6	A92162
22	1317.4	49.8	2542	8	ATU22428
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25	1285.2	48.6	2668	8	ATU18817
26	1270.8	48.0	1481	8	STU011891
27	1264.8	47.8	3015	6	EL4723
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29	1263.6	47.8	2364	6	EL4724
30	1260	47.6	2554	8	AF064560
31	1251.2	47.3	2918	8	RICBCE3
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35	1243.6	47.0	2970	8	AF286319
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37	1240.4	46.9	2853	8	TAU66376
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ALIGNMENTS

RESULT 1
STU011890
LOCUS
DEFINITION Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE A-6.
ACCESSION AJ011890
VERSION AJ011890.1 GI:4584512
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 2992)
AUTHORS Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,

STU011890 2992 bp mRNA Linear PLN 07-APR-1999
Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE

Pred. No. is the number of results predicted by chance to have a

Debet, M., Gidley, M. J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2992)
Jobling, S. A.
Direct Submission
Submitted (07-OCT-1998) Jobling S. A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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/cultivar="Desiree"
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/product="starch branching enzyme II"
/BC_number="2.4.1.18"
BASE COUNT 893 a 542 c 701 g 856 t
ORIGIN

Query Match 100.0%; Score 2646; DB 8; Length 2992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 200 GGATTCAGCAGTAATGGTGCAGGAGTATGATGTTCTGTTATCTTGTAAGAGCAC 259

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QY 361 CCGTCAAGTGAATCTTACAGGAAGTGTGAAGAGTGGATTTGTTTCTTACACTCAACTA 420
Db 500 CCGTCAAGTGAATCTTACAGGAAGTGTGAAGAGTGGATTTGTTTCTTACACTCAACTA 559
QY 421 CAAGAAGTGGTAACTGGAGAGCTTAAACATTAATAACTTCTGTAAGAGACAAATTAAT 480
Db 560 CAAGAAGTGGTAACTGGAGAGCTTAAACATTAATAACTTCTGTAAGAGACAAATTAAT 619
QY 481 GATGAATCTGATAGGATCAGAGAGGGGATCCCTCCAGCTGGATTTGTTTCTGAGAGATT 540
Db 620 GATGAATCTGATAGGATCAGAGAGGGGATCCCTCCAGCTGGATTTGTTTCTGAGAGATT 679
QY 541 TATGAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGATTTACAGTATTCACAG 600
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Db 920 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTTCGCCAAATAATATGGAATGGT 979
QY 841 TCTCCTCGCAATTCCTCATGGTTCAGAGTCAAGATAGTATGACACTCCATCAGGTTGT 900
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QY 121 TCCTTTTCACGGAAGATCTTGCTGAAAGTCTTCTTACAATTCGGAATTCGACACCTTCT 180
Db 265 TCCTTTTCACGGAAGATCTTGCTGAAAGTCTTCTTACAATTCGGAATTCGACACCTTCT 324
QY 181 ACAGTTGACATCGGGGAAAGTCTTGCTGAAAGTCTTCTTACAATTCGGAATTCGACACCTTCT 240
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QY 241 TCAACAGACCAATTTGAGTTCACTGACACATCTCCAGAAAATTCGCCAGCATCACTGAT 300
Db 385 TCACAGACCAATTTGAGTTCACTGACACATCTCCAGAAAATTCGCCAGCATCACTGAT 444
QY 301 GTAGATAGTTCAACAATGAACACGCTAGCCAGATTAACACTGAGAACGATGAGTGTGAG 360
Db 445 GTAGATAGTTCAACAATGAACACGCTAGCCAGATTAACACTGAGAACGATGAGTGTGAG 504
QY 361 CCGTCAAGTCACTTACAGGAAGTGTGAGAGCTGGATTTTGCCTCATCCTACACTA 420
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QY 421 CAAGAAGTGGTAAACTGGAGGAGTCTTAAACATTAATACTCTGGAAGAGACAAATTAAT 480
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QY 601 TACAAGAACTGAGGAGGCAATTGACAAGTATGAGGTGGTGGAAAGCCTTTCTCGT 660
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QY 661 GPTATGAAAAATGGTTCCTACTCGTAGTGTACAGGTATCACTTACCGTGTGAGTGGCT 720
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QY |||||
2641 GAAGAA 2646
Db |||||
2785 GAAGAA 2790

RESULT 3

AR123355-
LOCUS AR123355 3074 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169226.
ACCESSION AR123355
VERSION AR123355.1 GI:14108321
KEYWORDS
SOURCE unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Ek, B., Khosnoodi, J., Larsson, C.-T., Larsson, H. and Rask, L.
TITLE Starch branching enzyme II of potato
JOURNAL Patent: US 6169226-A 1 02-JAN-2001;
FEATURES location/Qualifiers
source 1..3074
BASE COUNT 902 a 558 c 712 g 896 t 6 others
ORIGIN

Query Match 97.5%; Score 2581; DB 6; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGTGTATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGATCAAACTAA 60
Db 189 ATGTGTATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGATCAAACTAA 248
QY 61 GGATTCAGAGTAATGTGATCGGAGAACTGATGTTCTGTTCTGTTCTGTTCTGTTCT 120
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489 GTAGATAGTTCAACAAATGGAACACCGCTAGCCAGATTTAAACTGAGAACGATGAG 548
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361 CCGTCAAGTGATCTTACAGGAGTGTGAAGAGCTGATTTGCTTTCATCAGTACAACTA 420
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669 GATGATCTGATAGGATCAGAGAGGAGGATCCCTCCACCTGGAGTGTGGTCAAGAGAT 728
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RESULT 4

STU011888

LOCUS

DEFINITION

STU011888 2982 bp mRNA linear PLN 07-APR-1999

Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE A-4.

ACCESSION

AJ011888

VERSION

SBEII gene; starch branching enzyme II.

KEYWORDS

Solanum tuberosum.

SOURCE

Solanum tuberosum.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE

1 (bases 1 to 2982)

Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M., Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.

A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II

Unpublished

2 (bases 1 to 2982)

Jobling, S.A.

Direct Submission

Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK

FEATURES

source

1..2982

location/Qualifiers

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BASE COUNT 888 a 529 c 703 g 862 t

Query Match
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Db 2808 GAAGAAGAAGAAGAAGTAGCAGTACTAGAGAAGTAGTAGTAAGAAGAA 2858

RESULT 6
A58162
LOCUS A58162 3003 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 12 from Patent WO9634968.
ACCESSION A58162
VERSION A58162.1 GI:3713887
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3003)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 12 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
COMMENT Other publication AU 550996 961121.
FEATURES
source
location/Qualifiers
1..3003
/organism="unidentified"
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BASE COUNT 895 a 535 c 706 g 867 t
ORIGIN

Query Match 96.4%; Score 2551; DB 6; Length 3003;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2589; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
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RESULT 7
STU011885 2955 bp mRNA linear PLN 07-APR-1999
LOCUS Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
DEFINITION A-1.
ACCESSION AJ011885
VERSION AJ011885.1 GI:4584502
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2955)
Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2955)
Jobling,S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
LOCATION/Qualifiers
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/cultivar="Desiree"
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Db 2720 GAAGTACAGTAGTAGAAGAACCCATTCGAAGAATCAAC 2757

RESULT 8
A58163 A58163 A58163 A58163
DEFINITION Sequence 13 from Patent WO9634968.
ACCESSION A58163
VERSION A58163.1 GI:3713888
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2975)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 13 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
COMMENT Other publication AU 550996 961121.
FEATURES Location/Qualifiers
source 1. 2975
BASE COUNT 870 a 548 c 693 g 864 t
ORIGIN

Query Match 95.0%; Score 2514; DB 6; Length 2975;
Best Local Similarity 98.0%; Pred. NO. 0;
Matches 2566; Conservative 0; Mismatches 50; Indels 2; Gaps 2;
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Db	1261	CAATAATACTTTAGTAGGAC	TGACCAATGTTTGCAT	CCACCGATAGTTGTTACCT	TCAT	1320
QY	1385	CTGAGCTCGTGTTATCAT	TGGATGTTGGATCCCG	CCCTTTAACTATGGAAC	TGGG	1444
Db	1321	CTGAGCTCGTGTTATCAT	TGGATGTTGGATCCCG	CCCTTTAACTATGGAAC	TGGG	1380
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Db	1381	AGGTACTTAGGTAICTTCT	CTCATAAATCGGAGAT	TGGTGGATTCGATTC	CAATTTGATG	1440
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Db	1441	GAATTAGATTTGATGGTG	CACATCAATGATGTTT	CACACGCAATTC	CGTGGAT	1500
QY	1565	TCACTGGAACTACGAGGA	TACTTTGGACTCGCA	ACTGATGTGGATGCT	TGTTGCTATC	1624
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QY	1685	ATGTTACGGAAATCCCGA	CAATTTGTTATCCCGT	CCAAAGGGGGCTGTG	GCTTTTCATC	1744
Db	1621	ATGTTACGGAAATCCCGA	CAATTTGTTATCCCGT	CCAAAGGGGGCTGTG	GCTTTTCATC	1680
QY	1745	ATCGGCTGCATATGGCA	ATTTGCTGATAA	ACGGATTGAGTTGCTCA	AGAAACGGGATGAGG	1804
Db	1681	ATCGGCTGCATATGGCA	ATTTGCTGATAA	ACGGATTGAGTTGCTCA	AGAAACGGGATGAGG	1740
QY	1805	ATTGGAGATGGGTGATAT	TGTTTCATACACT	GACAAATAGAGATGGT	CGGAAAAGTGTG	1864
Db	1741	ATTGGAGATGGGTGATAT	TGTTTCATACACT	GACAAATAGAGATGGT	CGGAAAAGTGTG	1800
QY	1865	TTTCATACGCTGAAAGT	CATGATCAAGCTCT	TAGTCGGTGTAA	AAACTATAGCATTC	1924
Db	1801	TTTCATACGCTGAAAGT	CATGATCAAGCTCT	TAGTCGGTGTAA	AAACTATAGCATTC	1860
QY	1925	TGATGGACAAGGATATGT	ATGATTTTATGGCT	CTGTGATAGACCGT	CAACATCATTAATAG	1984
Db	1861	TGATGGACAAGGATATGT	ATGATTTTATGGCT	CTGTGATAGACCGT	CAACATCATTAATAG	1920
QY	1985	ATCGTGGGATAGCATTTG	CACAGATGATTTAGG	TTGTAACTATGGGAT	TAGGAGGAGAG	2044
Db	1921	ATCGTGGGATAGCATTTG	CACAGATGATTTAGG	TTGTAACTATGGGAT	TAGGAGGAGAG	1980
QY	2045	GGTACCTAAATTTTCATG	GGAATGAATTCGGC	CCCTCAGTGGAT	TGATTTCCCTAGG	2104
Db	1981	GGTACCTAAATTTTCATG	GGAATGAATTCGGC	CCCTCAGTGGAT	TGATTTCCCTAGG	2040
QY	2105	CTGAACAACACCTCTCT	GATGGCTCAGTAAT	CCCGGAACCAATTCAGT	TATGATAAT	2164
Db	2041	CTGAACAACACCTCTCT	GATGGCTCAGTAAT	CCCGGAACCAATTCAGT	TATGATAAT	2100
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[illegible]

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387 TGAAGAGCTGGATTTGCTTCACTACATACAACTACAGAAAGGTTGGTAACTGGAGGAGTC 446
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447 TAAACATTAATACTCTCTGAAGAGACAATTAATGATGAATGATAGGATCAGAGAGAG 506
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421 GGGCATCCCTCCACCTGGACTTGGTCAGAGAGATTAAGAAATGACACCCCTTTTGACAAA 480
567 CTATCGTCAACACCTTGAATACAGGTAATCACAGTACAGAAACTGAGGAGGCAATTGA 626
481 CTATCGTCAACACCTTGAATACAGGTAATCACAGTACAGAAACTGAGGAGGCAATTGA 540
627 CAAGATGAGGGTGGTTGGAAGCTTTCTCGRGGTTATGAAAAATGGTTTCACTCG 686
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687 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTGGTCCCGAGTCAGTCCCTCAT 746
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747 TGGAGATTTCAACAATTTGGGACGCAATGCTGACATTAAGTACGTCGGAATGAATTTGGTGT 806
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927 CTACTCTTTACAGCTTCTGATGAATTTCCATATAATGGAATATAATGATGATCCACCGA 986
841 CTACTCTTTACAGCTTCTGATGAATTTCCATATAATGGAATATAATGATGATCCACCGA 900
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1047 TGAATCTCATATGGAATGAGTACTCGGAGCCPAAAAUUAACATACGTGAATTTTAG 1106
961 TGAATCTCATATGGAATGAGTACTCGGAGCCPAAAAUUAACATACGTGAATTTTAG 1020
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1167 TCAGAGCATCTTATACGCTAGTCTTGGTATCATGTCACAAATTTTGTGACCAAG 1226
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1141 CAGCGGTTTGGAAAGCCGACGACCTTAAGTCTTTGATGATAAAGCTCATGAGCTAGG 1200
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1981 TGAATCGCCACCTGAGTGGATGATTTCCCTAGGCTGAACCAACACCTCTCTGATGG 2040
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QY	1095	CGTGAATTTAGAGATGAAGTCTCTCCCTCGCATAAAAAGCGTGGGTACAAATCGCTGCA	1154	QY	2175	ATTGTGACCTGGGAGATGCAGAAATATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGCG	2234
Db	961	CGTGAATTTAGAGATGAAGTCTCTCCCTCGCATAAAAAGCGTGGGTACAAATCGCTGCA	1020	Db	2041	ATTGTGACCTGGGAGATGCAGAAATATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGCG	2100
QY	1155	AATTATGGGTATTCAGAGCATCTTATACGCTAGTCTTTGGTTATCAITCAITCAACAATTT	1214	QY	2235	TATGCAGTATCTTGAAGATAAATATGAGTTATGACTTTCAGAACACACAGTTCATATCAGC	2294
Db	1021	AATTATGGGTATTCAGAGCATCTTATACGCTAGTCTTTGGTTATCAITCAITCAACAATTT	1080	Db	2101	TATGCAGTATCTTGAAGATAAATATGAGTTATGACTTTCAGAACACACAGTTCATATCAGC	2160
QY	1215	TTTTGCACCAAGCAGCGCTTTTGGAGCGCCGACGACCTTAAGTCTTTGATGATGAAGC	1274	QY	2295	AAAGGATGAAGGAGATAGGATGATTTGATTTGAAAAAGAAACCTAGTCTTTTGTCTTTAA	2354
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QY	1275	TCATGAGCTAGGAATTTGCTCTCATGGACATTTGTTACAGCAGCATGCATCAATAATAC	1334	QY	2355	TTTTTACTGGACAAAAAAGCTATTTCAGACTATCGCATAGCCCTGTAAGCCTTGAAAAATA	2414
Db	1141	TCATGAGCTAGGAATTTGCTCTCATGGACATTTGTTACAGCAGCATGCATCAATAATAC	1200	Db	2221	TTTTTACTGGACAAAAAAGCTATTTCAGACTATCGCATAGCCCTGTAAGCCTTGAAAAATA	2280
QY	1335	TTTTAGATGGAGTGAACATGTTTGCAGTGCACCGATAGTGTACTTTCACTCTCGAGCTCG	1394	QY	2415	CAAGGTTGCTTGGACCTCAGATGATCCACCTTTTGGTGGCTTGGGAGATTTGATCATAA	2474
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QY	1395	TGCTTATCATTTGGATGCGGATTCGCCCTCTTTAACTATGGAACCTGGGAGTACTTAG	1454	QY	2475	TGCCGAATATTTTCACTTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATG	2534
Db	1261	TGCTTATCATTTGGATGCGGATTCGCCCTCTTTAACTATGGAACCTGGGAGTACTTAG	1320	Db	2341	TGCCGAATATTTTCACTTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATG	2400
QY	1455	GTATCTCTCTCAAAATCGAGATGTTGGTGGATGGCTTCAAAATTTGATGATTTAGATT	1514	QY	2535	TGCACCTTTGAAACACAGCTGGTCTATGCACTAGTAGACAAAAGAAAGAAAGAAAGA	2594
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QY	1575	CTAGAGGAATATTTGATTCCTCGCTCAAGAGGGGTTGGCTTTGATCTGATGCTGGT	1634	RESULT 12			
Db	1441	CTAGAGGAATATTTGATTCCTCGCTCAAGAGGGGTTGGCTTTGATCTGATGCTGGT	1500	A58169	A58169	2578 bp	DNA
QY	1635	CAACGATCTTATTCATGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATTTAGCGG	1694	DEFINITION	Sequence 19 from Patent WO9634968.		
Db	1501	CAACGATCTTATTCATGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATTTAGCGG	1560	ACCESSION	A58169		
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QY	1815	GGGTGATATTTTATCACTGACAAATAGAAGATGCTCGGAAAGTGTGTTTCATACGC	1874	AUTHORS	Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,		
Db	1681	GGGTGATATTTTATCACTGACAAATAGAAGATGCTCGGAAAGTGTGTTTCATACGC	1740	TITLE	Sidebottom, Christopher,M. and Westcott,R.J.		
QY	1875	TGAAGTCATGATCAAGCTAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1934	JOURNAL	IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION		
Db	1741	TGAAGTCATGATCAAGCTAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATG	1800	COMMENT	Patent: WO 9634968-A 19 07-NOV-1996;		
QY	1935	GGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTAATAGATGCTGGGAT	1994	FEATURES	NAT STARCH CHEM INVEST (US)		
Db	1801	GGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTAATAGATGCTGGGAT	1860	source	Other publication AU 550996 961121.		
QY	1995	AGCATTCACAAGATGATTTAGGCTTTAATATGAGGATTTAGGAGGAAAGGTTACCTAAA	2054	1. .2578	Location/Qualifiers		
Db	1861	AGCATTCACAAGATGATTTAGGCTTTAATATGAGGATTTAGGAGGAAAGGTTACCTAAA	1920	/organism="unidentified"			
QY	2055	TTTTTATGGGAAATCAATTCGCGACCTGAGTGGATTTGATTTCCCTAGGCTGAAACAA	2114	/db_xref="taxon:32644"			
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Db	1981	CCCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGATGATGATGATGATGATG	2040	Best Local Similarity 98.9%; Pred. No. 0;	Matches 2482; Conservative 0; Mismatches 27; Indels 0; Gaps 0;		

QY 315 AATGGACACCGTAGCCAGATTAATAACTCAGAACGATGACGTTGAGCGCTCAAGTGACT 374
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RESULT 13
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ACCESSION A58166
VERSION   A58166.1  GI:3713891
KEYWORDS .
SOURCE   unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2576)
AUTHORS  Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
          Sidebottom, Christopher,M. and Westcott,R.J.
TITLE    IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL  Patent: WO 9634968-A 16 07-NOV-1996;
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COMMENT  Other publication AU 5509996 961121.
FEATURES             Location/Qualifiers
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BASE COUNT  770 a 462 c 615 g 729 t
ORIGIN

Query Match      92.8%; Score 2455; DB 6; Length 2576;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2482; Conservative 0; Mismatches 25; Indels 2; Gaps 1;

QY      135  GATCTTGGCTGAAAGTCCTTTACAAATTCGGAATTCGGACCTCTACAGTTGCAGCATC 194
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QY      195  GGGGAAAGTCCTTGTGCTGGAACCCAGAGTAGTAGCTCTCATCTCAACAGACCAAT 254
Db      116  GGGGAAAGTCCTTGTGCTGGAACCCAGAGTAGTAGCTCTCATCTCAACAAACCAAT 175
QY      255  TGAGTTCACCTGAGACATCTCCAGAAATTCGCCAGCATCCAGCATCACTGATGATCTCAAC 314
Db      176  TGAGTTCACCTGAGACATCTCCAGAAATTCGCCAGCATCCAGCATCACTGATGATCTCAAC 235
QY      315  AATGGAACAGCTAGCCAGATTTAAACTGGAAGCATGACGTTGAGCGCTCAAGTGATCT 374
Db      236  AATGGAACAGCTAGCCAGATTTAAACTGGAAGCATGACGTTGAGCGCTCAAGTGATCT 295
QY      375  TACAGGAAGTGTGAAGAGCTGGATTTTGGTTCATCACTCAACTACAAGAGTGGTAA 434
Db      296  TACAGGAAGTGTGAAGAGCTGGATTTTGGTTCATCACTCAACTACAAGAGTGGTAA 355
QY      435  ACTGGAGAGCTTAAACATTAATACTCTCGAGAGACAATTATGATGAATCTGATAG 494
Db      356  ACTGGAGAGCTTAAACATTAATACTCTCGAGAGACAATTATGATGAATCTGATAG 415
QY      495  GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCC 554
Db      416  GATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCC 475
QY      555  CCTTTTGACAAACTATCGTCAACACCTTGATTAACAGTATTCACAGTACAAAGACTGAG 614
Db      476  CCTTTTGACAAACTATCGTCAACACCTTGATTAACAGTATTCACAGTACAAAGACTGAG 535
QY      615  GGAGGCAATTCACAGATGAGGTGGTTTGAAGCCTTTTCTCGTGGTTATGAAAAT 674
Db      1614  AATGCCACATTTTGTATTCGGCTCAAGATGGGGGTGTGGCTTTGACTATCGGTGCA 1673

536  GGAGGCAATTCACAGATGAGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAGAAAT 595
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596  GGGTTTCACCTCGTAGTCTACAGTATCAGTTACCGTGAAGTGGCTCTTGGTGCCAGATC 655
735  AGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCGCAAAATGCTGACATTTATGACTCG 794
656  AGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCGCAAAATGCTGACATTTATGACTCG 715
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1494  CTACAGGAATTAATTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1553
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QY 1405 TGGATGTGGATTTCCCGCTCTTTAACTATGAAACTGGGAGTACTTAGGTATCTTCTC 1464
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QY	2605	GAAGAAAGTAGCAGCAGTAGAAGAAAGTAGTGA	2634		
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RESULT 15					
LOCUS	AB071286	3123 bp	linear	PLN 11-SEP-2001	
DEFINITION	Ipomoea batatas SBE II mRNA for starch branching enzyme II, complete cds.				
ACCESSION	AB071286				
VERSION	AB071286.1	GI:15553090			
KEYWORDS					
SOURCE	Ipomoea batatas (cultivar:Kokei 14)	cDNA to mRNA.			
ORGANISM	Ipomoea batatas				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.				
REFERENCE	1	Kimura,T. and Saito,A.			
AUTHORS	Ipomoea batatas mRNA for starch branching enzyme II				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 3123)				
REFERENCE	Kimura,T. and Saito,A.				
AUTHORS	Direct Submission				
TITLE	Submitted (08-SEP-2001) Takashi Kimura, National Agricultural Research Center for Kyushu Okinawa Region; 2421 Suyu, Nishigoshi, Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp, Tel:81-96-242-1150).				
JOURNAL	Location/Qualifiers				
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ORIGIN					
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	Best Local Similarity	78.9%;	Pred. No. 0;		
	Matches 2061;	Conservative	0;	Mismatches 544;	Indels 6;
	Gaps	2;			
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 12:28:17 : Search time 551.364 Seconds
(without alignments)
10807.357 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2646	100.0	3033	17	Class A starch bra
2	2584.2	97.7	3074	18	Potato starch bran
3	2558.2	96.7	3231	17	Class A starch bra
4	2551	96.4	3003	17	Class A starch bra
5	2512.4	95.0	2975	17	Class A starch bra
6	2486.8	94.0	2563	23	Potato cDNA encodi
7	2471.2	93.4	2531	17	Class A starch bra
8	2468.4	93.3	2529	17	Class A starch bra
9	2465.8	93.2	2578	17	Class A starch bra

10	2451.8	92.7	2576	17	Class A starch bra
11	1429.4	54.0	3090	19	Full length cassav
12	1362	51.5	2913	19	Full length cassav
13	1290	48.8	2715	21	Arabidopsis thalia
14	1264.8	47.8	3015	19	Rice type IV starc
15	1251.2	47.3	2919	15	Rice starch branch
16	1243.6	47.0	2726	22	Nucleotide sequenc
17	1183.6	44.7	2640	19	DNA encoding maize
18	1180.4	44.6	2665	18	Plasmid pBE240 ins
19	1180.4	44.6	2725	19	Plasmid pBE240 ins
20	1167.2	44.1	3039	24	Zea mays starch br
21	1164	44.0	2968	22	Wheat starch bran
22	1044.6	39.5	2307	21	Nucleotide sequenc
23	1033	39.0	2087	18	DNA encoding part
24	1031.4	39.0	2165	18	Corn starch branch
25	956.6	36.2	1919	19	Corn starch branch
26	728.8	27.5	1452	21	cDNA encoding star
27	632.4	23.9	4563	22	Arabidopsis thalia
28	631.4	23.9	3128	16	Wheat starch bran
29	628.4	23.7	2487	18	Potato starch bran
30	628.4	23.7	2565	18	Corn starch branch
31	628.4	23.7	2763	19	Corn starch branch
32	628.4	23.7	2771	13	Zea mays starch br
33	628.4	23.7	2772	18	Branching enzyme D
34	617.2	23.3	2909	13	Plasmid pBE5 inse
35	610	23.1	2687	20	Potato amylose-amy
36	603	22.8	2733	15	wSBE I-D4 cDNA seq
37	603	22.8	2733	15	Rice starch branch
38	589	22.3	2713	19	Rice starch branch
39	578.2	21.9	3075	24	DNA encoding maize
40	576.6	21.8	2899	22	Human DNA sequenc
41	576.6	21.8	2955	24	Human shear stress
42	542	20.5	1809	18	Gene #2148 used to
43	542	20.5	1865	18	Corn starch branch
44	535.8	20.2	770	23	Corn starch branch
45	501.6	19.0	728	23	Potato starch bran

ALIGNMENTS

RESULT 1
AAT42630
ID AAT42630 standard; DNA; 3033 BP.
XX
AC AAT42630;
XX
DT 25-FEB-1997 (first entry)
XX
DE Class A starch branching enzyme (19con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT CDS 145..2793
FT FT /*tag= a
FT sig_peptide 145..288
FT FT /*tag= b
FT mat_peptide 289..2790
FT FT /*tag= c
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XX WO9634968-A2.
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XX 07-NOV-1996.
XX
XX 03-MAY-1996; 96WO-GB01075.
XX
XX 10-APR-1996; 96GB-0007409.
XX
XX 05-MAY-1995; 95GB-0009229.
XX

(NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
Sidebottom CM, Westcott RJ;
WPI; 1996-506170/50.
P-PSDB; AAW06399.
New potato plant starch having high amylose content - also class A
starch branching enzyme and corresp. DNA to alter the viscosity of
starch; for use in food, biodegradable products, adhesives, etc.
Claim 28-30; Page 42-46; 142pp; English.
Class A starch branching enzyme (SBE) has been obtained from
potatoes. In class A SBE mols., a flexible N-terminal domain,
is found, which is not found in class B mols.
Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;
Query Match 100.0%; Score 2646; DB 17; Length 3033;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGATACACTCTCTGGAGTTCGTTTCTCTACTCTTCCATCAGTGTACAAATCAAT 60
DB 145 ATGGTGATACACTCTCTGGAGTTCGTTTCTCTACTCTTCCATCAGTGTACAAATCAAT 204
QY 61 GGATTCAGCAGTAATGTGATCGAGGAATGCTAATGTTCTGTTCTTGGAAAGCAC 120
DB 205 GGATTCAGCAGTAATGTGATCGAGGAATGCTAATGTTCTGTTCTTGGAAAGCAC 264
QY 121 TCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTCAATTCGGAATTCGACCTTCT 180
DB 265 TCCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTCAATTCGGAATTCGACCTTCT 324
QY 181 ACAGTTCAGCATCGGGAAGTCTTGTGCTGGGAAACCCAGAGTATGATCTCTCATCC 240
DB 325 ACAGTTCAGCATCGGGAAGTCTTGTGCTGGGAAACCCAGAGTATGATCTCTCATCC 384
QY 241 TCAACAGACCAATTTGATTCACATGACATCTCCAGAAATTCGAGCATCACTGAT 300
DB 385 TCAACAGACCAATTTGATTCACATGACATCTCCAGAAATTCGAGCATCACTGAT 444
QY 301 GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATACTGAGAAGTGTGAG 360
DB 445 GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATACTGAGAAGTGTGAG 504
QY 361 CCGTCAAGTATCTTACAGGAAGTGTGAGAGAGTGGATTTTGCTTCACTACACTA 420
DB 505 CCGTCAAGTATCTTACAGGAAGTGTGAGAGAGTGGATTTTGCTTCACTACACTA 564
QY 421 CAAGAAGTGTAAACTGGAGAGTGTAAACATTAATACTTCTGGAAGACAAATTAAT 480
DB 565 CAAGAAGTGTAAACTGGAGAGTGTAAACATTAATACTTCTGGAAGACAAATTAAT 624
QY 481 GATGAATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGAGTGTGTCAGGAAGAT 540
DB 625 GATGAATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGAGTGTGTCAGGAAGAT 684
QY 541 TATGAATAGACCCCTTTTACAAACTATCGTCAACACCTTGATTCAGAGTATTCACAG 600
DB 685 TATGAATAGACCCCTTTTACAAACTATCGTCAACACCTTGATTCAGAGTATTCACAG 744
QY 601 TACAAGAACTGAGGGAGCAATTCACAAGTATGAGGTGTTTGGAAAGCCTTTTCTCGT 660
DB 745 TACAAGAACTGAGGGAGCAATTCACAAGTATGAGGTGTTTGGAAAGCCTTTTCTCGT 804
QY 661 GGTATGAAAAAATGGGTTTCACTCGTATGCTCAGGATATCACTTACCGTGAAGGGCT 720
DB 805 GGTATGAAAAAATGGGTTTCACTCGTATGCTCAGGATATCACTTACCGTGAAGGGCT 864
QY 721 CTTGGTGCACAGTCAGCTGCCCTCATTTGAGATTTCAACAATGGGACGCAATTCCTGAC 780

DB 865 CTTGGTGCACAGTCAGCTGCCCTCATTTGGAGATTTCAACAATGGGACGGAATTCCTGAC 924
QY 781 ATTATGACTCGGAATGAATTTGGTCTCTGGAGATTTTCTGCGCAATTAATGTGATGGT 840
DB 925 ATTATGACTCGGAATGAATTTGGTCTCTGGAGATTTTCTGCGCAATTAATGTGATGGT 984
QY 841 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGATAGATATGAGACATCTCCATCAGGTTT 900
DB 985 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGATAGATATGAGACATCTCCATCAGGTTT 1044
QY 901 AAGGATTCATTCCTGCTGGATCAACTACTCTTTTACAGTTCCTGATGAATTCATAT 960
DB 1045 AAGGATTCATTCCTGCTGGATCAACTACTCTTTTACAGTTCCTGATGAATTCATAT 1104
QY 961 AATGGAATACATTAATGATCCACCGAAGAGGAGGATATCTTCCAAACACCCAGGCCA 1020
DB 1105 AATGGAATACATTAATGATCCACCGAAGAGGAGGATATCTTCCAAACACCCAGGCCA 1164
QY 1021 AAGAAACCAAGTCGCTGAGAAATATGAATCTCATATTTGAATGAGTAGTCCGAGGCT 1080
DB 1165 AAGAAACCAAGTCGCTGAGAAATATGAATCTCATATTTGAATGAGTAGTCCGAGGCT 1224
QY 1081 AAAATTAACCTCATACGTGAATTTAGAGATGAAGTCTTCTCGCATAAAGAGCTGGG 1140
DB 1225 AAAATTAACCTCATACGTGAATTTAGAGATGAAGTCTTCTCGCATAAAGAGCTGGG 1284
QY 1141 TACAATGGCTGCAAAATATGGCTATTCAAGAGCATCTTATAGCTTAGTTTTGGTTAT 1200
DB 1285 TACAATGGCTGCAAAATATGGCTATTCAAGAGCATCTTATAGCTTAGTTTTGGTTAT 1344
QY 1201 CATGTCACAAATTTTTCACCAAGAGCCGTTTGGAGCCGCGAGACCTTAAGTCT 1260
DB 1345 CATGTCACAAATTTTTCACCAAGAGCCGTTTGGAGCCGCGAGACCTTAAGTCT 1404
QY 1261 TTGATTTGAAGTCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTTCAAGCCAT 1320
DB 1405 TTGATTTGAAGTCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTTCAAGCCAT 1464
QY 1321 GCATCAAAATATACITTTAGATGGACTGAACATTTTGTACTGCACCGATAGTTTACTTT 1380
DB 1465 GCATCAAAATATACITTTAGATGGACTGAACATTTTGTACTGCACCGATAGTTTACTTT 1524
QY 1381 CACTCTGAGCTCGTGGTTTATCATTTGGATTTGGGATTTCCCGCTCTTTAACTATGGAAC 1440
DB 1525 CACTCTGAGCTCGTGGTTTATCATTTGGATTTGGGATTTCCCGCTCTTTAACTATGGAAC 1584
QY 1441 TGGAGGTACTTAGTATCTTCTCAAAATGGAGATGGTGGTGGATCGGCTTCAAAATTT 1500
DB 1585 TGGAGGTACTTAGTATCTTCTCAAAATGGAGATGGTGGTGGATCGGCTTCAAAATTT 1644
QY 1501 GATGATTTAGATTTGATGGTGTGACATCAATGATGATATATTCACCGAGTATTCGGTG 1560
DB 1645 GATGATTTAGATTTGATGGTGTGACATCAATGATGATATATTCACCGAGTATTCGGTG 1704
QY 1561 GGATTCATCGGAACTACGAGGAATACITTTGAGCTGCAACTGATGATGCTCTGTG 1620
DB 1705 GGATTCATCGGAACTACGAGGAATACITTTGAGCTGCAACTGATGATGCTCTGTG 1764
QY 1621 TATCTGATGCTGGTCAAGCATCTTATTCATGGGCTTTTCCAGATGCAATTAACATTTG 1680
DB 1765 TATCTGATGCTGGTCAAGCATCTTATTCATGGGCTTTTCCAGATGCAATTAACATTTG 1824
QY 1681 GAAGATTTAGGGGAATGCGGACATTTTGTATTCCTGCTCCAGAGGGGGTGTGGCTTT 1740
DB 1825 GAAGATTTAGGGGAATGCGGACATTTTGTATTCCTGCTCCAGAGGGGGTGTGGCTTT 1884
QY 1741 GACTATCGCTGCTATATGCAATTTCTGATTAAGGATTTGAGTTCTCAAGAAACGGGAT 1800
DB 1885 GACTATCGCTGCTATATGCAATTTCTGATTAAGGATTTGAGTTCTCAAGAAACGGGAT 1944
QY 1801 CAGGATTCGAGAGTGGGTGATATTTTTCATACACTGACAAATAGAGATGGTTCGGAAG 1860

RESULT 2	
AAAT69587	
ID	AAAT69587 standard; cDNA; 3074 bp.
XX	
XX	AAAT69587;
AC	
XX	
XX	26-AUG-1997 (first entry)
DT	
XX	
XX	Potato starch branching enzyme II gene (bell).
DE	
XX	
XX	Starch branching enzyme II; bell gene; potato; transgenic plant;
KW	amylpectin; amylose; starch; ss.
XX	
OS	Solanum tuberosum.

SQ	Sequence	3074 BP;	902 A;	560 C;	710 G;	896 T;	6 other;
Query Match	97.7%;	Score	2584.2;	DB	18;	Length	3074;
Best Local Similarity	98.7%;	Pred.	No. 0;	Mismatches	0;	Indels	0;
Matches	2601;	Conservative					
QY	1	ATGGTGTTATACACTCTCTGAGTTCGTTTTCTTACTGTTCCTACTGTTCCATCACTGATCAGAAATCGTAATGTTTCTCTATTCTTGAAAAAGCGT					
Dd	189	ATGGTGTTATACACTCTCTGAGTTCGTTTTCTTACTGTTCCTACTGTTCCATCACTGATCAGAAATCGTAATGTTTCTCTATTCTTGAAAAAGCGT					
QY	61	GGATTTCAGCAGTGAATGCTGATCGAGGAATCGTAATGTTTCTCTATTCTTGAAAAAGCGT					
Dd	249	GGATTTCAGCAGTGAATGCTGATCGAGGAATCGTAATGTTTCTCTATTCTTGAAAAAGCGT					
QY	121	TCTCTTTTCACGGAAGATCTTTGGCTGAAAAGTCTTCTTACAATTCGAAATTCGAAATTCGCAGACTTC					
Dd	309	TCTCTTTTCACGGAAGATCTTTGGCTGAAAAGTCTTCTTACAATTCGAAATTCGCAGACTTC					
QY	181	ACAGTTGCAGCATCGGGGAAGTCTTGTCCTCTGAAACCCAGAGTGATAGCTTCCTTCATCT					
Dd	369	ACAGTTGCAGCATCGGGGAAGTCTTGTCCTCTGAAACCCAGAGTGATAGCTTCCTTCATCT					
QY	241	TCAACAGACCAAATTTGAGTTCACTGAGACATCTCCAGAAAAATTCGCCAGCACTCACTGAG					
Dd	429	TCAACAGACCAAATTTGAGTTCACTGAGACATCTCCAGAAAAATTCGCCAGCACTCACTGAG					

QY	301	GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATAAACTGAGAACGATGACGTTGAG	360		1569	CACCTCTGGAGCTCGTGGTTATCATTTGGATGGGATTTCCCGCTCTTTAACTATGGAAC	1628	
Db	489	GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATAAACTGAGAACGATGACGTTGAG	548		1441	TGGAGAGTACTTAGGTATCTTCTCTCAATTCGAGATGGTGGTGGATGGTTCAAATTT	1500	
QY	361	CGGTCAAGTGAATCTTACAGGAGAGTGTGAAGAGCTGGATTTGCTTCATCATCTACAACTA	420		1629	TGGAGAGTACTTAGGTATCTTCTCTCAATTCGAGATGGTGGTGGATGGTTCAAATTT	1688	
Db	549	CGGTCAAGTGAATCTTACAGGAGAGTGTGAAGAGCTGGATTTGCTTCATCATCTACAACTA	608		1501	GATCGAATTTAGATTTGATGGTGCATCATCAATGATGATATTCACCAACGGATATTCGGTG	1560	
QY	421	CAAGAGGTTGGTAACTGAGGAGTCTAACAATTAATTAATCTCTGAAGAGCAATTAAT	480		1689	GATCGAATTTAGATTTGATGGTGCATCATCAATGATGATATTCACCAACGGATATTCGGTG	1748	
Db	609	CAAGAGGTTGGTAACTGAGGAGTCTAACAATTAATTAATCTCTGAAGAGCAATTAAT	668		1561	GGATTCCTGGGAACACGAGGAGTACTTTGGACTCGCACTGATGGATGGTGGTG	1620	
QY	481	GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGGTCAAGAT	540		1749	GGATTCCTGGGAACACGAGGAGTACTTTGGACTCGCACTGATGGATGGTGGTG	1808	
Db	669	GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGGTCAAGAT	728		1621	TATCTGATGCTGGTCAACGATCTTATTCATGCGGCTTTTCCAGATGCAATTAACCAATGGT	1680	
QY	541	TATGAATAGACCCCTTTTGACAAACTATTCGTCAACACCTTGATTCAGGTTATTCACAG	600		1809	TATCTGATGCTGGTCAACGATCTTATTCATGCGGCTTTTCCAGATGCAATTAACCAATGGT	1868	
Db	729	TATGAATAGACCCCTTTTGACAAACTATTCGTCAACACCTTGATTCAGGTTATTCACAG	788		1681	GAAGATTTAGCGGAATGCCGACATTTTGTATTTCCCGTCCAGAGGGGGTGGTGGCTTT	1740	
QY	601	TACAAGAACTGAGGAGGCAATTGACAAGTATGAGGGTGGTGGTGGTGGTGGTGGTGGTGGT	660		1869	GAAGATTTAGCGGAATGCCGACATTTTGTATTTCCCGTCCAGAGGGGGTGGTGGCTTT	1928	
Db	789	TACAAGAACTGAGGAGGCAATTGACAAGTATGAGGGTGGTGGTGGTGGTGGTGGTGGTGGT	848		1741	CACATATCGCTGCATATGGCAATTCGTGATAAACGGATTCAGTTGCTCAAGAAACGGGAT	1800	
QY	661	GGTATCAAAAAATGGTCTTCACTCGTGTGCTACAGGTATCACTTACCGTGTGAGTGGCT	720		1929	CACATATCGCTGCATATGGCAATTCGTGATAAACGGATTCAGTTGCTCAAGAAACGGGAT	1988	
Db	849	GGTATCAAAAAATGGTCTTCACTCGTGTGCTACAGGTATCACTTACCGTGTGAGTGGCT	908		1801	GAGGATTTGAGAGTGGGTGATTTGTTTATATACACTGACAAATAGAGAATGGTTCGGAAGA	1860	
QY	721	CTTGGTGGCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAATTCGTAC	780		1989	GAGGATTTGAGAGTGGGTGATTTGTTTATATACACTGACAAATAGAGAATGGTTCGGAAGA	2048	
Db	909	CTTGGTGGCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAATTCGTAC	968		1861	TGCTTTTCACTACCGTGAAGATCATGCAAGCTAGTCGCTGATGATAAACTATGACATTC	1920	
QY	781	ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAAAATATTTGGATGGT	840		2049	TGCTTTTCACTACCGTGAAGATCATGCAAGCTAGTCGCTGATGATAAACTATGACATTC	2108	
Db	969	ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAAAATATTTGGATGGT	1028		1921	TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTA	1980	
QY	841	TCCTCTGCAATTCCTCATGGTCCAGAGTGAAGATGATGAGACATCCATCAGGTGTT	900		2109	TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTA	2168	
Db	1029	TCCTCTGCAATTCCTCATGGTCCAGAGTGAAGATGATGAGACATCCATCAGGTGTT	1088		1981	ATAGATCGTGGGATAGCATTCGACAAGATGATAGGCTTGAATAGGATAGGATAGGAGA	2040	
QY	901	AAGGATTCATTCCTGTTGGATCAACTACTCTTTACAGCTTCTGATGAAATCCCATAT	960		2169	ATAGATCGTGGGATAGCATTCGACAAGATGATAGGCTTGAATAGGATAGGAGA	2228	
Db	1089	AAGGATTCATTCCTGTTGGATCAACTACTCTTTACAGCTTCTGATGAAATCCCATAT	1148		2041	GAAGGTACCTTAATTTTCATGGGAAATGAATTCGCCACCTGATGGATGATTCCTCT	2100	
QY	961	AATGGAATACATTTATGATCCACCGAAGAGAGAGGTATATCTTCCAAACACCCAGGCCA	1020		2229	GAAGGTACCTTAATTTTCATGGGAAATGAATTCGCCACCTGATGGATGATTCCTCT	2288	
Db	1149	AATGGAATATATTAATGATCCACCGAAGAGAGAGGTATATCTTCCAAACACCCAGGCCA	1208		2101	AGGCTGAACAAACACCTCTCTGATGGCTCAGTAAATPCCCGGAAACCAATTCAGTTATGAT	2160	
QY	1021	AAGAAACCAAGTCGCTGAGAAATATATGATCTCATATTTGGAATGAGTAGTCCGAGCCT	1080		2289	AGGCTGAACAAACACCTCTCTGATGGCTCAGTAAATPCCCGGAAACCAATTCAGTTATGAT	2348	
Db	1209	AAGAAACCAAGTCGCTGAGAAATATATGATCTCATATTTGGAATGAGTAGTCCGAGCCT	1268		2161	AAATGCAGACGGAGATTTGACCTGGGAGATGCGAGAAATTAAGATACCGTGGTGGCA	2220	
QY	1081	AAAATTAACATACAGTGAATTTTAGAGATGAAGTCTTCTCTGCAATAAAAAAGCTGGG	1140		2349	AAATGCAGACGGAGATTTGACCTGGGAGATGCGAGAAATTAAGATACCGTGGTGGCA	2408	
Db	1269	AAAATTAACATACAGTGAATTTTAGAGATGAAGTCTTCTCTGCAATAAAAAAGCTGGG	1328		2221	GAATTTGACCGGCTTATGCACTATCTTCAAGATAAATGATGATTTATGACTTCAGAACAC	2280	
QY	1141	TACAATGGCTGCAAAATATGGCTATTAACAGACATTTCTTAATACGCTAGTTTGGTTAT	1200		2409	GAATTTGACCGGCTTATGCACTATCTTCAAGATAAATGATGATTTATGACTTCAGAACAC	2468	
Db	1329	TACAATGGCTGCAAAATATGGCTATTAACAGACATTTCTTAATGCTAGTTTGGTTAT	1388		2281	CAGTTTCATATCACGAAAGGATGAAGGATAGGATGATTTGTAATTTGAAAAAGGAACCTA	2340	
QY	1201	CATGTCACAAATTTTGGACCAAGCAGCGGTTTGGACCGCCGACGACCTTAAGTCT	1260		2469	CAGTTTCATATCACGAAAGGATGAAGGATAGGATGATTTGTAATTTGAAAAAGGAACCTA	2528	
Db	1389	CATGTCACAAATTTTGGACCAAGCAGCGGTTTGGACCGCCGACGACCTTAAGTCT	1448		2341	GTATTTGCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATTCGATAGCCTGCTG	2400	
QY	1261	TTGATTCATAAGCTCATAGCTAGGAATTTGCTCTCATGGACATTTGTTACAGAGCCAT	1320		2529	GTATTTGCTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATTCGATAGCCTGCTG	2588	
Db	1449	TTGATTCATAAGCTCATAGCTAGGAATTTGCTCTCATGGACATTTGTTACAGAGCCAT	1508		2401	AAGCTGAAATAACAAGTTGCCCTGGCACTCAGATGATCCACTTTTGGTGGCTTCGGG	2460	
QY	1321	GCATCAATAATATCTTTAGATGGACTGAACATGTTTGACTGCACCGGATGTTGTTACTTT	1380		2589	AAGCTGAAATAACAAGTTGCCCTGGCACTCAGATGATCCACTTTTGGTGGCTTCGGG	2648	
Db	1509	GCATCAATAATATCTTTAGATGGACTGAACATGTTTGACTGCACCGGATGTTGTTACTTT	1568		2461	AGAATTGATCAATAATGCGCAATATTTTCACCTTTGAAGGATGATGATGATGCTGCTCT	2520	
QY	1381	CACCTGAGCTCGTGGTTATCAATTTGGAATGGGATTCGCCGCTCTTTAACTATGGAAC	1440					

QY 1201 CATGTCACAAATTTTTCACCAAGCAGCCGTTTGGGAACGCCGACGACCTTAAAGTCT 1260
DB 1428 CATGTCACAAATTTTTCACCAAGCAGCCGTTTGGGAACGCCGACGACCTTAAAGTCT 1487
QY 1261 TTGATGATAAAGCTCATGAGCTAGGAATTTGTTCTCTCATGAGACATGTTTCACAGCCAT 1320
DB 1488 TTGATGATAAAGCTCATGAGCTAGGAATTTGTTCTCTCATGAGACATGTTTCACAGCCAT 1547
QY 1321 GCATCAAAATTAATCTTTAGATGAGCTGAACATGTTTGACGTGCACCGATAGTTGTTACTTT 1380
DB 1548 GCATCAAAATTAATCTTTAGATGAGCTGAACATGTTTGACGTGCACCGATAGTTGTTACTTT 1607
QY 1381 CACTCTGGAGCTCGTGGTTATCAATGGAATGCGGATTCGCCCTCTTTAACTACTATGGAAC 1440
DB 1608 CACTCTGGAGCTCGTGGTTATCAATGGAATGCGGATTCGCCCTCTTTAACTACTATGGAAC 1667
QY 1441 TGGAGGTACTTAGGTATCTCTCTCAAAATGCGAGATGGTGGTGGATGCTTCAAAATTT 1500
DB 1668 TGGAGGTACTTAGGTATCTCTCTCAAAATGCGAGATGGTGGTGGATGCTTCAAAATTT 1727
QY 1501 GATGGATTTAGATTTGATGCTGCACATCAATGATGATATTCACACGCGATATCGGTG 1560
DB 1728 GRTGGATTTAGATTTGATGCTGCACATCAATGATGATATTCACACGCGATATCGGTG 1787
QY 1561 GGATTCACCTGGGAACTACGAGAAATCTTTGGACTCGCAACTGATGCTGCTGTTG 1620
DB 1788 GGATTCACCTGGGAACTACGAGAAATCTTTGGACTCGCAACTGATGCTGCTGCTG 1847
QY 1621 TATCTGATGCTGGTCAACGATCTTATTCATGCGGCTTTTCCAGATGCAATACCATTGGT 1680
DB 1848 TATCTGATGCTGGTCAACGATCTTATTCATGCGGCTTTTCCAGATGCAATACCATTGGT 1907
QY 1681 GAGATCTTAGCGAATGCGGACATTTGTTATCCCGTCCCAAGAGGGGGTGGTGGCTTT 1740
DB 1908 GAGATCTTAGCGAATGCGGACATTTGTTATCCCGTCCCAAGATGGGGTGGTGGCTTT 1967
QY 1741 GACTATCGGCTGCATATGCAATGCTGATAAAGGATTTGAGTTGCTCAAGAAACGGGAT 1800
DB 1968 GACTATCGGCTGCATATGCAATGCTGATAAAGGATTTGAGTTGCTCAAGAAACGGGAT 2027
QY 1801 GAGATTTGAGAGTGGGTGATATTTGTTCACTACATGACATGACAAATAGATGTCGGAAG 1860
DB 2028 GAGATTTGAGAGTGGGTGATATTTGTTCACTACATGACATGACAAATAGATGTCGGAAG 2087
QY 1861 TGTCTTTACACGCTGAAAGTCATGATCAAGCTCTAGTCGGGTGATAAACTATAGCATTC 1920
DB 2088 TGTCTTTACACGCTGAAAGTCATGATCAAGCTCTAGTCGGGTGATAAACTATAGCATTC 2147
QY 1921 TGGCTGATGGACAGGATATGATGATTTTATGCTCTGGATAGACCGTCAACATCAPTA 1980
DB 2148 TGGCTGATGGACAGGATATGATGATTTTATGCTCTGGATAGACCGTCAACATCAPTA 2207
QY 1981 ATAGATCGTGGATAGCATTCACCAAGATGATTAGGCTTGAACATGCGGATAGGAGGA 2040
DB 2208 ATAGATCGTGGATAGCATTCACCAAGATGATTAGGCTTGAACATGCGGATAGGAGGA 2267
QY 2041 GAAGGTACCTAAATTTTCATGGGAAATGAATTCGCCACCTGAGTGGATGATTCCCT 2100
DB 2268 GAAGGTACCTAAATTTTCATGGGAAATGAATTCGCCACCTGAGTGGATGATTCCCT 2327
QY 2101 AGGCTGAACACACCTCTCTGATGGCTCAGTATATCCCGGAAACCAATTCAGTTATGAT 2160
DB 2328 AGGCTGAACACACCTCTCTGATGGCTCAGTATATCCCGGAAACCAATTCAGTTATGAT 2387
QY 2161 AAATGTCAGACGAGATTTGACTGGGATGACGAAATATTAAGATACCGTGGGTGCA 2220
DB 2388 AAATGTCAGACGAGATTTGACTGGGATGACGAAATATTAAGATACCGTGGGTGCA 2447
QY 2221 GAATTTGACCGGCTATGCACTATCTTCAAGATAAAATGAGTTTATGACTTCAGAACAC 2280
DB 2448 GAATTTGACCGGCTATGCACTATCTTCAAGATAAAATGAGTTTATGACTTCAGAACAC 2507

QY 2281 CAGTTTCATATCAGAAAGGATGAAGGAGATAGGATGATGTTATTTGAAAAAGGAACCTA 2340
DB 2508 CAGTTTCATATCAGAAAGGATGAAGGAGATAGGATGATGTTATTTGAAAAAGGAACCTA 2567
QY 2341 GTTTTGTCTTTAATTTTCACTGGACAAAAGCTATTTCAGACTATCCGATAGGCTGCTG 2400
DB 2568 GTTTTGTCTTTAATTTTCACTGGACAAAAGCTATTTCAGACTATCCGATAGGCTGCTG 2627
QY 2401 AAGCTGGAAAATCAAGGTTGCCCTTGCACTCAGATGATCCACTTTTGTGGTGGCTTCGG 2460
DB 2628 AAGCTGGAAAATCAAGGTTGCCCTTGCACTCAGATGATCCACTTTTGTGGTGGCTTCGG 2687
QY 2461 AGAATTGATCATATGCCGAATATTTTCCCTTTGAAGATGGTATGATGATCGTCTCGT 2520
DB 2688 AGAATTGATCATATGCCGAATATTTTCCCTTTGAAGATGGTATGATGATCGTCTCGT 2747
QY 2521 TCAATTATGGTGTATGACACCTTTGTAACACACAGCTGGTCTATGCACCTAGTAGACAAGAA 2580
DB 2748 TCAATTATGGTGTATGACACCTTTGTAACACACAGCTGGTCTATGCACCTAGTAGACAAGAA 2807
QY 2581 GAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAGTA 2631
DB 2808 GAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGAAGAAGAA 2858

RESULT 4
AA142634
ID AA142634 standard; DNA; 3003 BP.
XX
AC AA142634;
XX
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (10con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
OS Solanum tuberosum.
XX
PN W09634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
XX
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
XX New potato plant starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 38-39; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX
XX Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;
SQ

Query Match 96.4%; Score 2551; DB 17; Length 3003;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2589; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 1 ATGGGTATATACACTCTCTGGAGTTTCGTTTTCCTACTGTTCCATCATGATGACAAATCAAT 60

[illegible]

Db	1223	AAAAATTAACTCATACGCTGAATTTTATAGAGATGAAGTTCTTCTCCGATAAAAAAGCTTGG	1298
QY	1140	GTACAATGCGCTGCAAAATATAGCGTATTCAAGACGATTCCTTATTACGCTAGCTTTTGGTTA	1199
Db	1283	GTACAAATGGGTGCAAAATATAGGCTATTCAAGACGATTCCTTATTATGCTAGCTTTGGTTA	1342
QY	1200	TCATGTCACAAATTTTITGCACCAAGCAGCCGTTTGGACGCCGCGACACCTTAAGTC	1259
Db	1343	TCATGTCACAAATTTTITGCACCAAGCAGCCGTTTGGACGCCGCGACACCTTAAGTC	1402
QY	1260	TTTGATTGATTAAGCTCATAGCTAGGAATTTGTTTCTCAITGACATTTGTTTCACAGCCA	1319
Db	1403	TTTGATTGATTAAGCTCATAGCTAGGAATTTGTTTCTCAITGACATTTGTTTCACAGCCA	1462
QY	1320	TGCATCAAAATAACTTTTAGATGAGCTGAACATGTTTGACATGACACCATAGTTGTTACTT	1379
Db	1463	TGCATCAAAATAACTTTTAGATGAGCTGAACATGTTTGACATGACACCATAGTTGTTACTT	1522
QY	1380	TCACCTCTGGAGCTCGTGTTATCATTTGGATTTGGGATTCGGCTCTPTTAACTATGAAA	1439
Db	1523	TCACCTCTGGAGCTCGTGTTATCATTTGGATTTGGGATTTGGGCTCTPTTAACTATGAAA	1582
QY	1440	CTGGGAGTACTTAGGTAICTTCTCTCAATTCGAGATGGTGGTTGATCGGTCAAAAT	1499
Db	1583	CTGGGAGTACTTAGGTAICTTCTCTCAATTCGAGATGGTGGTTGATCGGTCAAAAT	1642
QY	1500	TGATGGATTTAGATTTGATGGTGATCAATGATCTATATATTCACACCGATATCGGT	1559
Db	1643	TGATGGATTTAGATTTGATGGTGATCAATGATCTATATATTCACACCGATATCGGT	1702
QY	1560	GGGATTCACCTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGATGCTGTGT	1619
Db	1703	GGGATTCACCTGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGATGCTGTGT	1762
QY	1620	GTATCTGATCTGCTCAACGATCTTATTCATGGGCTTTTCCAGAGATGCAATTAACATGG	1679
Db	1763	GTATCTGATCTGCTCAACGATCTTATTCATGGGCTTTTCCAGAGATGCAATTAACATGG	1822
QY	1680	TGAAGATGTTTAGCGGAATGCGGACATTTTCTATTCCGCTCAAGAGGGGGTCTGGCTTT	1739
Db	1823	TGAAGATGTTTAGCGGAATGCGGACATTTTCTATTCCGCTCAAGATGGGGGGTCTGGCTTT	1882
QY	1740	TGACTATCGGCTGCATATGGCAATTCGCTGATAACGGAATGAGTTGCTCAAGAAACGGGA	1799
Db	1883	TGACTATCGGCTGCATATGGCAATTCGCTGATAAATGATGATGCTCAAGNAACGGGA	1942
QY	1900	TGAGGATTTGAGAGTGGGTGATTTGTTCACTACACTGACAAATAGAGAATGGTCGGAAAA	1859
Db	1943	TGAGGATTTGAGAGTGGGTGATTTGTTCACTACACTGACAAATAGAGAATGGTCGGAAAA	2002
QY	1860	GTGTGTTTCATACGCTCAAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATT	1919
Db	2003	GTGTGTTTCATACGCTCAAAAGTCATGATCAAGCTCTAGTCGGTGATAAACHATATAGCATT	2062
QY	1920	CTGGCTCATGGCAAGATATGATGATTTATTTGCTCTGGATAGACCGTCAACATCATTT	1979
Db	2063	CTGGCTCATGGCAAGATATGATGATTTATTTGCTCTGGATAGACCGTCAACATCATTT	2122
QY	1980	AATAGATCGTGGGATAGCATTTGACACAGATGATTAGGCTTTGAACTATGGGATTAGGAGG	2039
Db	2123	AATAGATCGTGGGATAGCATTTGACACAGATGATTAGGCTTTGAACTATGGGATTAGGAGG	2182
QY	2040	AGAAGGTACTATAATTTTCATGGGAATCAATTCGGCCACCCCTGAGTGGATTGATTTCCC	2099
Db	2183	AGAAGGTACTATAATTTTCATGGGAATCAATTCGGCCACCCCTGAGTGGATTGATTTCCC	2242
QY	2100	TAGGGCTGAAACAACACCTCTCTGATGGCTCAGTAATTCGCCGGAACCAACTTCACTATGA	2159
Db	2243	TAGGGCTGAAACAACACCTCTCTGATGGCTCAGTAATTCGCCGGAACCAACTTCACTATGA	2302
QY	2160	TAAATCGACACGGAGATTTGACCTGGGAGATCGAGATATTTAAGATACCGTGGGTTGCA	2219
Db	2303	TAAATCGACACGGAGATTTGACCTGGGAGATCGAGATATTTAAGATACCGTGGGTTGCA	2362

1164 ANGAACCAAGTCGCTGAGAATATATGAATCTCATATGGAATGAGTAGTCGGAGCCT 1223
1081 AAAATTAACTCATACGCTGAATTTTAGAGATGAAGTCTCTCCATCAAAAAGCCTGGG 1140
1224 ARAATTAACTCATACGCTGAATTTTAGAGATGAAGTCTCTCCATCAAAAAGCCTGGG 1283
1141 TACAATCGCTGCAAAATTTAGGCTATTCAAGAGCATCTTAATACGCTAGTTTGGTTAT 1200
1284 TACAATCGCTGCGAATTTAGGCTATTCAAGAGCATCTTAATACGCTAGTTTGGTTAT 1343
1201 CATCTCAAAATTTTTCACCAAGCAGCGCTTTTGAACGCCCGCAGACCTTTAAGTCT 1260
1344 CATCTCAAAATTTTTCACCAAGCAGCGCTTTTGAACGCCCGCAGACCTTTAAGTCT 1403
1261 TTGATTGATAAAGCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTCAGAGCAT 1320
1404 TCGATTGATAAAGCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTCAGAGCAT 1463
1321 GCATCAAAATTAATCTTTAGTAGGACTGAACATGTTTGACTGCACCGATAGTTACTTT 1380
1464 GCATCAAAATTAATCTTTAGTAGGACTGAACATGTTTGACTGCACCGATAGTTACTTT 1523
1381 CACTCTGGAGCTGCTGTTATCATTGCATGTGGGATTCGCCCTCTTTTAATAGTGAAC 1440
1524 CACTCTGGAGCTGCTGTTATCATTGCATGTGGGATTCGCCCTCTTTTAATAGTGAAC 1582
1441 TGGAGGCTACTTAGGTATCTTCTCAAAATCGAGATGTTGGTGGATGCTCAAAATTT 1500
1583 TGGAGGCTACTTAGGTATCTTCTCAAAATCGAGATGTTGGTGGATGCTCAAAATTT 1642
1501 GATGGATTAGATTGATGTTGACATCAATGATGATATATTCACCACGGATATCGGTG 1560
1643 GATGGATTAGATTGATGTTGACATCAATGATGATATATTCACCACGGATATCGGTG 1702
1561 GGATTCACCTGGGAACACGAGGATATCTTGGACTCGCACTGATGTGGATGCTGTGTG 1620
1703 GGATTCACCTGGGAACACGAGGATATCTTGGACTCGCACTGATGTGGATGCTGTGTG 1762
1621 TATCTGATGCTGTGCAACGATCTTATTCATGGCTTTTCCAGATGCAATTTACCATTGT 1680
1763 TATCTGATGCTGTGCAACGATCTTATTCATGGCTTTTCCAGATGCAATTTACCATTGT 1822
1681 GAAGATGTTAGCGGAATGCGACATTTGTATTCGCTCCAAAGAGGGGGTGTGGCTTT 1740
1823 GAAGATGTTAGCGGAATGCGACATTTGTATTCGCTCCAAAGAGGGGGTGTGGCTTT 1882
1741 GACTATCGCTGCATATGCAATTTGCTGATACAGGATTCAGTTGCTCAAGAAACGGAT 1800
1883 GACTATCGCTGCATATGCAATTTGCTGATACAGGATTCAGTTGCTCAAGAAACGGAT 1942
1801 GAGGATGCGAGAGTGGGTGATATTTGTTACACTGACAAATAGAGATGGTCCGAAAG 1860
1943 GAGGATGCGAGAGTGGGTGATATTTGTTACACTGACAAATAGAGATGGTCCGAAAG 2002
1861 TGTGTTTCATACGCTGAAGTCAATGATCAAGCTCTAGTCCGTCATATAAACTATAGCATTC 1920
2003 TGTGTTTCATACGCTGAAGTCAATGATCAAGCTCTAGTCCGTCATATAAACTATAGCATTC 2062
1921 TGGCTGATGGCAAGSATATGATGATTTATGCTCTGGATCGATAGACCGTCAACATCATTA 1980
2063 TGGCTGATGGCAAGSATATGATGATTTATGCTCTGGATCGATAGACCGTCAACATCATTA 2122
1981 ATAGATCGTGGATGAGTTCACCAAGATGATTAGGCTTGTAACTATGGGATTAGGAGCA 2040
2123 ATAGATCGTGGATGAGTTCACCAAGATGATTAGGCTTGTAACTATGGGATTAGGAGCA 2182
2041 GAAGGCTACCTAAATTTTTCATGGCAATGAATTCGCCACCTCGAGTGGATTGATTCCTCT 2100
2183 GAAGGCTACCTAAATTTTTCATGGCAATGAATTCGCCACCTCGAGTGGATTGATTCCTCT 2242
2101 AGGCTGACACACCTCTCTGATGGCTCAGTAATTCGCCGGAACCAATTCAGTTATGAT 2160

Db 2243 AGGCGTAGCCACACACCTTTCTGATGGCTCAGTAATTCGCGAAACCAATTCAGTTATGAT 2302
QY 2161 AAATTCAGACGAGATTTTACCTGGGAGATGCAGAAATATTTAAAGATACCGTGGGTTGCAA 2220
Db 2303 AAATTCAGACGAGATTTTACCTGGGAGATGCAGAAATATTTAAAGATACCGTGGGTTGCAA 2362
QY 2221 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATATGATGATTTTGAAGAGGAAACCTA 2280
Db 2363 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATATGATGATTTTGAAGAGGAAACCTA 2422
QY 2281 CAGTTTCATATCACCAAGAGATGAAGGAGATAGGATGATTTGATTTGAAAAGGAAACCTA 2340
Db 2423 CAGTTTCATATCACCAAGAGATGAAGGAGATAGGATGATTTGATTTGAAAAGGAAACCTA 2482
QY 2341 GTTTTGTCTTTAATTTTCTGACTGGACAAAAAGCTATTTCAGACTATTCGCATAGCCTGCTG 2400
Db 2483 GTTTTGTCTTTAATTTTCTGACTGGACAAAAAGCTATTTCAGACTATTCGCATAGCCTGCTG 2542
QY 2401 AAGCCTGGAATAACAGGTTGCCCTTGGACTCAGATGATCCACHTTTTGGTGGCTTCGGG 2460
Db 2543 AAGCCTGGAATAACAGGTTGCCCTTGGACTCAGATGATCCACHTTTTGGTGGCTTCGGG 2602
QY 2461 AGAATTGATCATAATGCCGAATATTTCAACCTTTTGAAGGATGATGATGATCGTCCCTGCT 2520
Db 2603 AGAATTGATCATAATGCCGAATATTTCAACCTTTTGAAGGATGATGATGATCGTCCCTGCT 2662
QY 2521 TCATTTATGTTGATGACCTTTGAAACAGCAGTGGTCTATGACACTAGTAGACAAAGAA 2580
Db 2563 TCATTTATGTTGATGACCTTTGAAACAGCAGTGGTCTATGACACTAGTAGACAAAGAA 2722
QY 2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGATGACAGC 2618
Db 2723 GAAGTAGCAGTAGTAGAAGAAGCAACCATTTGAAGAATGAAC 2760

RESULT 6
ABK50301
ID ABK50301 standard; cdna; 2563 bp.
AC ABK50301;
XX
DT 15-JUL-2002 (first entry)
XX
DE Potato cDNA encoding starch branching enzyme, SBE II.
XX
KW Potato; starch branching enzyme; SBE II; glucan branching enzyme;
KW GBE; ss; gene; plant; transgenic; antisense; food industry;
XX
OS Solanum tuberosum.
XX
PH Key Location/Qualifiers
FT CDS 3..2552
FT /*tag= a
FT /product= "SBE II"
FT /partial
XX
PN GB2360521-A.
XX
PD 26-SEP-2001.
XX
PF 20-MAR-2000; 2000GB-0006733.
XX
PR 20-MAR-2000; 2000GB-0006733.
XX
PA (DANI-) DANISCO AS.
XX
PI Poulsen P, Sorensen IS;
XX
DR WPI; 2001-650142/75.
DR P-PSDB; AAU80169.
XX

PT New transformed plants with reduced endogenous starch branching enzyme
PT and heterologous glucan branching enzyme activities, useful for
PT producing starch with improved properties, which is in the food, paper
PT and chemical industries -
XX
XX Example 1: Page 31-35; 6lpp; English.

XX The invention relates to a transformed organism, preferably a transformed
CC plant, having a reduced endogenous starch branching enzyme (SBE)
CC activity, and having a heterologous glucan branching enzyme (SBE)
CC activity. The reduced SBE activity is effected via expression of a
CC nucleotide sequence that is antisense to at least part of a SBE exon.
CC Also included are a method of producing starch with altered
CC characteristics comprising (a) providing a plant having reduced
CC endogenous SBE activity, and having heterologous SBE activity
CC (b) propagating the plant of (a) and optionally (c) obtaining starch
CC from the plant; starch obtainable from the transformed plant; and
CC a nucleic acid construct system capable of directing the expression
CC of all or part of one or more antisense SBE exons and optionally one or
CC more heterologous SBE. The transformed plants are useful for producing
CC starch with modified and improved properties, which is an important raw
CC material and used in the food, paper and chemical industries. The
CC present sequence encodes Potato SBE II, used to make transgenic plants of
CC the invention.

XX Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

Query Match 94.0%; Score 2486.8; DB 23; Length 2563;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2512; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 65 TCAGCAGTATGTGATCGGAGGAGTCTAAATGTTCTGTATCTTGTAAGGACACCTCTC 124
DB 1 TCAGCAGTATGTGATCGGAGGAGTCTAAATGTTCTGTATCTTGTAAGGACACCTCTC 60
QY 125 TTTACGAGAGATCTTGGCTGAAAGTCTTCTTACAAATTCGAAATTCGACCTCTACAG 184
DB 61 TTTACGAGAGATCTTGGCTGAAAGTCTTCTTACAAATTCGAAATTCGACCTCTACAG 120
QY 185 TTGACGATCGGGGAAAGTCTTGTGCTGGACCCAGCTGATGATGCTCTCAPCCCTCAA 244
DB 121 TTGACGATCGGGGAAAGTCTTGTGCTGGACCCAGCTGATGATGCTCTCAPCCCTCAA 180
QY 245 CAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAATTCGCCAGCATCACTGATGATG 304
DB 181 CAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAATTCGCCAGCATCACTGATGATG 240
QY 305 ATAGTTCAACAATGGAAACGCTAGCCAGATTAACCTGAGAGATGACGTTGAGCCGT 364
DB 241 ATAGTTCAACAATGGAAACGCTAGCCAGATTAACCTGAGAGATGACGTTGAGCCGT 300
QY 365 CAAGTGATCTTACAGGAAGTGTGAAGAGCTGGAATTTGGTTTCATCACTACAACTACAAG 424
DB 301 CAAGTGATCTTACAGGAAGTGTGAAGAGCTGGAATTTGGTTTCATCACTACAACTACAAG 360
QY 425 AAGTGTAACCTGGAGGAGTCTAAACATTAATATCTCTGAGAGACAAATTAATGATG 484
DB 361 AAGTGTAACCTGGAGGAGTCTAAACATTAATATCTCTGAGAGACAAATTAATGATG 420
QY 485 AATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGACTTGGTCAGAGATTTATG 544
DB 421 AATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGACTTGGTCAGAGATTTATG 480
QY 545 AAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATTAACAGGTATTACAGATACA 604
DB 481 AAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATTAACAGGTATTACAGATACA 540
QY 605 AGAACTGAGGAGGAGGAAATGACAAGATGAGGGTGTGGAGCCCTTTCTCGTGGTT 664
DB 541 AGAACTGAGGAGGAGGAAATGACAAGATGAGGGTGTGGAGCCCTTTCTCGTGGTT 600
QY 665 ATGAAAAATGGGTTTCACTCTAGTGTACAGTATCACATTCCTGAGTGGGCTCTTG 724

DB 601 ATGAAAAATGGGTTTCACTCGTAGTGCTACAGGATACATTCACCGTAGTGCGCTCCTG 560
QY 725 GTCCCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAAATTTGGGAGCGCAAAATGCTACATTA 784
DB 661 GTCCCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAAATTTGGGAGCGCAAAATGCTACATTA 720
QY 785 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATTAATGTCGATGGTTCTC 844
DB 721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATTAATGTCGATGGTTCTC 780
QY 845 CTGCAATTCCTCATGGTCCAGAGTGAAGATAGTATGAGACATCTCCATCAGGTGTTAAGG 904
DB 781 CTGCAATTCCTCATGGTCCAGAGTGAAGATAGTATGAGACATCTCCATCAGGTGTTAAGG 840
QY 905 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTCTGATGAATTTCCCAATTAATG 964
DB 841 ATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTCTGATGAATTTCCCAATTAATG 900
QY 965 GAATACATATGATPCCACCGAGAGAGAGGTATATCTTCCACACCCACGCGCAAGA 1024
DB 901 GGATATATTTATGATPCCACCGAGAGAGAGGTATATCTTCCACACCCACGCGCAAGA 960
QY 1025 AACCAAGTCGTCGAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGCTAAAA 1084
DB 961 AACCAAGTCGTCGAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGCTAAAA 1020
QY 1085 TTAACATCATACGCTGAATTTTAGAGATGAAGTCTTCTCCGATAAAAAGCTTGGGTACA 1144
DB 1021 TTAACATCATACGCTGAATTTTAGAGATGAAGTCTTCTCCGATAAAAAGCTTGGGTACG 1080
QY 1145 ATGGCTGCGAAATATGCGTATTCAGAGACATCTTATTACCGTAGTCTTGGTTATCATG 1204
DB 1081 ATGGCTGCGAAATATGCGTATTCAGAGACATCTTATTATGCTAGTCTTGGTTATCATG 1140
QY 1205 TCACAAATTTTTCACCAAGCAGCCGTTTGGAGCCCGCAGACGCTTAAGTCTTTGA 1264
DB 1141 TCACAAATTTTTCACCAAGCAGCCGTTTGGAGCTCCGACGACCTTAAGTCTTTGA 1200
QY 1265 TTGATAAGCTCATGAGCTAGGAATTTGTTCTTCATCGGACATTTGTCACAGCATGAT 1324
DB 1201 TTGATAAGCTCATGAGCTAGGAATTTGTTCTTCATCGGACATTTGTCACAGCATGAT 1260
QY 1325 CAATAATACCTTAGATGGAGTGAACATTTTGTGCTGCAACGATGTTGTTACTTTCAT 1384
DB 1261 CAATAATACCTTAGATGGAGTGAACATTTTGTGCTGCAACGATGTTGTTACTTTCAT 1320
QY 1385 CTGAGCTCGTGGTTATCATTTGGATTTGGGATTCGCGCTCTTTAACTATGAGAACTGG 1444
DB 1321 CTGAGCTCGTGGTTATCATTTGGATTTGGGATTCGCGCTCTTTAACTATGAGAACTGG 1380
QY 1445 AGGTACTTAGTATCTTCTCCTCAATGCGGATGTTGGTGGATGCGTTCAAAATTTGATG 1504
DB 1381 AGGTACTTAGTATCTTCTCCTCAATGCGGATGTTGGTGGATGCGTTCAAAATTTGATG 1440
QY 1505 GATTTAGATTTGATGGTGTGACATCAATGATGTATTTCAACGAGATTTATCGGTGGAT 1564
DB 1441 GATTTAGATTTGATGGTGTGACATCAATGATGTATTTCAACGAGATTTATCGGTGGAT 1500
QY 1565 TCACCTGGAACTACGAGGAATTTTGGACTTCGCAACTGATGTGGATGCTGTGTGTATC 1624
DB 1501 TCACCTGGAACTACGAGGAATTTTGGACTTCGCAACTGATGTGGATGCTGTGTGTATC 1560
QY 1625 TGATGCTGCTCAAGATCTTATTCATGGCTTTTCCAGATGCAATTAACATTTGTTGAAG 1684
DB 1561 TGATGCTGCTCAAGATCTTATTCATGGCTTTTCCAGATGCAATTAACATTTGTTGAAG 1620
QY 1685 ATGTTAGCGGAATCGGACATTTTGTATTCGCGTCCAAAGAGGGGGTGTGCTGGCTTGA 1744
DB 1621 ATGTTAGCGGAATCGGACATTTTGTATTCGCGTCCAAAGATGCGGGTGTGCTGGCTTGA 1680
QY 1745 ATCGGCTGCATATGCAATTTGCTGTAATAACGAGTTGAGTTGCTCAAGAAACGGGATGAG 1804
DB 1681 ATCGGCTGCATATGCAATTTGCTGTAATAATGATTTGAGTTGCTCAAGAAACGGGATGAG 1740

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.
XX W09634968-A2.
XX 07-NOV-1996. 96WO-GB01075.
XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
XX 05-MAY-1995; 95GB-0009229.
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX Example 1; Page 51-53; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
Query Match 93.3%; Score 2468.4; DB 17; Length 2529;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2481; Conservative 10; Mismatches 36; Indels 0; Gaps 0;
QY 87 GAATGCTAATGTTCTGTATCTTGTGAAAGACACTCTCTTACGGAAGATCTTGGCTGA 146
DB 1 GGATGCTAATGTTCTGTATCTTGTGAAAGACACTCTCTTACGGAAGATCTTGGCTGA 60
QY 147 AAAGTCTTCTTACAATTCGGAATTCGGACCTTCTACAGTTGCGAGCATCGGGGAAGTCCT 206
DB 61 AAAGTCTTCTTACAATTCGGAATTCGGACCTTCTACAGTTGCGAGCATCGGGGAAGTCCT 120
QY 207 TGTGCTGGAACCCAGAGTGATAGCTCCTCATCTCTCAACAGACCAATTTGAGTTCACTGA 266
DB 121 TGTGCTGGAATCCAGAGTGATAGCTCCTCATCTCTCAACAGACCAATTTGAGTTCACTGA 180
QY 267 GACATCTCCAGAAAATTCCTCCAGCATCAACTGATGATAGATAGTTCAACAAATGGAACACGC 326
DB 181 GACATCTCCAGAAAATTCCTCCAGCATCAACTGATGATAGATAGTTCAACAAATGGAACACGC 240
QY 327 TAGCCAGATTAACACTGAGAAGATGACGTTGAGCGGTCAAGTGATCTTACAGGAAGTGT 386
DB 241 TAGCCAGATTAACACTGAGAAGATGACGTTGAGCGGTCAAGTGATCTTACAGGAAGTGT 300
QY 387 TGAAGAGCTGGATTTTGTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 446
DB 301 TGAAGAGCTGGATTTTGTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 360
QY 447 TAAACATTAATACTCTTGAAGACAAATTTATGATGAATCTGATAGGATCAGAGAGAG 506
DB 361 TAAACATTAATACTCTTGAAGACAAATTTATGATGAATCTGATAGGATCAGAGAGAG 420
QY 507 GGGCATCCCTCACTGGACTTGGTTCAGAAATTTATGAAATAGACCCCTTTTGACAAA 566
DB 421 GGGCATCCCTCACTGGACTTGGTTCAGAAATTTATGAAATAGACCCCTTTTGACAAA 480
QY 567 CTATCGTCAACACCTTGATTACAGGTATTCAGATACAGAAACTGAGGAGGCAATTGA 626
DB 481 CTATCGTCAACACCTTGATTACAGGTATTCAGATACAGAAACTGAGGAGGCAATTGA 540

QY 627 CAAGTATCAGGGTGGTTTGAAGCCCTTTTCGTTGGTTATGAAAAAATGGTTTCACTCG 686
DB 541 CAAGTATCAGGGTGGTTTTCAGAGCTTTTTCGTTGGTTATGAAAAAATGGTTTCACTCG 600
QY 687 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTTGGTCCAGTCCAGTCCGCTCAT 746
DB 601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTTGGTCCAGTCCAGTCCGCTCAT 660
QY 747 TGGAGATTTCAACAATTTGGGACGCAATTCGACATTAATGACTCGGAATGAATTTGGTGT 806
DB 661 TGGAGATTTCAACAATTTGGGACGCAATTCGACATTAATGACTCGGAATGAATTTGGTGT 720
QY 807 CTGGGAGATTTTCTGCCAAATAATGTGGATGGTCTCTCCCAATTCCTCATGGTCCAG 866
DB 721 CTGGGAGATTTTCTGCCAAATAATGTGGATGGTCTCTCCCAATTCCTCATGGTCCAG 780
QY 867 AGTGAAGATAGGTATGGACACTCCATCAGGTGTTAAGGATTCATTCCTGTTGGATCAA 926
DB 781 AGTGAAGATAGGTATGGACACTCCATCAGGTGTTAAGGATTCATTCCTGTTGGATCAA 840
QY 927 CTACTCTTTTACAGCTTCTCTGATGAAATTCCTATAATGGAATACATTAATGATCCACCGA 986
DB 841 CTACTCTTTTACAGCTTCTCTGATGAAATTCCTATAATGGAATACATTAATGATCCACCGA 900
QY 987 AGAGGAGAGGTATTAICTTCCAAACCCACGCCCAAGAAACCAAGTCGCTGAGAAATA 1046
DB 901 AGAGGAGAGGTATTAICTTCCAAACCCACGCCCAAGAAACCAAGTCGCTGAGAAATA 960
QY 1047 TGAATCTCATATTTGGAATGAGTACGCGGACCTTAAATTAACHTCATACGTGAATTTAG 1106
DB 961 TGAATCTCATATTTGGAATGAGTACGCGGACCTTAAATTAACHTCATACGTGAATTTAG 1020
QY 1107 AGATGAAGTCTTCTCTCGCATATAAAAGCTTGGTACAAATCGCTGCAAAATTAATGGCTAT 1166
DB 1021 AGATGAAGTCTTCTCTCGCATATAAAAGCTTGGTACAAATCGCTGCAAAATTAATGGCTAT 1080
QY 1167 TCAAGAGCATCTTAATACGCTAGTTTGGTATCATGTCACAAATTTTTCGACCAAG 1226
DB 1081 TCAAGAGCATCTTAATATGCTAGTTTGGTATCATGTCACAAATTTTTCGACCAAG 1140
QY 1227 CAGCGGTTTGGAGCGCCGACGACCTTAAGTCTTTGATTTGATTAAGCTCATGAGCTAGG 1286
DB 1141 CAGCGGTTTGGAGCGCCGACGACCTTAAGTCTTTGATTTGATTAAGCTCATGAGCTAGG 1200
QY 1287 AATTGTTGTCICATGGACATTTGTTACAGCCATGCAATCAAAATTAATTAATGATGACT 1346
DB 1201 AATTGTTGTCICATGGACATTTGTTACAGCCATGCAATCAAAATTAATTAATGATGACT 1260
QY 1347 GAACATGTTTGAATGACATGACCGATAGTTGTTACTTTCATCTGGAGCTCGTGGTTAATG 1406
DB 1261 GAACATGTTTGAATGACATGACCGATAGTTGTTACTTTCATCTGGAGCTCGTGGTTAATG 1320
QY 1407 GATGTTGGATTTCCCGCTCTTTAACTATGAAACTGGAGGACTTAGGTATCTCTCTC 1466
DB 1321 GATGTTGGATTTCCCGCTCTTTAACTATGAAACTGGAGGACTTAGGTATCTCTCTC 1380
QY 1467 AAAICGAGATGGTGGTGGATCGCTCAAAATTTGATGATTTAGATTTGATGGTGTGAC 1526
DB 1381 AAAICGAGATGGTGGTGGATCGCTCAAAATTTGATGATTTAGATTTGATGGTGTGAC 1440
QY 1527 ATCAATGATGATATTTACACACCGATTAATCGGTGGGATTCACGGAACCTACAGGAATA 1586
DB 1441 ATCAATGATGATATTTACACACCGATTAATCGGTGGGATTCACGGAACCTACAGGAATA 1500
QY 1587 CTTTGGACTCGCAACTGATGTGATGCTGTGTGATCTCATGCTGCTCAACCATCTTAT 1646
DB 1501 CTTTGGACTCGCAACTGATGTGATGCTGTGTGATCTCATGCTGCTCAACCATCTTAT 1560
QY 1647 TCATGGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATTTAGCGGAATGCGGACAT 1706
DB 1561 TCATGGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATTTAGCGGAATGCGGACAT 1620

QY 1707 TTGATATCCGCTCCAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTGC 1766
DB 1621 TTGATATCCGCTCCAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTGC 1680
QY 1767 TGATAACGGAATGAGTTGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATGT 1826
DB 1681 TGATAAATGAGTTGAGTTGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATGT 1740
QY 1827 TCATACACTGACAAATAGAGATGGTCGGAAAGTGTGTTTCATAGCTCAAACTCATGA 1886
DB 1741 TCATACACTGACAAATAGAGATGGTCGGAAAGTGTGTTTCATAGCTCAAACTCATGA 1800
QY 1887 TCAAGCTCTAGTCGGGTGATAAACTATAGCATTTCTGGCTGATGACAAAGATATGATGA 1946
DB 1801 TCAAGCTCTAGTCGGGTGATAAACTATAGCATTTCTGGCTGATGACAAAGATATGATGA 1860
QY 1947 TTTTATGGCTCTGGATAGACCGTCACATCATTAATAGATCGTGGGATAGCATGTCACAA 2006
DB 1861 TTTTATGGCTCTGGATAGACCGTCACATCATTAATAGATCGTGGGATAGCATGTCACAA 1920
QY 2007 GATCATTAGGCTTGTAACTAGGATGAGTGGAGAGAGGTGACCTAAATTTTCATGGGAAA 2066
DB 1921 GATCATTAGGCTTGTAACTAGGATGAGTGGAGAGAGGTGACCTAAATTTTCATGGGAAA 1980
QY 2067 TGAATTCGGCCACCCCTGAGTGGATGATTTCCCTAGGGCTGAACAACACCTCTCTGATGG 2126
DB 1981 TGAATTCGGCCACCCCTGAGTGGATGATTTCCCTAGGGCTGACCAACACCTCTCTGATGG 2040
QY 2127 CTCAGTAATCCCGGAAACCAATTCAGTTATGATAAATGACAGGGAGATTTGACCTGGG 2186
DB 2041 CTCAGTAATCCCGGAAACCAATTCAGTTATGATAAATGACAGGGAGATTTGACCTGGG 2100
QY 2187 AGATGACAGATATTAAGATACCGTGGTTCAGAGAAATTCACCGGCTATGACAGTATCT 2246
DB 2101 AGATGACAGATATTAAGATACCGTGGTTCAGAGAAATTCACCGGCTATGACAGTATCT 2160
QY 2247 TGAAGATAATATGAGTTTATGACTTCAGAACACCGATTCATATCAGAAAGGATGAAG 2306
DB 2161 TGAAGATAATATGAGTTTATGACTTCAGAACACCGATTCATATCAGAAAGGATGAAG 2220
QY 2307 AGATGATGATGTTTATGAGAAAGAAACCTAGTTTGTCTTTTAAATTTTCACTGGAC 2366
DB 2221 AGATGATGATGTTTATGAGAAAGAAACCTAGTTTGTCTTTTAAATTTTCACTGGAC 2280
QY 2367 AAAAGCTATTCAGACTATCGCATAGCTGCTGAAGCCTGGAATAATACAGGTTGCGTT 2426
DB 2281 AAATAGCTATTCAGACTATCGCATAGCTGCTGAAGCCTGGAATAATACAGGTTGCGTT 2340
QY 2427 GGACTCAGATGATCCACTTTTGGTGGCTGCGGAGAAATTCATATGATGCGCAATATTT 2486
DB 2341 GGACTCAGATGATCCACTTTTGGTGGCTGCGGAGAAATTCATATGATGCGCAATATTT 2400
QY 2487 CACCTTTGAAGGATGGTATGATGATGCTGCTGCTCAATATGATGCTGATGACCTGTAA 2546
DB 2401 CACCTTTGAAGGATGGTATGATGATGCTGCTGCTCAATATGATGCTGATGACCTGTAA 2460
QY 2547 AACAGCAGTGTCTATGACCTAGTAGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2606
DB 2461 AACAGCAGTGTCTATGACCTAGTAGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2520
QY 2607 AGAAGTA 2613
DB 2521 NGAAGAA 2527

RESULT 9

AA42631

ID AA42631 standard; DNA: 2578 BP.

XX

AC AA42631;

XX

DT 25-FEB-1997 (first entry)

XX

DE XX Class A starch branching enzyme (psbe2con.seq - clone psU90).
KW Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
KW anylose; viscosity; potato; ss.
OS Solanum tuberosum.
FH Key Location/Qualifiers
FT CDS 24..2567
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
PN WO9634968-A2.
XX 07-NOV-1996.
XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
DR P-PSDB; AAW06400.
XX New potato plant starch having high amylose content - also class A
starch branching enzyme and corresp. DNA to alter the viscosity of
starch; for use in food, biodegradable products, adhesives, etc.
XX Claim 32; Page 55-56; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
potatoes. In class A SBE mols., a flexible N-terminal domain,
is found, which is not found in class B mols.
XX Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;

Query Match 93.2%; Score 2465.8; DB 17; Length 2578;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2482; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 135 GATCTTGGCTGAAAAGTCTTCTTACAAATTCGAATTCGAGCTTCTACAGTTGCAGCATC 194
DB 56 GATCTTGGCTGAAAAGTCTTCTTACAAATTCGAATTCGAGCTTCTACAGTTGCAGCATC 115
QY 195 GGGGAAAGTCTTGTGCTGGAAACCCAGAGTGATAGCTCCTCATCTCAACAGACCAATT 254
DB 116 GGGGAAAGTCTTGTGCTGGAAACCCAGAGTGATAGCTCCTCATCTCAACAGACCAATT 175
QY 255 TGAGTTCACTGAGACATCTCCAGAAAATTCGCCAGATCACTGATGATGATGATGATGAT 314
DB 176 TGAGTTCACTGAGACATCTCCAGAAAATTCGCCAGATCACTGATGATGATGATGATGAT 235
QY 315 AATGGAACACGCTACCCAGATTAACACTGAGAACCATGACGTTGAGCCGTCAAGTGATCT 374
DB 236 AATGGAACACGCTACCCAGATTAACACTGAGAACCATGACGTTGAGCCGTCAAGTGATCT 295
QY 375 TACAGGAAAGTGTGAGAGCTGGATTTTGGCTTTCATCACTTACAACTACAGAGGTGGTAA 434
DB 296 TACAGGAAAGTGTGAGAGCTGGATTTTGGCTTTCATCACTTACAACTACAGAGGTGGTAA 355
QY 435 ACTGGAGGAGTCTAAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 494
DB 356 ACTGGAGGAGTCTAAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 415
QY 495 GATCAGAGAGAGGGGCGCATCCCTCCAGCTTGGTCTCAGAGATTTATGAAATAGACCC 554

Db 416 GATCAGAGAGGGGATCCCTCCACCTGGACTGGTCAGAGATTTATGAATAGACCC 475
QY 555 CCTTTTGACAAACATATCGTCAACACCTTGATTACAGGTATTACAGTACAAAGAACTGAG 614
Db 476 CCTTTTGACAAACATATCGTCAACACCTTGATTACAGGTATTACAGTACAAAGAACTGAG 535
QY 615 GGAGGCAATTCACAAATGAGGTGGTTTGGAGCCCTTTCTCTGTTGTTATGAATAAT 674
Db 536 GGAGGCAATTCACAAATGAGGTGGTTTGGAGCCCTTTCTCTGTTGTTATGAATAAT 595
QY 675 GGGTTTCACTCGTATAGTGTACAGGTATACCTTACCGTGGTGGTCTTGGTCCAGTC 734
Db 596 GGGTTTCACTCGTATAGTGTACAGGTATACCTTACCGTGGTGGTCTTGGTCCAGTC 655
QY 735 AGCTGCCCTCATTCGAGATTCACAAATGGGAGCGCAAAATGCTGACATATGACTCGAA 794
Db 656 AGCTGCCCTCATTCGAGATTCACAAATGGGAGCGCAAAATGCTGACATATGACTCGAA 715
QY 795 TGAATTTGGTCTGGGAGATTTTCTGCCAAATAAATGTGGATGTTCTCTCGAATTC 854
Db 716 TGAATTTGGTCTGGGAGATTTTCTGCCAAATAAATGTGGATGTTCTCTCGAATTC 775
QY 855 TCATGGTCCAGAGTGAAGATACGTATGGACATCCATCAGGTGTTAAGGATTCATTC 914
Db 776 TCATGGTCCAGAGTGAAGATACGTATGGACATCCATCAGGTGTTAAGGATTCATTC 835
QY 915 TGCTTGGATCAACTACTCTTACAGCTTCTCGATGAATCCATTCATATGAATACATTA 974
Db 836 TGCTTGGATCAACTACTCTTACAGCTTCTCGATGAATCCATATGAATGAATATATTA 895
QY 975 TGATCCCGGAGAGGAGGTATATCTTCCACACCCAGCGCAAGAAACCAAGTC 1034
Db 896 TGATCCCGGAGAGGAGGTATATCTTCCACACCCAGCGCAAGAAACCAAGTC 955
QY 1035 GCTGAGATATATGAATCTCATATGGAATGAGTAGTCCGAGAGCTAAATTAACATTA 1094
Db 956 GCTGAGATATATGAATCTCATATGGAATGAGTAGTCCGAGAGCTAAATTAACATTA 1015
QY 1095 CGTGAATTTTAGAGTGAAGTCTTCTCGCATAAAGCTTGGTACATGTCACAAATTT 1154
Db 1016 CGTGAATTTTAGAGTGAAGTCTTCTCGCATAAAGCTTGGTACATGTCACAAATTT 1075
QY 1155 AATTATGGCTATTCAAGAGCATTTATTACGCTAGTTTGGTTATCATGTCACAAATTT 1214
Db 1076 AATTATGGCTATTCAAGAGCATTTATTATGCTAGTTTGGTTATCATGTCACAAATTT 1135
QY 1215 TTTTGACCAAGCAGCGTTTGGAGCCCGGAGCCTTAAAGTCTTTGATTGATAAAGC 1274
Db 1136 TTTTGACCAAGCAGCGTTTGGAGCCCGGAGCCTTAAAGTCTTTGATTGATAAAGC 1195
QY 1275 TCATGAGCTAGGAATTTGCTTCTCATGGACATTTTCAGAGCATGTCACAAATATAC 1334
Db 1196 TCATGAGCTAGGAATTTGCTTCTCATGGACATTTTCAGAGCATGTCACAAATATAC 1255
QY 1335 TTTAGATGGACTGAACATGTTGACATGACCGCATGTTTACTTTTACCTCTGGAGTCG 1394
Db 1256 TTTAGATGGACTGAACATGTTGACCGCACCGCATGTTTACTTTTACCTCTGGAGTCG 1315
QY 1395 TGCTTATCATGATGCGGATTTCCCGCTTTTAACTATGGAACCTGGAGGTACTTAG 1454
Db 1316 TGCTTATCATGATGCGGATTTCCCGCTTTTAACTATGGAACCTGGAGGTACTTAG 1375
QY 1455 GTATCTTCTCAATTCGAGATGGTGGTTGGATGGTTCCTCAAAATTCATGGATTAGATT 1514
Db 1376 GTATCTTCTCAATTCGAGATGGTGGTTGGATGGTTCCTCAAAATTCATGGATTAGATT 1435
QY 1515 TGAATGTCACATCAATCATGTATATTCACCGGATTTACCGTGGGATTCACCTGGAA 1574
Db 1436 TGAATGTCACATCAATCATGTATATTCACCGGATTTACCGTGGGATTCACCTGGAA 1495
QY 1575 CTACGAGGATACCTTTGGACTCGCACTGANTGGATGCTGTTGTATCTGATGCTGTT 1634

RESULT 10
AAT42636

Db 1496 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTGTATCTGATGCTGT 1555
QY 1635 CAACGATCTTATTCATGGGCTTTTCCAGATGCAATTCACATTTGGTGAAGATTTAGCGG 1694
Db 1556 CAACGATCTTATTCATGGGCTTTTCCAGATGCAATTCACATTTGGTGAAGATTTAGCGG 1615
QY 1695 AATGCCGACATTTGTATTCOCGTCCAAAGAGGGGGTGTGGCTTTGACTATCGGTGCA 1754
Db 1616 AATGCCGACATTTGTATTCOCGTTCACAGATGGGGTGTGGCTTTGACTATCGGTGCA 1675
QY 1755 TATGCCAATTCGTGATAAACGATTTAGTTGCTCAAGAACCGGATGAGGATTTGAGAT 1814
Db 1676 TATGCCAATTCGTGATAAACGATTTAGTTGCTCAAGAACCGGATGAGGATTTGAGAT 1735
QY 1815 GGGTGATATTTGTTCATACACTGACAAATAGAAAGATGGTCCGAAAAAGTGTGTTTCATCGC 1874
Db 1736 GGGTGATATTTGTTCATACACTGACAAATAGAAAGATGGTCCGAAAAAGTGTGTTTCATCGC 1795
QY 1875 TGAAGTCAATGATCAAGCTTAGTCGGTGATAAACTATAGCAATTTCTGGCTGAIGGACAA 1934
Db 1796 TGAAGTCAATGATCAAGCTTAGTCGGTGATAAACTATAGCAATTTCTGGCTGAIGGACAA 1855
QY 1935 GGATATGATGATTTTATGGCTCTGGATAGACCTCAACATCATTAAATAGATCTGGGAT 1994
Db 1856 GGATATGATGATTTTATGGCTCTGGATAGACCTCAACATCATTAAATAGATCTGGGAT 1915
QY 1995 AGCATGTCACAAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAGGTACTATAA 2054
Db 1916 AGCATGTCACAAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAGGTACTATAA 1975
QY 2055 TTTTCATGGGAATGAATTCGGCCACCTTGAGTGGAATTCCTTCCCTAGGGCTGAACAA 2114
Db 1976 TTTTCATGGGAATGAATTCGGCCACCTTGAGTGGAATTCCTTCCCTAGGGCTGAACAA 2035
QY 2115 CCTCTCTGATGGCTCAGTAATCCCGGAAACCAATTCAGTTATGATATATATGATGATGAT 2174
Db 2036 CCTCTCTGATGATGATTAATCCCGGAAACCAATTCAGTTATGATATATATGATGATGAT 2095
QY 2175 AATTGACCTGGGAGATGCAGAAATTTAAGATACCGTGGGTTGCAAGAAATTTGACCGGCC 2234
Db 2096 AATTGACCTGGGAGATGCAGAAATTTAAGATACCGTGGGTTGCAAGAAATTTGACCGGCC 2155
QY 2235 TATCGATGATCTTGAAGATAATATGAGTTTATGACTTCAGAACACCACTGATATATACG 2294
Db 2156 TATCGATGATCTTGAAGATAATATGAGTTTATGACTTCAGAACACCACTGATATATACG 2215
QY 2295 AAAGGATGAAGAGATAGGATGATTTTGAAGAAAGAAACCTAGTTTGTCTTAA 2354
Db 2216 AAAGGATGAAGAGATAGGATGATTTTGAAGAAAGAAACCTAGTTTGTCTTAA 2275
QY 2355 TTTTCATCGCAAAAAAGCTATTCAGACTATPCGATAGCCCTGCTGAAGCCTGGAAATA 2414
Db 2276 TTTTCATCGCAAAAAAGCTATTCAGACTATPCGATAGCCCTGCTGAAGCCTGGAAATA 2335
QY 2415 CAAGGTTGCCCTGGACATCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATATAA 2474
Db 2336 CAAGGTTGCCCTGGACATCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATATAA 2395
QY 2475 TGCCGAATATTTTCAACCTTTGAAGGATGATATGATGATGCTCTGCTCAATATGATGTA 2534
Db 2396 TGCCGAATATTTTCAACCTTTGAAGGATGATATGATGATGCTCTGCTCAATATGATGTA 2455
QY 2535 TGCCCTTTGAAACACAGCAGTGTCTATGCACTAGTAGACAAAGAAAGAAAGAA 2594
Db 2456 TGCCCTTTGAAACACAGCAGTGTCTATGCACTAGTAGACAAAGAAAGAAAGAA 2515
QY 2595 AGAAGAGAGAGAGAGAGTACACAGTACAGAGAGAGTATGATAGTATAGAGAA 2643
Db 2516 AGAAGAGAGAGAGTACAGTACAGAGAGAGTATGATAGTATAGAGAGAA 2564

AA142636 standard; DNA; 2576 BP.
AA142636;
03-MAR-1997 (first entry)
Class A starch branching enzyme (85con.seq) cloned in QE32.
Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
amylose; viscosity; potato; ss.
Solanum tuberosum.
w09634968-A2.
07-NOV-1996.
03-MAY-1996; 96WO-GB01075.
10-APR-1996; 96GB-0007409.
05-MAY-1995; 95GB-0009229.
(NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
Sidebottom CM, Westcott RJ;
WPI; 1996-506170/50.
New potato plant starch having high amylose content - also class A
starch branching enzyme and corresp. DNA to alter the viscosity of
starch; for use in food, biodegradable products, adhesives, etc.
Example 1; Page 49-51; 142pp; English.
Class A starch branching enzyme (SBE) has been obtained from
potatoes. In class A SBE mols., a flexible N-terminal domain,
is found, which is not found in class B mols.
Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;
Query Match 92.7%; Score 2451.8; DB 17; Length 2576;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2480; Conservative 0; Mismatches 27; Indels 2; Gaps 1;
QY 135 GATCTTGGCTGAAAAGTCTTTACAAATCCGAATCCGACTTCTACAGTTGCAGCATC 194
DB 56 GATCTTGGCTGAAAAGTCTTTACAAATCCGAATCCGACTTCTACAGTTGCAGCATC 115
QY 195 GGGGAAAGTCTTGTGCTGGAACCCAGAGTGATGCTCCATCCTCAACAGCAAT 254
DB 116 GGGGAAAGTCTTGTGCTGGAACCCAGAGTGATGCTCCATCCTCAACAGCAAT 175
QY 255 TGAGTTACATGACATCTCCAGAAATCCCGAGATCACTGATGATAGTATGATCAAC 314
DB 176 TGAGTTACATGACATCTCCAGAAATCCCGAGATCACTGATGATAGTATGATCAAC 235
QY 315 AATGGAACAGCTAGCCAGATTAACACTGAGAGGATGAGCTTGAGCGCTCAAGTGATCT 374
DB 236 AATGGAACAGCTAGCCAGATTAACACTGAGAGGATGAGCTTGAGCGCTCAAGTGATCT 295
QY 375 TACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTCAACAGAGGTTGGTAA 434
DB 296 TACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTCAACAGAGGTTGGTAA 355
QY 435 ACTGGAGAGCTTAAACATTAATACCTCTGAGAGACATTAATGATGATGATAG 494
DB 356 ACTGGAGAGCTTAAACATTAATACCTCTGAGAGACATTAATGATGATGATAG 415
QY 495 GATCAGAGAGAGGGGCTCCCTCCACCTGGACTTGGTGGAGAGATTTATGAATAGACCC 554
DB 416 GATCAGAGAGAGGGGCTCCCTCCACCTGGACTTGGTGGAGAGATTTATGAATAGACCC 475

QY 555 CCTTTGACAAACTATCGTCAACACCTTGATGATACAGGTATTTACAGTACAGAAACCTGAG 614
DB 476 CCTTTGACAAACTATCGTCAACACCTTGATGATGATGATGATGATGATGATGATGATGAT 535
QY 615 GGAGGCAATTGACAACTATGAGGCTGTTGGAGGCTTTCTGCTGGTTATGAAAAAT 674
DB 536 GGAGGCAATTGACAACTATGAGGCTGTTGGAGGCTTTCTGCTGGTTATGAAAAAT 595
QY 675 GGGTTTCACCTGCTAGTGTCTACAGGTATCACTTACCTGAGTGGGCTCTTGGTCCCACTC 734
DB 596 GGGTTTCACCTGCTAGTGTCTACAGGTATCACTTACCTGAGTGGGCTCTTGGTCCCACTC 655
QY 735 AGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCGAAATGCTGACATTTAGCTCGGAA 794
DB 656 AGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCGAAATGCTGACATTTAGCTCGGAA 715
QY 795 TGRATTTGGTGTCTGGAGATTTTCTGCCAAATAATGATGATGATGATGATGATGATGATGAT 854
DB 716 TGRATTTGGTGTCTGGAGATTTTCTGCCAAATAATGATGATGATGATGATGATGATGATGAT 775
QY 855 TCATGGGTCAGAGTGAAGATACGTATGGACACTCCATCAGGTCTTAAGGATTCATTC 914
DB 776 TCATGGGTCAGAGTGAAGATACGTATGGACACTCCATCAGGTCTTAAGGATTCATTC 835
QY 915 TGCTTGATCAACTACTCTTTTACAGCTTCTGATGAAATTCATATTAATGATGATGATGATGAT 974
DB 836 TGCTTGATCAACTACTCT--TACAGCTTCTGATGAAATTCATATTAATGATGATGATGAT 893
QY 975 TGATCCACCCGAGAGGAGGTATATCTTCCACACCCGAGCGCAAGAACCAAGTC 1034
DB 894 TGATCCACCCGAGAGGAGGTATATCTTCCACACCCGAGCGCAAGAACCAAGTC 953
QY 1035 GCTGAGAAATATGAATCTCATATTTGGAATGAGTAGTCCGAGGCTTAAATTAATCATATA 1094
DB 954 GCTGAGAAATATGAATCTCATATTTGGAATGAGTAGTCCGAGGCTTAAATTAATCATATA 1013
QY 1095 CGTGAATTTAGATGAAGTTCTTCTCCGATGAAATGAGTGGTACATGCGCTGCA 1154
DB 1014 CGTGAATTTAGATGAAGTTCTTCTCCGATGAAATGAGTGGTACATGCGCTGCA 1073
QY 1155 AATATGCTATTCAGAGCATTTCTTATAGCTAGTTTGGTTATCATGTACAAATTT 1214
DB 1074 AATATGCTATTCAGAGCATTTCTTATAGCTAGTTTGGTTATCATGTACAAATTT 1133
QY 1215 TTTTGCAACAGAGCCGCTTTTGAAGCCCGAGACCTTAAGTCTTTGATGATGATGATGATGAT 1274
DB 1134 TTTTGCAACAGAGCCGCTTTTGAAGCCCGAGACCTTAAGTCTTTGATGATGATGATGATGAT 1193
QY 1275 TCATGAGCTAGAAATTTGTTGTTCTCATGGACATTTCTCACAGCCATGATGATGATGATGATGAT 1334
DB 1194 TCATGAGCTAGAAATTTGTTGTTCTCATGGACATTTCTCACAGCCATGATGATGATGATGATGAT 1253
QY 1335 TTTAGATGAGTGAACATGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394
DB 1254 TTTAGATGAGTGAACATGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
QY 1395 TGGTTATCATTTGAGTGGGATTCCTGCTTTTAACTATGATGATGATGATGATGATGATGATGATGAT 1454
DB 1314 TGGTTATCATTTGAGTGGGATTCCTGCTTTTAACTATGATGATGATGATGATGATGATGATGATGAT 1373
QY 1455 GTAATCTCTCTCAATGCGAGATGTTGTTGTTGATGATGATGATGATGATGATGATGATGATGAT 1514
DB 1374 GTAATCTCTCTCAATGCGAGATGTTGTTGTTGATGATGATGATGATGATGATGATGATGATGAT 1433
QY 1515 TGATGGTGTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
DB 1434 TGATGGTGTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
QY 1575 CTACAGGAATACCTTTGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1634
DB 1494 CTACAGGAATACCTTTGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553
QY 1635 CAACGATCTTATTCATGGGCTTTTCCAGATGCAATTTACCATTTGTTGATGATGATGATGATGATGAT 1694

Db 440 GAGAGCTCTTGATGGAAGATGATAAGAAATGTTGAGGAGATCAAGTAAAAAAGAGTCG 499
QY 364 TCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTACAACTACAA 423
Db 500 ----- 499
QY 424 GAAGGTGGTAAACTGGAGGAGCTAAACATTAATAACTTCTGGAAGAGACAAATATTGAT 483
Db 500 -----GTCCCATTTGCATGAGACAAATTAGCAAT 526
QY 484 GAATCTGATAGATCAGAGAGGAGGCGCATCCCTCCACCTGGACTGGCTGGTCAGAGATTTAT 543
Db 527 GGAAGAAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCGAGAAATAT 586
QY 544 GAAATAGACCCCTTTTGCAGAACTATCGTCAACACCTTGATTACAGGTATTACACAGTAC 603
Db 587 GACATAGATCCAAAGCTTGGCAGGTTCCTCGTCAGCATCTTGACTACCGATATTACAGTAC 646
QY 604 AAGAAACTGAGGAGGCAATTTGACAAAGTATGAGGGTGGTTGGAAAGCCTTTTCTCGTGGT 663
Db 647 AAAAGGCTCGGTGAGGAAATTCACAAAGTATGAAGTGGTGGATGCATCTCTCTGTGA 706
QY 664 TATGAAGAAATGGTTTCACTCGTACTGCTACAGGTATCACTTACCGTGGTGGTCTT 723
Db 707 TTGAAAGATTTGGTTTACCGAGTGAACAGGAATTAACCTTATAGGGAATGGGCACCT 766
QY 724 GGTGCCAGTCACTGCCCTCATTTGGAGATTTTCAACAATTTGGACGCAAAATGCTGACATT 783
Db 767 GGAGCTACGTGGGCTGCNCTTATGGAGATTTCAACAATTTGGAATCCTATGAGATGTC 826
QY 784 ATGACTCGGAATGAAATTTGGTGTCTGGAGATTTTCTGCGCAATTAATGTTGGATGTTCT 843
Db 827 ATGACTCGGAATGAGTTTGGTGTCTGGAGATTTTTCGCAATTAACGAGATGGTCA 886
QY 844 CTTGCAATCTCTCATGCTGCACAGTGAAGATAGTATGACATCTGCACCTCATTCAGTGAAG 903
Db 887 CCACCAATTCCTCATGTTCTCGAGTAAGATAGCATGATGATCACTCCATCGCATCAAA 946
QY 904 GATTCCATTCCTGCTGGATCAACTACTCTTTTACAGCTTCCCTGATGAATTTCCATATAAT 963
Db 947 GATTCAATTCCTGCTGGATCAAGTTCTCAGTTTCAGGCACCTGGTGAATCCCATACAAT 1006
QY 964 GGAATACATTTATGATCCACCCGAGGAGGAGGTATATCTTCAACACCCACGCCCAAAG 1023
Db 1007 GCCATATACTATGATCCACCAAGAGGAGGAAGTATGTGTCAAAATCCTCAGGCCAAAG 1066
QY 1024 AAACCAAGTCGCTGAGATATATGAATCTCATTTGGAATGAGTACTCCGGAGCCTAAA 1083
Db 1067 AGACCAAAATCATTAGATTTATGAATCTCATGTTGGGATGAGTATGAGGCCAATA 1126
QY 1084 ATTAACATCACTACGTTGAATTTTAGAGATGAAGTCTTCTCCTCGCATAAAAAGCTGGGTAC 1143
Db 1127 ATTAACATATGCAACTTTAGAGATGATATGCTTCTCGCATCAAAAAGCTGGGTAC 1186
QY 1144 AATGCGTGAATTTAGCTATTCAGAGCATCTTTATACGCTAGCTTTGGTATATCAT 1203
Db 1187 AATGCTGTTGAGATCATGGTATTCAGAGCATTCCTTATGCTAGTTTGGGTACCAT 1246
QY 1204 GTCAAAATTTTTCACCAAGCAGCCGTTTGGAAAGCCGCGACGACCTTAAGTCTTTG 1263
Db 1247 GTCAAACTTTTTCACCTAGCAGCCGATTTGGAATCTCTGATGATTCAAGCTTTA 1306
QY 1264 ATTGATAAGCTATGAGCTAGGAATTTGTTCTCATGAGCATTTGTTACAGCCATGCA 1323
Db 1307 ATACATAAAGCTATGATGTTAGGCTGCTTGTCTCATGGATATTTGTTATGATGCGG 1366
QY 1324 TCAAAATATCTTTAGATGGACTGAACATGTTTACCTGACCGAGTATGTTACTTTTCA 1383
Db 1367 TCAAAATATAGTTTGGATGGGCTGAACATGTTTATGATGGTACGGATGACTACTTCCAC 1426
QY 1384 TCTGAGCTGTGTTTATCATTTGATGTTGGGATTCGCGCCCTTTTAACTATGGAACCT 1443
Db 1427 TCGGATCACGGGGTCATCAITTTGTTGGGACTCTCGCCCTTTTCAACTATGGAAGCTGG 1486

QY 1444 GAGGTACTTAGGTATCTTCTCTCAAAATCCAGATGGTGGTGGATGCGTTCAAATTTGAT 1503
Db 1487 GAGGTGCTAAGATTTCTTCTTCAAAATGCAAGATGGTGGTGGAGAGTACAGGTTTAT 1546
QY 1504 GGATTTAGATTTGATGGTGTGACATCAATGATGATTAATTCACACGAGTATTCGGTGGGA 1563
Db 1547 GGTTTATAGATTTGATGGGTGACTTCCATGATGTACATCCCTCCATGGTTCAGGTAGCT 1606
QY 1564 TTCACCTGGGAACACAGGAAATACTTTGGACTCGCACTGATGTGGAATGCTGTGTGAT 1623
Db 1607 TTTTACTGGCACTACAAATGAGTACTTTGGATATGCAACTGATGTAGATGCTGTGATTTAT 1666
QY 1624 CTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCAGATGCAATTCATTTGTTGAA 1683
Db 1667 TTGATGCTTGTGAATGATATGATTCACGGTCTTTTCCCTGAGGCTGTACCATTTGGTAA 1726
QY 1684 GATGTTAGCGGAATCGGACATTTTGTATTCCCTCCAAAGAGGGGGTGTGGCTTTGAC 1743
Db 1727 GATGTTAGCGGAAGAACCAACATTTTGCATTCAGTGGAGATGGTGTGTTGATTTGAT 1786
QY 1744 TATCGGCTGCATATGGCAATTTGCTGATPAAACGGATGAGTTGCTCAAGAACGGGATGAG 1803
Db 1787 TACGCTCCACATGGCCATTTGCCGATAAATGGATTCAGATTTCTTTAAGAGAGAGATGAG 1846
QY 1804 GATTTGAGAGTGGTGTATTTGTTACATACACTGACAATPACAGATGCTCGGAAAGCTGT 1863
Db 1847 GACTGGAAATGGTGTACATTTGTGCATACACTCCACCAAGAGGTTGGTGGAAAAATGT 1906
QY 1864 GTTTCATACCTGAAAGTCAATGATCAAGCTCTAGTCGGTGTATATAAACTATAGCATTTCTGG 1923
Db 1907 GTTGCTTATGCTGAAAGTCATGACCAAGCTCTTGTGGTGACAAACTATTTGCATTTTGG 1966
QY 1924 CTGATGACAAAGATATGATGATTTTATGCTCTGGATAGACCGTCAACATCATTAATA 1983
Db 1967 CTGATGACAAAGACATGTACGACTTCATGGCTCGTGACAGACCATCTACTCTCTTATA 2026
QY 1984 GATCTCGGATAGCATTTGCACAGATGATAGGCTTTGTAATATGATGGATAGGAGGAGAA 2043
Db 2027 GATGCTGGAATAGCATTTGCACAAATGATCAGGCTTATTCACCTGGGCTTAGCGGAGAA 2086
QY 2044 GGTACCTTAATTTTCATGGGAATGAATTCGCCACCTGAGTGGATGATTTCCCTAGG 2103
Db 2087 GGATTTTGAATTTTATGGGAATGAATTTGACATCTGATGATGATTTTCCAAAGA 2146
QY 2104 GCTGAACAAACACCTCTCTGATGGCTCAGTAATCCCGGAACCAATTCAGTTATGATAAA 2163
Db 2147 GGGATCGACATCTGCCCAATGTTAAAGTAAATTCAGGGAACACCACTATGATATAA 2206
QY 2164 TGCAGCGGAGATTTGACCTGGGAGATGCAGAAATTTTAAAGATACCGTGGGTTCGAAGA 2223
Db 2207 TGGCTGCTGATGATTTGATCTAGGTGATGACAGACTATCTAAGATATCATGGAATGCAAG 2266
QY 2224 TTTTACCGGCTATGCTAGTATCTTGAAGATAAAATGATGATTTATGATCTCAGAACACCG 2283
Db 2267 TTTGATCAGGCAATGCAACATCTTTGAAGAAGCCCTATGCTTTCATGACTCTGAGCACCG 2326
QY 2284 TTTATATCAGAAAGGATGAGAGATGAGTATGATTTGATTTGAAAGGAAACCTAGTT 2343
Db 2327 TATATATCAGGAGGATGAGAGATGCGGATGATGCTTTGAGAGGGGAAACCTGTT 2386
QY 2344 TTTCTCTTTTAAATTTTCACTGGACAAAAAGCTATTTCAGACTATCGCATAGCCTGCTGAAG 2403
Db 2387 TTTGATTTCAACTTTTTCATTTGACTTAACAGCTATTCAGATTTACCGAGTGGCTGCTCAAG 2446
QY 2404 CCTGGAATAATAAGGTTGCTTGGACTTCAGATGATCCACTTTTGGTGGGCTTCGGGAGA 2463
Db 2447 TCAGGAAAGTACAAGATTTTGGACCTCGGATGATGGCTTGTGTTGGAGGCTTCAACAGG 2506
QY 2464 ATTGATCATATGCGGAATATTTTACCTTTGAGGATGATGATGATGCTGCTGTTCA 2523
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 QY 1869 ATACGCTGAAGATCARTATCAAGCTCTAGTGGTGATAAACTATAGCAATTCCTGGCTGAT 1928
 Db 1787 TTATGCTGAAGATCAGACAGGCCCTTGTGGTGACAAAACATTTGCAATTTGGCTGAT 1846
 QY 1929 GGACAGGATATGATGATTTATGCTCTGGATAGACCGTCAACATCATATATAGATCG 1988
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 QY 1989 TGGGATAGCATTCACAAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAAGGTA 2048
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AAC45939

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XX AAC45939;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

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Score 48.8%; DB 21; Length 2715;

Pred. No. 0;

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QY	623	TTGACAAGTATGAGGTGGTTTGGAGCCCTTTTCTCGTGGTTAGAAAAATGGTTTGA	682
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QY	683	CTCGTAGTGTACAGGTATCACTTACCTGAGTGGGCTCTTGGTCCCGAGTCAGTGGCC	742
Db	623	CTCGAGCCCGACTGTGTATCACTTACCGGAGTGGGCGAGTACGAGGAGCATCAC	682
QY	743	TCATTGGAGATTCACAAATTTGGAGCGCAATGCTGACATTTATGACTCGGAATGATTTG	802
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QY	803	GTGTCGGGAGATTTTCTGCGCAAAATATGATGTGATGTTCTCTCTCAATTCCTCATGGGT	862


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:31:27 ; Search time 115.381 seconds
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1369.8	51.8	1393	US-09-087-277-3	Sequence 3, Appli
4	1369.8	51.8	1393	US-09-087-277-3	Sequence 3, Appli
5	1180.4	44.6	2665	US-09-257-894-1	Sequence 1, Appli
6	1180.4	44.6	2725	US-08-941-445A-14	Sequence 14, Appli
7	1033	39.0	2087	US-09-257-894-9	Sequence 9, Appli
8	1031.4	39.0	2165	US-09-257-894-8	Sequence 8, Appli
9	631.4	23.2	3128	US-08-716-449-1	Sequence 1, Appli
10	628.4	23.7	2487	US-09-257-894-19	Sequence 19, Appli
11	628.4	23.7	2565	US-09-257-894-24	Sequence 24, Appli
12	628.4	23.7	2763	US-08-941-445A-16	Sequence 16, Appli
13	628.4	23.7	2772	US-09-257-894-12	Sequence 12, Appli
14	617.2	23.3	2502	US-08-104-158-1	Sequence 1, Appli
15	542	20.5	1809	US-09-257-894-25	Sequence 25, Appli
16	542	20.5	1865	US-09-257-894-20	Sequence 20, Appli
17	368.8	13.9	11478	US-08-981-803-29	Sequence 29, Appli
18	368.8	13.9	11478	US-08-983-440-29	Sequence 29, Appli
19	358.6	13.6	5402	US-08-221-017B-194	Sequence 194, App
20	103.8	3.9	414	US-09-257-894-2	Sequence 2, Appli
21	71	2.7	2426	US-08-528-026C-3	Sequence 3, Appli
22	66.6	2.5	16442	US-08-781-891-208	Sequence 208, App
23	63.6	2.4	5394	US-08-688-376-1	Sequence 1, Appli
24	63.6	2.4	4403765	US-09-103-840A-2	Sequence 2, Appli
25	63.6	2.4	4411529	US-09-103-840A-1	Sequence 1, Appli
26	58.4	2.2	405	US-08-299-074A-1	Sequence 1, Appli
27	58.4	2.2	405	US-09-399-773-1	Sequence 1, Appli

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c 32	57	2.2	43795	3	US-08-742-185-101	Sequence 101, App
c 33	56.4	2.1	252	2	US-08-623-906A-1	Sequence 1, Appli
c 34	55.6	2.1	7218	1	US-08-232-463-14	Sequence 14, Appli
c 35	55.4	2.1	2223	1	US-08-257-073-4	Sequence 4, Appli
c 36	53	2.0	571	4	US-09-257-894-16	Sequence 16, Appli
c 37	53	2.0	1276	4	US-09-177-325-2	Sequence 2, Appli
c 38	53	2.0	1276	4	US-09-411-812A-2	Sequence 2, Appli
c 39	53	2.0	1276	4	US-09-590-113-2	Sequence 2, Appli
c 40	53	2.0	3211	4	US-08-574-959A-8	Sequence 8, Appli
c 41	53	2.0	3211	4	US-09-357-014-8	Sequence 8, Appli
c 42	53	2.0	3901	2	US-08-574-959A-6	Sequence 6, Appli
c 43	53	2.0	3901	4	US-09-357-014-6	Sequence 6, Appli
c 44	52	2.0	3337	1	US-08-072-610-1	Sequence 1, Appli
c 45	52	2.0	3337	2	US-08-719-822B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-087-277-1

Sequence 1, Application US/09087277B

Patent No. 6169226

GENERAL INFORMATION:

APPLICANT: EK, BO

APPLICANT: KHOSNODI, Jamshid

APPLICANT: LARSSON, Clas-Tomas

APPLICANT: LARSSON, Hakan

APPLICANT: RASK, Lars

TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,277B

EARLIER FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER FILING DATE: 1996-11-28

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9601506-0

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3074

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:bell gene

OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

OTHER INFORMATION: (potato)

NAME/KEY: CDS

LOCATION: (189)..(2825)

FEATURE:

NAME/KEY: sig_peptide

LOCATION: (189)..(332)

FEATURE:

NAME/KEY: mat_peptide

LOCATION: (333)..(2825)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (92)..(2156)

OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are

OTHER INFORMATION: n wherein n = A, C, G or T.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (285)..(287)

OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val

OTHER INFORMATION: or Phe.

FEATURE:

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; NAME/KEY: misc.feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc.feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Query Match          97.5%; Score 2581; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 249 GGATTGAGCAGTAAATGGTGTATCGGAGGAATGCTTAATGTTCTGTATTTCTTTGAAAAAGCAC 308
QY 121 TCTCTTTACGGAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGACCTTCT 180
DB 309 TCTCTTTACGGAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGACCTTCT 368
QY 181 ACAGTTGCGACATCGGGGAAGTCCCTGTGCTGGACCCAGAGTGTATGCTCCTCATCC 240
DB 369 ACAGTTGCGACATCGGGGAAGTCCCTGTGCTGGACCCAGAGTGTATGCTCCTCATCC 428
QY 241 TCAACAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAAATTCGCCAGCATCAACTGAT 300
DB 429 TCAACAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAAATTCGCCAGCATCAACTGAT 488
QY 301 GTAGATAGTTCAACAATGGAACGCTAGCCAGATTAACACTGAGACGATGAGTTGAG 360
DB 489 GTAGATAGTTCAACAATGGAACGCTAGCCAGATTAACACTGAGACGATGAGTTGAG 548
QY 361 CCGTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTGCTTCATCACTACAACCTA 420
DB 549 CCGTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTGCTTCATCACTACAACCTA 608
QY 421 CAAGAAGTGGTAAACTGGAGAGTCTTAAACATTAATATCTTCTGGAAGACAAATATT 480
DB 609 CAAGAAGTGGTAAACTGGAGAGTCTTAAACATTAATATCTTCTGGAAGACAAATATT 668
QY 481 GATGAATCTGATAGATCAGAGAGAGGGGATCCCTCCACTGGACCTTGGTTCAGAAATTT 540
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QY 601 TACAAGAACTGAGGGAGCAATGTACAAGTATGAGGGTGTGTTTGAAGCCCTTTTCTCGT 660
DB 789 TACAAGAACTGAGGGAGCAATGTACAAGTATGAGGGTGTGTTTGAAGCCCTTTTCTCGT 848
QY 661 GGTATGAAAAAATGGTTTCACCTCAGTGTACAGGTATCACTTACCGTGAGTGGGCT 720
DB 849 GGTATGAAAAAATGGTTTCACCTCAGTGTACAGGTATCACTTACCGTGAGTGGGCT 908
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DB 909 CTTGGTCCCGAGTCAGTGCCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGAC 968
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QY 841 TCTCCTGCAATTTCTCTATGGGTCCAGAGTGAAGATAGTATGGACACTCCATCAGGTGT 900
DB 1029 TCTCCTGCAATTTCTCTATGGGTCCAGAGTGAAGATAGTATGGACACTCCATCAGGTGT 1088
QY 901 AAGGATTCCTATCTCTGCTTGGATCAACTACTCTTTTACAGCTTCTCTGATGAAATTCATAT 960
DB 1089 AAGGATTCCTATCTCTGCTTGGATCAACTACTCTTTTACAGCTTCTCTGATGAAATTCATAT 1148
QY 961 AATGGAATACATATGATCCACCGAAGAGAGAGTATATFCTTCCAAACCCACGGCCA 1020
DB 1149 AATGGAATATATGATCCACCGAAGAGAGAGTATATFCTTCCAAACCCACGGCCA 1208
QY 1021 AAGAAACCAAGTCGCTGAGNATATATGAATCTCATATTTGAAATGAGTAGTCCGAGCCT 1080
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QY 1081 AAAATTAACCTACATACGTGAATTTTGGAGATGAAGTCTTCTCTCGCATATAAAAAGCTTGGG 1140
DB 1269 AAAATTAACCTACATACGTGAATTTTGGAGATGAAGTCTTCTCTCGCATATAAAAAGCTTGGG 1328
QY 1141 TACAATCGGTGCAAAATTTATGGCTATTTCAGAGCATTTCTTATTAACGTAGTTTGGTAT 1200
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DB 1389 CATGTCACAAATTTTTTGGACCAAGCAGCCGTTTGGACGCCGCGACGACCTTAAGTCT 1448
QY 1261 TTGATTGATAAAGTCTATGAGTAGAATTTTCTCTCATGAGCATTTGTTTACAGCCAT 1320
DB 1449 TTGATTGATAAAGTCTATGAGTAGAATTTTCTCTCATGAGCATTTGTTTACAGCCAT 1508
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QY 1381 CACTCTGGAGTCTGCTGGTTATCATTTGATGTTGGGATTCGCCCTCTTTAATATGGAAC 1440
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QY 1741 GACTATCGCTGCAATGATGGCAATGCTGATAAAGGATTTGATTTGCTCAAGAAACGGGAT 1800
DB 1929 GACTATCGCTGCAATGATGGCAATGCTGATAAAGGATTTGATTTGCTCAAGAAACGGGAT 1988
QY 1801 GAGGATTTGAGAGTGGGTGATTTGTTTCATCATGCAAAATAGAGTGTGCGGAAAAG 1860
DB 1989 GAGGATTTGAGAGTGGGTGATTTGTTTCATCATGCAAAATAGAGTGTGCGGAAAAG 2048
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QY 1921 TGGCTGATGGACAGGATATGATGATTTATGCTCTGGATAGACCGGTCAACATCATTA 1980
Db 2109 TGGCTGATGGACAGGATATGATGATTTATGCTCTGGATAGACCGGTCAACATCATTA 2168
QY 1981 ATAGATCTGGGATAGACATTCACAAAGATGATAGGCTTGTAACATGGATAGGAGA 2040
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QY 2101 AGGCTGAACACACCTCTCTGATGGCTCAGTAATCCCGGAACCAATTCAGTTATGAT 2160
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Db 2349 AAATGCAGACGGAGATTTGACCTGGGAGATGCAGAAATTTAAAGATACCGTGGTGCAG 2408
QY 2221 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATTAAGATTCAGATTCAGAACAC 2280
Db 2409 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATTAAGATTCAGATTCAGAACAC 2468
QY 2281 CAGTTTATATCACCAGGAGGATGAGGATAGGATGATGATTTGAAAAGGAAACCTA 2340
Db 2469 CAGTTTATATCACCAGGAGGATGAGGATAGGATGATGATTTGAAAAGGAAACCTA 2528
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Db 2529 GTTTTGTCTTTAATTTTCACTGGACAAAAGCTATTTCAGACTATCGCATAGCGCTG 2588
QY 2401 AAGCTGGAATAACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTCGG 2460
Db 2589 AAGCTGGAATAACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTCGG 2648
QY 2461 AGAATTCATCATATCGGATATTTTCACTTTGAAGATGATGATGATGATGATGATGAT 2520
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RESULT 2

US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakau
; APPLICANT: RASK, Lars
; FILE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29

; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

Query Match 97.5%; Score 2581; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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Db 189 ATGGTGATACACCTCTGAGTTCGTTTCTTCTACTGTTCATCAGTGACAAATCTAAT 248
QY 61 GGATTCAGCAGTAATGGTATCGGAGGAAGTCTTGTGCTTGGAAACCCAGAGTATAGTCTCATCC 120
Db 249 GGATTCAGCAGTAATGGTATCGGAGGAAGTCTTGTGCTTGGAAACCCAGAGTATAGTCTCATCC 308
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Db 489 GTAGTAGTTCAACATGGAAACAGCTAGCAGATTAATAACTGAGACGATGAGTGTAG 548
QY 361 CCCTCAAGTAGTCTTACAGGAAGTGTGAAGAGCTGATTTTCTTCACTACACAACTA 420
Db 549 CCCTCAAGTAGTCTTACAGGAAGTGTGAAGAGCTGATTTTCTTCACTACACAACTA 608

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QY 609 CAAGAAGGNGTAACTGAGGAGTCTAAACATTAATTAATCTCTGAAGAGACAAATATT 668
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QY 481 GATGAATCTGATAGGATCAGAGAGAGGGGCAICCCCTCCACCTGGACTTGGTTCAGAGATT 540
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QY 669 GATGAATCTGATAGGATCAGAGAGAGGGGCAICCCCTCCACCTGGACTTGGTTCAGAGATT 728
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QY 541 TATGAATAGACCCCTTTTGACAAACTATCGTCAACACTTCACTTACAGGATTTACACAG 600
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QY 729 TATGAATAGACCCCTTTTGACAAACTATCGTCAACACTTCACTTACAGGATTTACACAG 788
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QY 601 TACAAGAACTGAGGAGGCAATTTGACAACTATGAGGGTGGTGGTGGTGGTGGTGGTGGT 660
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QY 901 AAGGATTCATTCCTGCTGATCACTACTCTTTACAGTCTTCTGATGAAATPCCATAT 960
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QY 1089 AAGGATTCATTCCTGCTGATCACTACTCTTTACAGTCTTCTGATGAAATPCCATAT 1148
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QY 2341 GTTTTGTCTTTAATTTTCACTGCGACAAAGACCTATTCAGACTATCGCATACCCCTGCTG 2400
DB |||||
QY 2529 GTTTTGTCTTTAATTTTCACTGCGACAAAGACCTATTCAGACTATCGCATACCCCTGCTG 2588
DB |||||
QY 2401 AAGCTGGAATAATCAAGTTGCTTGGACTCAGATGATTTCCACTTTTGGTGGCTTCGG 2460
DB |||||
QY 2589 AAGCTGGAATAATCAAGTTGCTTGGACTCAGATGATTTCCACTTTTGGTGGCTTCGG 2648
DB |||||
QY 2461 AGAATTTGATCAATAATGCGGAATTTTCCACTTTTGAAGGATGATGATGATGATGATGATGAT 2520
DB |||||
QY 2649 AGAATTTGATCAATAATGCGGAATTTTCCACTTTTGAAGGATGATGATGATGATGATGATGAT 2708
DB |||||
QY 2521 TCAATTTGTTGATGACCTTGTAAACACAGCTGCTGATGCACTAGTAGACAAAGAA 2580
DB |||||
QY 2709 TCAATTTGTTGATGACCTTGTAAACACAGCTGCTGATGCACTAGTAGACAAAGAA 2768
DB |||||
QY 2581 GAAGAAGAGAAAGAAAGAAAGAAAGTAGCAGGATGAGAGAAAGTAGTA 2634
DB |||||

Db 2769 GAAGAAGAAGAAGAAGTAGCAGTAGTAGAGAGAGAGAGAGAGAGAA 2822

US-09-087-277-3

Sequence 3, Application US/09087277B

Patent No. 6169226

GENERAL INFORMATION:

APPLICANT: EK, Bo

APPLICANT: KHOSNOODI, Jamshid

APPLICANT: LARSSON, Clas-Iomas

APPLICANT: LARSSON, Hakan

APPLICANT: RASK, Lars

TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,277B

CURRENT FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER FILING DATE: 1996-11-28

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9601506-0

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 1393

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: bell gene fragment

OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

OTHER INFORMATION: (potato)

FEATURE:

NAME/KEY: CDS

LOCATION: (2)..(1393)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (424)..(1150)

OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,

OTHER INFORMATION: C, G or T.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (422)..(424)

OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (890)..(892)

OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys

OTHER INFORMATION: of Phe.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1148)..(1150)

OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.

US-09-087-277-3

Query Match 51.8%; Score 1369.8; DB 4; Length 1393;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 1377; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 819 TCTGCCAAATATATGGATGGTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 878

Db 1 TCTGCCAAATATATGGATGGTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

QY 879 TATGGACACTCCATCAGGTGTTAAGGATTCCTTCCTGATGATCCATTCCTGTTGGATCAACTACHTTTTACA 938

Db 61 TATGGACACTCCATCAGGTGTTAAGGATTCCTTCCTGATGATCCATTCCTGTTGGATCAACTACTCTTTACA 120

QY 939 GCTTCTCTGATGAATTCCTATATAATGGAATACATATATGATCCACCCGACAGAGAGGTTA 998

Db 121 GCTTCTCTGATGAATTCCTATATAATGGAATACATATATGATCCACCCGACAGAGAGGTTA 180

QY 999 TATCTTCCACACCCACGSCCAAGAAAGTGGCTGAGATATATGATCTCATAT 1058

Db 181 TATCTTCCACACCCACGSCCAAGAAAGTGGCTGAGATATATGATCTCATAT 240

QY 1059 TGGATAGTAGTTCGGGAGCCTAAATTAACCTATACCTGATGATTTTATGAGATGAAGTTCT 1118

Db 241 TGGATAGTAGTTCGGGAGCCTAAATTAACCTATACCTGATGATTTTATGAGATGAAGTTCT 300

QY 1119 TCCTCGCATAAAAAGCTTGGGTACATGCGCTGCAAAATTAATGGCTATTAAGAGCATTC 1178

Db 301 TCCTCGCATAAAAAGCTTGGGTACATGCGCTGCAAAATTAATGGCTATTAAGAGCATTC 360

QY 1179 TTATTAGCTAGTTTGGTTATCATGTCACAAAATTTTTCACCAACGACGCGTTTGG 1238

Db 361 TTATTAGCTAGTTTGGTTATCATGTCACAAAATTTTTCACCAACGACGCGTTTGA 420

QY 1239 AACGCCGACGACCTTAACTCTTTGATTGATTAAGCTCATGAGCTAGGATTTGTTCT 1298

Db 421 AACNCCGACGACCTTAACTCTTTGATTGATTAAGCTCATGAGCTAGGATTTGTTCT 480

QY 1299 CATGGACATTTTTCACAGCCATGATCAATAAATTAATTTAGATGGACTGAACATTTGA 1358

Db 481 CATGGACATTTTTCACAGCCATGATCAATAAATTAATTTAGATGGACTGAACATTTGA 540

QY 1359 CTGCACCGATAGTTTGTACTTTTCACTCTGGAGCTCGTGGTTATCATGGATGGGATTC 1418

Db 541 CGGCACAGATAGTTTGTACTTTTCACTCTGGAGCTCGTGGTTATCATGGATGGGATTC 600

QY 1419 CCGCTCTTTAACTATGGAACCTGGAGGTTACTTAGGTATCTCTCAAAATCGAGATG 1478

Db 601 CCGCTCTTTAACTATGGAACCTGGAGGTTACTTAGGTATCTCTCAAAATCGAGATG 660

QY 1479 GTGGTTGGATCGCTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGA 1538

Db 661 GTGGTTGGATCGCTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGA 720

QY 1539 TATTCACACGGATTATCGGTGGATTCACCTGGAACCTACGAGAAATACITTTGACATCGC 1598

Db 721 TACTCACCGATTATCGGTGGATTCACCTGGAACCTACGAGAAATACITTTGACATCGC 780

QY 1599 AACTGATGTGATGCTGTTGTGATCTGATGCTGGTCAACGATCTTATTCATGGCTTTT 1658

Db 781 AACTGATGTGATGCTGTTGTGATCTGATGCTGGTCAACGATCTTATTCATGGCTTTT 840

QY 1659 CCAGATGCAATTAACATTTGGTGAAGATTTAGCGGAATCCGACATTTTGTATTCCTG 1718

Db 841 CCAGATGCAATTAACATTTGGTGAAGATTTAGCGGAATCCGACATTTTGTATTCCTG 900

QY 1719 CCAAGAGGGGGTGTGGCTTTGACTATCGCTCATGCTGATGCTGATGCTGATGCTGATGCTGAT 1778

Db 901 TCAAGATGGGGTGTGGCTTTGACTATCGCTCATGCTGATGCTGATGCTGATGCTGATGCTGAT 960

QY 1779 TGAGTTGCTCAAGAAACGGGATGAGGATTCGAGAGTGGGTGATGTTTATGCTATACACTGAC 1838

Db 961 TGAGTTGCTCAAGAAACGGGATGAGGATTCGAGAGTGGGTGATGTTTATGCTATACACTGAC 1020

QY 1839 AATAGAGATGCTCGGAAGTGTGTTTATCATGCTGAAAGTCAATGATCAAGCTCTAGT 1898

Db 1021 AATAGAGATGCTCGGAAGTGTGTTTATCATGCTGAAAGTCAATGATCAAGCTCTAGT 1080

QY 1899 CGGTGATAAATCATAGCTATTCGCTGATGGCAAGGATGATGATGATGATGATGATGATGATGAT 1958

Db 1081 CGGTGATAAATCATAGCTATTCGCTGATGGCAAGGATGATGATGATGATGATGATGATGATGAT 1140

QY 1959 GGATAGACCTCAACATCATTAATAGATCGTGGATGAGATTCGACAAAGATGATGATGATGATGAT 2018

Db 1141 GGATAGACCTCAACATCATTAATAGATCGTGGATGAGATTCGACAAAGTCAATGATGATGATGAT 1200

QY 2019 TGTAACTATGGGATTTAGGAGGAGAGGTTACCTTAAATTTTCAATGGGAAATGAATTCGSCCA 2078

Db 1201 TGTAACTATGGGATTTAGGAGGAGAGGTTACCTTAAATTTTCAATGGGAAATGAATTCGSCCA 1260

QY 2079 CCTGATGATGATTTTCCCTAGGCTGAACACACCTCTCTGATGGCTGATGATGATGATGATGATGAT 2138

Db 1261 CCTGAGTGGATTGATTTCCCTAGGCGTGAACAACACCTCTCTGTATGGCTCAGTAATTC 1320
QY 2139 CGGAACCAATTCAGTTATGATAAATGCGACGAGATTTGACCTGGGAGATCGAGAATA 2198
Db 1321 CGGAACCAATTCAGTTATGATAAATGCGACGAGATTTGACCTGGGAGATCGAGAATA 1380
QY 2199 TTTAAGATACCGT 2211
Db 1381 TTTAAGATACCGT 1393

RESULT 4

US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: betaII gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is xaa wherein xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is xaa wherein xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is xaa wherein xaa = Pro.
US-09-658-499-3

Query Match 51.8%; Score 1369.8; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 137; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 819 TCTGCCAAATAATCGATGGTCTCTCGCAATTCCTCATGGGTCACAGTGAAGATACG 878
Db 1 TCTGCCAAATAATCGATGGTCTCTCGCAATTCCTCATGGGTCACAGTGAAGATACG 60
QY 879 TATGGACATCCATCAGGTGTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACA 938
Db 61 TATGGACATCCATCAGGTGTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACA 120

QY 939 GCTTCCTGATGAATTCOCATATATATGAATATACATATATGATCCACCCGAGAGAGAGTA 998
Db 121 GCTTCCTGATGAATTCOCATATATATGAATATATGATCCACCCGAGAGAGAGTA 180
QY 999 TATCTTCCACACCCGAGGCGCARAGAACCAAGTCGCTGAGATATATGAATCTCATAT 1058
Db 181 TATCTTCCACACCCGAGGCGCARAGAACCAAGTCGCTGAGATATATGAATCTCATAT 240
QY 1059 TGAATGAGTAGTCCGGAGGCTAAATTAATCTCATACGTGAATTTAGAGATGAAGTTCT 1118
Db 241 TGAATGAGTAGTCCGGAGGCTAAATTAATCTCATACGTGAATTTAGAGATGAAGTTCT 300
QY 1119 TCCTCGCATAAAAAGCTTGGGTACAAATGCGCTGCAAAATATATGCTATTCAGAGCATTC 1178
Db 301 TCCTCGCATAAAAAGCTTGGGTACAAATGCGCTGCAAAATATATGCTATTCAGAGCATTC 360
QY 1179 TTATACGCTAGTTTGGTTATCATGTCACAAATTTTTCACCAACAGCAGCCGTTTGG 1238
Db 361 TTATATGCTAGTTTGGTTATCATGTCACAAATTTTTCACCAACAGCAGCCGTTTGA 420
QY 1239 AAGCGCGAGCAGCCTTAAGTCTTGTGATTGATAAAGCTCATGAGCTAGGAATTTGTGTCT 1298
Db 421 AACNCCGAGCAGCCTTAAGTCTTGTGATTGATAAAGCTCATGAGCTAGGAATTTGTGTCT 480
QY 1299 CATGGACATTTTCACAGCCCATGCATCAAAATAAATCTTATAGTGGACTGACATGTTGA 1358
Db 481 CATGGACATTTTCACAGCCCATGCATCAAAATAAATCTTATAGTGGACTGACATGTTGA 540
QY 1359 CTGCAACGATAGTTTACTTTCCTGAGCTCGTGGTTATCATGTTGATGGATCGGATTC 1418
Db 541 CGGCACAGATAGTTTACTTTCCTGAGCTCGTGGTTATCATGTTGATGGATCGGATTC 600
QY 1419 CCGCTCTTTAACTATGGAACCTGGAGGCTACTTAGGTATCTTCTCAAAATGGAGATG 1478
Db 601 CCGCTCTTTAACTATGGAACCTGGAGGCTACTTAGGTATCTTCTCAAAATGGAGATG 660
QY 1479 GTGTTGGATCGGTTCAAAATTTGATGATTTAGATTTGATGGTGTGACATCAATGATGA 1538
Db 661 GTGTTGGATCGGTTCAAAATTTGATGATTTAGATTTGATGGTGTGACATCAATGATGA 720
QY 1539 TATTCACACGATTTATCGGTGGGATTCACCTGGGAACCTACGAGAAATCTTTGGACTCGC 1598
Db 721 TACTCACACGATTTATCGGTGGGATTCACCTGGGAACCTACGAGAAATCTTTGGACTCGC 780
QY 1599 AACTGATGTGGATCGTGTGTATCTGATCTGGTCAACGATCTATCTATGAGGCTTTT 1658
Db 781 AACTGATGTGGATCGTGTGTATCTGATCTGGTCAACGATCTATCTATGAGGCTTTT 840
QY 1659 CCCAGATGCAATTTACCATTTGGTGRAGATTTAGCGGAATCGGACATTTCTATCCGCT 1718
Db 841 CCCAGATGCAATTTACCATTTGGTGRAGATTTAGCGGAATCGGACATTTCTATCCGCT 900
QY 1719 CCAAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGCGAATTCGTGATAACGAT 1778
Db 901 TCAGATGGGGGTGTGGCTTTGACTATCGGCTGCATATGCGAATTCGTGATAACGAT 960
QY 1779 TGAGTTGCTCAAGAAACCGGATGAGGATTTGGAGAGTGGGTGATATTTCTATACACTGAC 1838
Db 961 TGAGTTGCTCAAGAAACCGGATGAGGATTTGGAGAGTGGGTGATATTTCTATACACTGAC 1020
QY 1839 AAATAGAGATGGTCCGGAAGAGTGTGTTTCATACGCTGAAAGTCATGATCAAGTCTAGT 1898
Db 1021 AAATAGAGATGGTCCGGAAGAGTGTGTTTCATACGCTGAAAGTCATGATCAAGTCTAGT 1080
QY 1899 CGGTGATAAAACTATAGCATTTCTGGCTGATGCAAGGATATGATGATTTTATGGCTCT 1958
Db 1081 CGGTGATAAAACTATAGCATTTCTGGCTGATGCAAGGATATGATGATTTTATGGCTCT 1140
QY 1959 GGATAGACCGTCAACATCATTTAATAGATTCGTGGGATAGCATTTGCACAGATGATAGCT 2018
Db 1141 GGATAGACCNCTCAACATCATTTAATAGATTCGTGGGATAGCATTTGCACAGATGATAGCT 1200
QY 2019 TGTAACATGGAATTAGGAGGAGAGGCTACCTAAATTTTCATGGGAATGAATTCGGCA 2078

1620 GTATCTGATCGTGGTCAACGATCTTATTCATGGCTTTCCAGATGCAATACCAATGG 1679
1521 TTACTTGTGCTGGTAAATGATTAATCATGACCTTTATCTGAGCGTGAACCAATGG 1580
1680 TGAAGATGTAGCGGAATGCCACATTTTGTATTCCTCCGTCACAGAGGGGGTGTGGCTT 1739
1581 TGAAGATGTAGTGGGAATGCCATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1640
1740 TGAATATCGCTGCTGATATGCAATTTCTGATTAACAGGATGATGCTCTCAAGAAAGGGA 1799
1641 TGAATATCGGATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1700
1800 TGAAGATGTAGCGGAATGCCACATTTTGTATTCCTCCGTCACAGAGGGGGTGTGGCTT 1859
1701 TGAATATCGGATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
1860 GTGTGTTTCATAGCTGAAAGTATGATCAAGCTCTAGTGGGTCATTAAGTATGATGCTT 1919
1761 GTGTGTTTCATAGCTGAAAGTATGATCAAGCTCTAGTGGGTCATTAAGTATGATGCTT 1820
1920 CTGGCTGATGGAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1979
1821 TTGGTGTGATGGAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1880
1980 AATAGATCGTGGATAGCATTCACAGATGATGATGATGATGATGATGATGATGATGATGAT 2039
1881 CATGATCGTGGATAGCATTCACAGATGATGATGATGATGATGATGATGATGATGATGAT 1940
2040 AGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
1941 AGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
2100 TAGGGTGAACACACTCTCTGATGCTCAGTAATCCCGGAAACCAATTCAGTTATGA 2159
2001 AGAAGTCCGCAAGACTTCCAGTGGTAAGTTATTCAGGGAATTAACACAGTATGA 2060
2160 TAAATGACAGCGGAGATTTGACCTGGGAGATGAGAAATATTAAGTATGATGATGATGATGAT 2219
2061 CAATGTCGTCGAGATTTGACCTGGGATGATGATGATGATGATGATGATGATGATGATGAT 2120
2220 AGAATTTGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2279
2121 AGAATTTGATCAGCAATGCAATCTTGGACAAAATATCAATTCATGATGATGATGATGAT 2180
2280 CCAGTTCATATCAGGAAGATGAAGGATAGGATGATGATGATGATGATGATGATGATGATGAT 2339
2181 CCAGTATATTTCCGGAACATGAGGAGGATAGGATGATGATGATGATGATGATGATGATGATGAT 2240
2340 AGTTTGTGCTTAAATTTTCACTGGACAAAGCTATTCAGATGATGATGATGATGATGATGATGAT 2399
2341 GGTATTTGTGCTTCAACTTCCACTGCAACACAGCTATTTGACATGATGATGATGATGATGATGAT 2300
2400 GAAGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2459
2301 AAAGCTTGGGGTGTATAGGTGCTTGGACCTGGGCTGATGATGATGATGATGATGATGATGATGAT 2360
2460 GAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2519
2361 CAGATCCATCAGCCAGCGAGCACTTCACCGCGGACTGTTCCGATGATGATGATGATGATGATGAT 2420
2520 TTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2573
2421 TTCATCTCGGTTTATACCAAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2474

RESULT 6

US-08-941-445A-14

; Sequence 14, Application US/08941445A

; Patent No. 6107060

; GENERAL INFORMATION:

; APPLICANT: Keeling, Peter

; APPLICANT: Guan, Hanping

TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 44.6%; Score 1180.4; DB 3; Length 2725;

Best Local Similarity 72.7%; Pred. No. 0;

Matches 1523; Conservative 0; Mismatches 571; Indels 0; Gaps 0;

QY 480 TGATGAATCTCATAGGATCAGAGAGGGGATCCCTCCACTGGACCTTGGTCAAGAT 539
DB 393 TGATGCTCAACCTTGACAGAGATCGATGGTCCGCCACCAAGCGATGACAAAAAT 452
QY 540 TTATGAATAGACCCCTTTTGGACAAATATCGTCAACACCTTGATTCAGGTATTCACA 599
DB 453 ATTCAGATTCACCCCATGTTGCAAGGCTATAAGTACCATCTTGATATCGGTACAGCT 512
QY 600 GTACAAGAACTGAGGAGGCAATGACAAGTATGAGGGTGGTTTGGAGGCTTTTCG 659
DB 513 CTATAGAAGATCCGTTTCAGACATGATGACAAGAGAGGCTTGGAGGCTTTCGCG 572
QY 660 TGGTATGAAAAAATGGGTTTCACTCGTAGTCTACAGGTATCATCTTACCGTGTGGG 719
DB 573 TAGTATGAGAAGTTTGGATTAAATGCCAGCGCGAGGTATCATATCGAGAATGGGC 632
QY 720 TCTGGTCCCGACGTCAGCTGCCCTCATTTGGAGATTTCAACATTTGGGACGCAATGCTGA 779
DB 633 TCCTGGAGCAATTTCTGCGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 692

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/257,894
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/091,052
;; FILING DATE: JUNE 10, 1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Majarian, William R.
;; REGISTRATION NUMBER: 41,173
;; REFERENCE/DOCKET NUMBER: BB-1066-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4926
;; TELEFAX: 302-773-0164
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2087 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-09-257-894-9

Query Match 39.0%; Score 1033; DB 4; Length 2087;

Best Local Similarity 73.7%; Pred. No. 1.3e-290;

Matches 1315; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY	480	TGATGATCTGATGAGATCAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAGAT	539
DB	303	TGATGCTCAGCCCTTGACAGAGTTGAGTGGTCCCTCCACCAAGCGATGGACAAAAT	362
QY	540	TTATGAATAGACCCCTTTTGACAACTATGTCACACCTGATGATGATGATGATGATG	599
DB	363	ATTCAGATTGACCCCAATGTTGCAAGCTATAAGTACCATCTTGATGATGATGATG	422
QY	600	GTACAGAACTCAGGAGGCAATGACAGTATGAGGTTGAGTGGTGGTGAAGCCCTTTC	659
DB	423	CTATAGAAGAACTCCGTTACAGACATGATGAACATGAAGAGGGCTTGAAGCCCTTC	482
QY	660	TGTTTATGAAAAATGGTTTCTACTGATGATGATGATGATGATGATGATGATGATG	719
DB	483	TAGTATGAGAACTTGGATTTAATGCCAGCGGAGGATACACATATCGAGATGGC	542
QY	720	TCTTGTGCGCATCAGCTGCCCTCAATGAGATTTCAACAATGGGACGCAATGCTGA	779
DB	543	TCCTGGAGCATTTCTGACAGATTTGTTGGTGGTGAATTCACAACTGGGATCCAAATG	602
QY	780	CATTATGACTCGGAATCAATTTGTTGCTCGGAGATTTTCTGCCAATATGTTGGATG	839
DB	603	TCGTATGAGCAAAATGAGTTTGGTGTTCGGGAATTTTCTGCCAATATGTTGGATG	662
QY	840	TTCTCTGCAATTCCTCATGGGTCAGAGTGAAGATACGATGACACTCCATCAGGTGT	899
DB	663	TACATCACCATTCTTCATGATCTCGTGAAGGTGAGATGATGATGATGATGATGATG	722
QY	900	TAGGATTCATTCCTGCTGGATCACTACTCTTTACAGCTTCCTGATGAAATCCATA	959
DB	723	AAAGGATTCATTCAGCTGATCAAGTATGATGATGATGATGATGATGATGATGATG	782
QY	960	TATGGAATACATATGATCAACCGGAGAGGAGGATATATCTTCCACACCCACGGCC	1019
DB	783	TGATGGATTTATATGATCCTCTGAAGAGGTAAAGTATGTTGATCAGGATGCGCAAC	842
QY	1020	AAAGAACCAAGTCGCTGAGATATATGATATGATGATGATGATGATGATGATGATG	1079
DB	843	TAAACGACCAAAATCATTCGGATATATGATGATGATGATGATGATGATGATGATG	902
QY	1080	TAAATTAATCACTAGTGAATTTTGAAGATGAAGTCTTCTCCGCGATAAAGAGCTGG	1139
DB	903	GAAGATAACACATATGTAAGTATGAGGATGAGTCTCCCAAGAAATAAAAGCTTGG	962
QY	1140	GTCAATGCGCTGCAATTTATGCTATTCAAGAGCAATCTATTACCTACTTTTGTGTA	1199

DB	963	ATCAATGTCAGTGCATAATAATGGCAATCCAAGAGCACTCATATATATGGAAGCTTTGGATA	1022
QY	1200	TCATGTCACAAAATTTTTTTCACCAAGCAGCCGTTTTTGGACGCCGCCGACACCTTAAGTC	1259
DB	1023	CAATGTAACATAATTTTTTTCGCGCAAGTAGTCTGTTTGGTATCCCAAGAGATTGAAGTC	1082
QY	1260	TTTCAATGATAAAGCTCATAGCTAGGATAGGAATGTTGTTCTCATGAGCATTTTTCACAGCCA	1319
DB	1083	TTTGAATGATAGAGACATGAGCTTGGTTGCTAGTCTCATGATGATGTTTTCATAGTCA	1142
QY	1320	TGCATCAAAATAATCTTATGATGACATGACATGTTGACTGTCACCGATGATGTTTACTT	1379
DB	1143	TGGCTCAAGTAATCTCTGGATGGTTGAATGGTTTTTGTATGTTGATACATACATATGAT	1202
QY	1380	TCATCTCTGAGCTCGTGGTTATCATTTGATGATGATGATGATGATGATGATGATGATG	1439
DB	1203	TCAGTGGTCCACGTCGACATGATGATGATGATGATGATGATGATGATGATGATGATG	1262
QY	1440	CTGGGAGGTACTTAGGTATCTCTCAAAAGCGAGATGGTGGTGGATGATGATGATGATG	1499
DB	1263	CTGGGAAGTTTTAAGATTTCTCTCCAATGCTAGATGATGATGATGATGATGATGATGATG	1322
QY	1500	TGATGATTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1559
DB	1323	TGATGTTTCCGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1382
QY	1560	GGATTCATCTGGGAACACGAGGATATCTTGGACTCGCAACTGATGATGATGATGATGATG	1619
DB	1383	AACATTTACGGGAACCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG	1442
QY	1620	GTAATGATGCTGCTCAACGATCTTATCATGATGATGATGATGATGATGATGATGATGATG	1679
DB	1443	TTACTTCTGATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1502
QY	1680	TGAAGATGTTAGCGGAATGCGGACATTTTGTATTCCTGCTCAAGAGGGGCTGTTGGCTT	1739
DB	1503	TGAAGATGTTAGTGAATGCTACATTTGCCCTTCCCTGTTACAGATGTTGGGATGATG	1562
QY	1740	TGATATCGGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1799
DB	1563	TGATATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1622
QY	1800	TGAGATGAGAGTGGTGTATGTTTCATACACTGACAAATAGAGATGTCGGAATA	1859
DB	1623	TGAACCTGGAAGATGGGTGATATTGTCACACTGACAAATAGAGGTTGGTTAGAGAA	1682
QY	1860	GTGTGTTTCATACGCTGAAAGTCAATGATCAAGCTCTAGTGGTGTATGATGATGATGATG	1919
DB	1683	GTGTGTAACCTTATCTGAAAGTCAATGATCAAGCTCTAGTGGTGTATGATGATGATGATG	1742
QY	1920	CTGCTGATGGACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1979
DB	1743	TTGTTTATGAGACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1802
QY	1980	AATGATGCTGGGATAGCATGTCACAGATGATGATGATGATGATGATGATGATGATGATG	2039
DB	1803	CATGATGCTGGGATAGCATTACATGATGATGATGATGATGATGATGATGATGATGATGATG	1862
QY	2040	AGAAGGTGATCAATTTTATGGAATGAATTCGGCCACCTGAGTGGATGATGATGATGATG	2099
DB	1863	AGAGGCTATCTTAAATTCATGGAATGATGATGATGATGATGATGATGATGATGATGATG	1922
QY	2100	TAGGCTGAACACACCTCTCTGATGCTGATGATGATGATGATGATGATGATGATGATGATG	2159
DB	1923	AAGAGTCCGCAAGAGCTTCCAGTGGTAAAGTTTATTCAGGGGATTAACACAGATTATGA	1982
QY	2160	TAAATCAGAGGAGATTTGACCTGGGAGATGACAAATATTTAAGATACCGTGGTGTGCA	2219
DB	1983	CAATGCTGCGAAGATTGACCTGGGATGATGATGATGATGATGATGATGATGATGATGATG	2042
QY	2220	AGAATTTGACCGGCTAGTATCTTGAAGATATAATATGATGATGATGATGATGATGATG	2264
DB	2043	AGACTTTCATCAGGCAATGCAACATCTTGACCAAAATATGATGATGATGATGATGATG	2087

RESULT 8

US-09-257-894-8/C

; Sequence 8, Application US/09257894

; Patent No. 6376749

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Klein, Theodore M.

; APPLICANT: Hubbard, Natalie L.

; APPLICANT: Lightner, Jonathan E.

; TITLE OF INVENTION: No. 6376749el Starches via Modification of

; TITLE OF INVENTION: Expression of Starch Biosynthesis

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 95

; SOFTWARE: Version 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/257,894

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/091,052

; FILING DATE: JUNE 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Majarian, William R.

; REGISTRATION NUMBER: 41,173

; REFERENCE/DOCKET NUMBER: BB-1066-A

; TELEPHONE: 302-992-4926

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2165 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-257-894-8

Query Match 39.0%; Score 1031.4; DB 4; Length 2165;
Best Local Similarity 73.6%; Pred. No. 4e-290;
Matches 1314; Conservative 0; Mismatches 471; Indels 0; Gaps 0;

QY	480	TGATGATCTGATAGGATCAGAGAGAGAGGGGCATCCCTCCACCTGGACTGGCTCAGAAGAT	539
DB	1785	TGATGCTCAAGCCCTTGAACAGAGCTCGAGTGTCCCTCCACCAAGCGATGACAAAT	1726
QY	540	TTATGAATAGACCCCTTTTGACAACTATCGTCAACACTTGTACAGCTTGTACAGATTCACA	599
DB	1725	ATTCAGATGGCCCCATGTGTGACGCTATAGATCCATTCCTTGAATCGGTACAGCCT	1666
QY	600	GTACAGAACTGAGGAGGCAATTCACAGATGAGGGTGTGAGGCTTTTGAAGCCCTTCTCG	659
DB	1665	CTATGAAGAATCCGTTTCACACTTGTACAGATGATGACAGAGAGGGCTTGAAGCCCTTCTCG	1606
QY	660	TGTTATGAATAAATGGTTTCTACTGCTGTACAGCTATCCTTACCTTACCTGAGTGGGC	719
DB	1605	TAGTTATGAAGATTTGGATTTAATGCCAGCGGGAAGGTATCAGATTCAGAAATGGGC	1546
QY	720	TCTTGGTCCAGTACGCTGCTCATTTGGAGATTTCACAATTTGAGAGCAATGCGCAATGCTGA	779
DB	1545	TCTTGGAGCATTTTCTGACAGATTTGGTGGTGTGACGTCACCAACTGGGATCCCAATGCAGA	1486

QY	780	CATTATGACTCGGAATGAATTTGGTCTGGAGATTTTCTGCCAAATAATCTGGATGG	839
DB	1485	TCGTATGACGCAAAATGAGTTTGGTCTTTGGCAATTTTCTGCCAAATAATCTGGATGG	1426
QY	840	TTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGATAGGACATCCCATAGGTG	899
DB	1425	TACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGATGGATCTCCATCAGGAT	1366
QY	900	TAAAGATTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTCCTGATGAATTTCCA	959
DB	1365	AAAGATTCAATTCAGCTTGGATCAAGTACTAGTGCAGGCCCCAGGAGAAATACCATTA	1306
QY	960	TAAATGAATACATTAATGATCCACCGAGAGAGAGAGGTATATCTTCCACACCCCGAGCC	1019
DB	1305	TGATGGATTTATTAATGATCTCTGAAAGAGTTAAAGTATGTTTCAGGCTAGCGCAACC	1246
QY	1020	AAAGAAACCAAGTCGCTGAGAAATATGAATCTCATATTGGAATGATGATGTCGAGCC	1079
DB	1245	TAAACGACCAAAATCATTCGGGATATATGAACACATGTCGGAATGAGTAGCCCGGAACC	1186
QY	1080	TAAATTAACCTACATAGCTGAATTTAGAGATCAAGTTCTTCTCCCAATAAAGACCTGG	1139
DB	1185	GAAGATAACACATATGTAATCTTTAGGGATGAGTCTCCCAAGATAAATAAATCTGG	1126
QY	1140	GTACAAATCGCTGCAAAATATGGCTATTCAAGAGCAATCTTATTACGCTAGTTTGGTTA	1199
DB	1125	ATACAATGCAATGCAAAATATGGCAATCCAAAGAGCACTCATATATGGAAGCTTTGGATA	1066
QY	1200	TCATGTCACAAATTTTTCACCAAGAGAGCGGTTTGGAGCGCCGAGAGCTTAAGTC	1259
DB	1065	CCATGTAACATAATTTTTCGCGCAAGTAGTCTGTTTGGTACCCAGAGATTTGAAGTC	1006
QY	1260	TTGATTCATAAAGCTCATAGCTAGGAATTTGTTCTCTCATGGACATTTGTCACAGCA	1319
DB	1005	TTTGAATGATAGAGACATGAGCTTGGTTGCTAGTTCTCATGGATGGTTTCATAGTCA	946
QY	1320	TGCATCAAAATATCTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTGTTACTT	1379
DB	945	TGCGTCAAGTAAATATCTCTGGATGGTTGAATGGTTTTCATGGATGGTTTCATAGTCA	886
QY	1380	TCATCTGGAGCTGCTGTTTATCATTTGATGGATTCGCGCTCTTACTATGGAATA	1439
DB	885	TCACAGTGTCCACGTGGCCATCACTGGATGGGATTTCTGCTTATTAACATATGGAA	826
QY	1440	CTGGAGGATCTTAGGTATCTCTCAAAATGCGAGATGGTGGTTGGATGGTTCAAAAT	1499
DB	825	CTGGGAAGTTTAAAGATTTCTCTCTCAATGCTAGATGGTGGCTCGAGGAAATATAGTT	766
QY	1500	TGATGGATTTAGATTTGATGGTGTGACATCAATGATATATTCACCACGATTTATCGGT	1559
DB	765	TGATGGTTTCCGTTTTCATGTTGAGCTCCATCATGATACATCACTCACCAGGATTTAAGT	706
QY	1560	GGATTCACATGGGAACATACAGGAAATCTTTGGACTCGACACTGATGATGATGCTGTGT	1619
DB	705	ACATTTACGGGAACCTCAATGAGTATTTGGCTTTGCCACCGATAGATGAGTGGT	646
QY	1620	GTAATGATGCTGTGCTCAACGATCTTATTCATGGCTTTTCCACGATCAATTCACATGG	1679
DB	645	TTACTTGAATGCTGTAATGATCTAATTCATGAGCTTATTCCTGAGGCTGTACCAATGG	586
QY	1680	TGAAGATGTTAGCGGAATCCGACATTTTGTATTCGCTCCAAAGAGGGGCTGTGSCIT	1739
DB	585	TGAAGATGTTAGTGAATGCTATCTTTCCTTCTGTTACAGATGCTGGGTGGGTAGTTT	526
QY	1740	TGACTATCGCTCATATGCAATTCCTGATAACGAGTTGAGTTGCTCAAGAAACGGA	1799
DB	525	TGACTATCGATCATATGCTGTGGCTGCAAAATGAGTTGACTTCTCTCAAGCAAAATGA	466
QY	1800	TGAGGATGGAGATGGGTGATATTTGTTCATACACTGACAAATAGAGATGTCGGAATA	1859
DB	465	TGAAGATGGAGATGGGTGATATTTGTTCACACTGACAAATAGGAGGTGGTTAGAGAA	406

Db 2124 ATATACGAGCTGCAGCCCAAGCTGGAGATATTCAGAGCAATTCAGGTACCGGATGAAA 2065
QY 598 CAGTACAAGAACTGAGGAGGCAATTCAGCACTATGAGGCTGGTTGGAGGCTTTCT 657
Db 2064 AGATTCTTAGAGCAGAAAGATCAATTCAGAAATGAGGAGAGICTTGAACTCTTTCT 2005
QY 658 CPTGGTTTGAATAATGGTTTCACTCGTCTAGTACAGGTATCACTTACCSTGAGTGG 717
Db 2004 AAGGCTATTTGAAATTTGGGAATTAACAATAGAGGATGGAATCTATCTGTAATGG 1945
QY 718 GCTCTTGGTCCAGCAGCTGCTGCTCATTCAGTATTCAGGATTTCAACAATTTGGGAGCAATGCT 777
Db 1944 GCACCTGCTCGCAGGAGGAGAGCTATTGCTGACTTCAATGACTGGAATGCTGCAAA 1885
QY 778 GACATATGACTCGGAATGAAATTTGGTCTGGGAGATTTTCTGCCAAATATGCTGAT 837
Db 1884 CATAGATGAGAGGATTAATTTGGTGTGTTGGTCAATCAAAAT--TGACCATGTCAAA 1828
QY 838 GGTTCCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db 1827 GGGAAACCTGCCATCCCTCAATTCAGAGTTAAATTTGCTTTCTACATGGTGGAGTA 1768
QY 898 GTTAAGATTCATTCCTGCTGGATCACTACTCTTTACAGCTTCCTGANGAAT---- 953
Db 1767 TGGGTTGATCGTATTCAGCATTTGATTGTCGACTGTGATGCTCTAAATTTGGA 1708
QY 954 --TCCATATATGGAATACATATGATCCACCCAGAGAGAGGTATATCTTCCAAAC 1011
Db 1707 GTCCTCATGAGGTGTCAITGGGATCCCTGCTCTCTGCTCTGAAAGGTACACATTTAAGCAT 1648
QY 1012 CCAGGCGCAAGAACCAAGTCCGCTGAGAAATATGAAATCTCATATTTGGAATAGTAGT 1071
Db 1647 CCTCGGCTTCAAGGCTGCTGCTCCAGCTATCTATGAGCCCATGAGGTATGAGTGGT 1588
QY 1072 CCGAGGCTTAAATTAATCACTCATAGTGAATTTAGAGATGAAGTTCTTCCTCGCATRAAA 1131
Db 1587 GAAAAGCAGCAGTAGACATATAGGAAATTCAGACAAATGTTTGGCCACGATAGGA 1528
QY 1132 AAGCTTGGGTACATGCGCTGCAATATGCTATTCAGAGCATCTTATTAAGCTAGT 1191
Db 1527 GCAATATCTACACACAGTTCAGTTGATGCGAGTTATGGAGCATTCGTACTATGCTCT 1468
QY 1192 TTGGTTATCATGTCACAAATTTTTCACCAAGAGCGCTTTTGGAAACGCGGACGAC 1251
Db 1467 TTCGGTACCATGTGACAAATTTCTTTCGGGTAGCAGCAGATCAGGCACACACAGAGAC 1408
QY 1252 CTTAAGCTTTGATGTAAAGCTCATCAGCTAGAAATGTTGTTCTCATGAGCATGCT 1311
Db 1407 CTCAAATATCTTGTGATAAGGCACACAGTTTGGGTTTGGAGTTCTGATGATGTTGTC 1348
QY 1312 CACAGCCTATCAATAATTAATTTAGATGAGTGAACATGTTTG-----ACTGC 1362
Db 1347 CATAGCCATGCAAGTAATTAATGTCACAGATGTTTAAATGCTATGATGTTGGACAAAGC 1288
QY 1363 ACCGATGTTGTTACTTTCATCTGGAGCTGCTGTTATCATTTGATGATGTTGGATCCGCG 1422
Db 1287 ACCCAAGAGTCTCTATTTTCATGCGGAGATAGAGTTTATCAAACTTTGGGATAGTCGG 1228
QY 1423 CTCCTTAACTATGGAACCTGGGAGCTATAGGTATCTTCTCTCAATCGGAGATGGTGG 1482
Db 1227 CTGTCAACTATGCTAACTGGGAGTATTAAGTTCTTCTTCTTAACCTGAGATTTGG 1168
QY 1483 TTGATGCTGTCACAAATTTGATGATTTAGATTTGATGCTGACATCAATGATGATAT 1542
Db 1167 TTGATGATTTCACTTTTGTGCTTCCGATTTGATGAGTTATCATCAATGCTGATCAT 1108
QY 1543 CACACGATTTATCGGTGGATTTCACTGGGACTACAGGATATCTTTGGCTCGCACT 1602
Db 1107 CACCATGATCAATGTGGGGTTTACTGGAACTACCAGGAATTTTCAGTTTGGACACA 1048
QY 1603 GATGGAATGCTGTGTGATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCCA 1662
Db 1047 GCTGTGGAGCAGTTGTTTACATGATGCTTGCAACCATTAATGCACAACTCTTGCA 988

QY 1663 GATGCAATTAACCATTTGCTGAGATGTTTAGCGGAATGCGGACATTTTGTATTCCTCCGTC 1722
Db 987 GAAGCAACTCTTGTGCTGAAGATGTTTCAGGCATGCGCGTCTTTTTCGCGCCAGTTGAT 928
QY 1723 GAGGGGGTGTGCTGTTGACTATCGCTGCAATGCAATTTGCTGATAAACGGAATGAG 1782
Db 927 GAAGGTGGGTGTTGCTTACTATCGCTGCAATGCTATCCCTGATAGATGATGATGAC 868
QY 1783 TTGCTCAAGAAACGGGATG---GCAATTTGAGAGTGGTGTATATTTGTCATPACACTGACA 1839
Db 867 TACCTGAAGATAAAGATGACTCTGAGTGGTGCATGCTGATGATGATGATGATGATGAT 808
QY 1840 AATAGAAGATGCTGCGAAAGTGTGTTTATACCTGAAAGTCAATGATGATGATGATGATGAT 1899
Db 807 AACAGGAGATATCTGAAATAATGCTATGCTGAGAGCCATGATGATGATGATGATGAT 748
QY 1900 GGTGATTAACATATAGCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1959
Db 747 GGCACAAAACCTATGCTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 688
QY 1960 GATAGACCGCTCAACATCAATTAATAGATGCTGGGATAGCAATTCACAAAGATGATGATGAT 2019
Db 687 TTGAGCCTGCTTCACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
QY 2020 GTAACATGCTGCTGAGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
Db 627 ATCAATGCTGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 568
QY 2080 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2139
Db 567 CCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
QY 2140 GGAACCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2199
Db 540 GGGACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 2200 TTAGATACCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2259
Db 480 TTGCGTACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
QY 2260 GAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2319
Db 420 TCTTCTCTTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
QY 2320 GTATTTGAAAAGGAAACCTAGTTTGTGCTTAAATTTTCTGATGATGATGATGATGATGAT 2379
Db 360 GTCTTTGAAAGTGGAGATTTACTTTTGTGTTTCAATTTTCAATTTTCAATTTTCAATTT 301
QY 2380 GACTATCGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2439
Db 300 GCTCAAAAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
QY 2440 CCACCTTTTGTGCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2491
Db 240 CTGGTCTCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189

RESULT 11

US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company

STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-257-894-24

Query Match 23.78; Score 628.4; DB 4; Length 2565;

Best Local Similarity 59.78; Pred. No. 8.8e-173;

Matches 1177; Conservative 0; Mismatches 741; Indels 54; Gaps 5;

QY	538	ATTATGAATAGACCCCTTTTGACAAACTATCGTCAACACACCTTGATTACAGTATCA	597
DB	253	ATATACGACCTGGACCCCAAGCTGGAGATATCAAGGACCATTTACGATACCGGATGAA	312
QY	598	CAGTACAGAACTGAGGGAGGCAATTCAGAGATGAGGTGGTTTGGAGCGTTTCT	657
DB	313	AGATTCCTAGAGCAGAAAGATCAATTCGAAGAAATGAGGAGTCTTGAATCTTTCT	372
QY	658	CGTGGTTATGAAAATGGCTTTCACCTCGTAGTCCTACAGGTATCATTACCGTGAGTG	717
DB	373	AAAGGCTATTGAAATTTGGATTAATACAAATGAGGATGGAACCTGTATATCGTGAATGG	432
QY	718	GCPTTGGTGCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAATGCT	777
DB	433	GCACCTGCTGCGCAGGAGGAGAGCTTATTTGGTACCTCAATGACGTGGAATGGTCAAC	492
QY	778	GACATTATGACTCGGAATGAATTTGGTCTGGAGATTTTCTGCCAAATATATGTGGAT	837
DB	493	CATAAGATGAGAGGATAAATTTGGTTTGGTTCGATCAAAAAT---TGACCATTGCAAA	549
QY	838	GGTTCTCTCCATTCCTCATGGTCCAGAGTCAAGATAGTATGACACTCCATCAGGT	897
DB	550	GGGAACCTGCCATCCCTCAAAATCCAAAGTTAAATTTCTTCTTACATGTTGGAGTA	609
QY	898	GTTAAGGATTCATTCCTGCTGGATCACTACTCTTTACAGCTTCTCTGATGAAT---	953
DB	610	TGGGTTGATGGTATTCAGCATGATTCTGTTATCGGACTGTTGATGCCCTTAATTTGA	669
QY	954	---TCCATTAATGGAATACATATGATPCCACCGAAGAGAGAGGATATPCTTCCACAC	1011
DB	670	GCTCCCTATGATGGTGTTCATGGGATCCCTCGCTTCTTGAAGGATACATTTANGCAT	729
QY	1012	CCACGGCCCAAGAAACCAAGTCCGTGAGATATGATATCTCATATTTGGAATGAGTAGT	1071
DB	730	CCTCGGCCCTCAAGCCCTGCTGCTCCAGCTATCTATCAAGCCCATGTAGTATGAGTGG	789

QY	1072	CGGAGCCCTAAATTAACATCACTACGTAATTTAGAGATGAAGTTCTTCTCCTCGCATAAA	1131
DB	790	GAAGAAGCCAGAGTAAAGCACAATATAGGGAATTTGCAGACAATGTGTTCACGACATACA	849
QY	1132	AAGCTTGGTACAAATGCGCTGCAAAATATGCGTATTTCAAGACCATCTTATTTACGGTAGT	1191
DB	850	GCAATAAATACTACACACAGTTCAGTTGATGGAGTATTTGGAGCATTCCTACTATGCTTCT	909
QY	1192	TTTGGTTATCATGTCACAAATTTTTCACCAACAGCAGCGCTTTTGGAAACGCCCGACGAC	1251
DB	910	TTGCGGTACCATGTGACAAATTTCTTGGGTTAGCAGCAATCAGGACACACACAGGAGAC	969
QY	1252	CTTAAGTCTTTGATTGATTAAGCTCATGAGCTAGGAATTTGTTCTCTCATGACACATGTT	1311
DB	970	CTCAAAATATCTTTGTTGATAAGGCACACAGTTTGGGTTTGGAGTTCTCTGATGGATTTGTC	1029
QY	1312	CACAGCCATCATCAAAATAATCTTTAGATGGAGTGAACATGTTG-----ACTGC	1362
DB	1030	CATAGCCATGCAAGTAATAATGTCACAGATGGTTTAAATGGCTATGATGTTGGACAAAGC	1089
QY	1363	ACCGATAGTCTTTACTCTGAGCTCGTGGTATCATTTGATGTTGGATTCGCGC	1422
DB	1090	ACCAAGAGTCTTATTTTCATGCGGAGATAGAGTTATCATAACTTTGGATAGTGG	1149
QY	1423	CTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCAAAATGCGAGATGGTG	1482
DB	1150	CTGTCAACTATGCTAACTGGGAGTATTAAGGTTCTTCTTCTTAACTGAGATATGG	1209
QY	1483	TTGGATCGTTTCAAAATTTGATGGATTTAGATTTGATGGTGGTGCATCAATGATGATAT	1542
DB	1210	TTGGATGAATTCATGTTTGGCTTCGATTTGATGGAGTTTACATCAATGCTGATCAT	1269
QY	1543	CACCAGGATTTATCGTGGGATTCCTGAGGAACTACGAGGAAATCTTTGGACTCGCAACT	1602
DB	1270	CACCATGATCAATGTTGGGTTTACTTGAACATACAGGATATTTTTCAGTTTGGACACA	1329
QY	1603	GATGTGATGCTGTGTGTATCTGATGCTGCTGCTCAACGATCTTATTCATGGGCTTTTCCA	1662
DB	1330	GCTGTGATGAGTGTGTTTACATGATGCTTCAAACTTTTAAATGCAAACTCTTGGCA	1389
QY	1563	GATCAATTCATGTTGGAAGATTTAGCGGAATCGGACATTTTGGATTTCCGCTCCA	1722
DB	1390	GAACCAACTGTTGTTGCTGAAGATGTTTTCAGGATGCGCGCTTTTGGCGCCAGTGTAT	1449
QY	1723	GAGGGGTGTGTGCTTTGATCTGCTGATGCTGCAATTTGCTGATTAACGAGTTGAG	1782
DB	1450	GAAGTGGGTGGGTTTGACTATCGCTGCGCAATGGCTATCCCTGATAGATGATGAC	1509
QY	1783	TTGCTCAAGAACCGGATGA---GGATTGGAGATGGTGTATATTTTTCATACACTGACA	1839
DB	1510	TACCTGAAGAAATAAGATGACTCTGAGTGTGCTGATGGTGAATAGGCACTATTGACT	1569
QY	1840	AATAGAAGATGGTTCGGAAGGTACCTTAAATTTTCATGCTGAAAGTCTATGATCAAGCTC	1899
DB	1570	AACAGGAGATATCTGAAATGATGCTGATGCTGAGAGCCATGATCACTCTTATGTT	1629
QY	1900	GGTGATAAACTATGACATCTTGGCTGATGACGAAGATATGATATGATTTTATGGCTCTG	1959
DB	1630	GGGACAAAATCTTTCATTTCTCTGATGACAAAGAAATGATACACTGGCACTGTCAGAC	1689
QY	1960	GATAGACCGTCAACATCATTAATAGATCGTGGGATACCATGTCACAGATGATTAGGCTT	2019
DB	1690	TTGAGGCTCTTCCCTACCTACATGATGTCGAGGATTTGCACTCCAAAAGATGATTCATC	1749
QY	2020	GTAATGATGGATTAGGAGAGAGGTACCTTAAATTTTCATGCTGGAATGATTCGCGCAC	2079
DB	1750	ATCAGATGCCCCCTGGAGGTGATGGCTACTTGAATTTTATGGAAATGATTTTGGTCA	1809
QY	2080	CCTGAGTGGATGATTTCCCTAGGGGTGAACACCTCTCTGATGGCTCAGTAATCCCC	2139
DB	1810	CCAGATGGATTCACITTCACAGAA-----	1836
QY	2140	GGAACCAATTCAGTTATGATAAATGACAGGAGATTTGACCTGGGAGATGAGGAATAT	2199

Db 1837 GGAACAACCTGGAGCTATGATAAATGACAGCAGACAGTGGAGCCTGTGGACACTGATCAC 1896
QY 2200 TTAAGATACCGTGGGTGCAAGAAATTTGACCGCCCTATGCAGTATCTTGAAGATAAATAT 2259
Db 1897 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGTTCGATGAGAGATTT 1956
QY 2260 GAGTTTATGACTTCAGAACACACCACTTCATATCAGCAAGAGATGAAGAGATAGGATGATT 2319
Db 1957 TCCTTCCTTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAGGTATT 2016
QY 2320 GTATTTGAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCACTGGGACAAAAGCTATTCA 2379
Db 2017 GTCTTTGAACGTGGAGATTAGTTTGTCTTTTCAATTTCCATCCCAAGAAACCTTACGAG 2076
QY 2380 GACTATCGCATACCTTCGCTTGAAGCCCTGGGAAATACAAAGTTTGCCTTTGGACTCAGATGAI 2439
Db 2077 GGTACAAAGTGGATGCGATTTCCTTGGGAAATACAGATAGCCCTGGACTCTGATGCT 2136
QY 2440 CCACCTTTTGGTGGCTTCGGGAGAAATGATCAATAAGCCGAATTTTCACT 2491
Db 2137 CTGCTCTCGTGACATGGAAGAGTTGGCCACGACGCTGGATCACTTCACT 2188

RESULT 12

US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: 2..190
; FEATURE:

; NAME/KEY: mat_peptide
; LOCATION: 191..2467
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..2470
; US-08-941-445A-16

Query Match 23.7%; Score 628.4; DB 3; Length 2763;
Best Local Similarity 59.7%; pred. No. 9.2e-173;
Matches 1177; Conservative 0; Mismatches 741; Indels 54; Gaps 5;

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Db 251 ATATACACCTGGACCCCAAGCTGGAGATATTCAGGACCAATTCAGGTACCGGATGAAA 310
QY 598 CAGTACAGAAACCTGAGGGAGCAATTCACAAGTATGAGGGTGGTTGGAGCCCTTTTCT 657
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QY 658 CGTGGTTATGAAAAATGGGTTTCACGCTAGTGTCTACAGATATCACTTACCGTAGTGG 717
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QY 718 GCTCTTGGTCCCGACGCTGCGCTCATTCGAGATTTCAACAATTTGGAGCGCAATGCT 777
Db 431 GCACCTGCTGCGAGAGGCGAGAGCTTATTTGGTCACTTCAATGACTGGATGGTGCRAAC 490
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QY 954 --TCCATATAATGGAATACATTAATGATCCACCGAAGAGAGAGATATATCTTCCAAAC 1011
Db 668 GCTCCCTATGATGGTGTTCATTTGGATCCTCTGCTCTGAAAGGTACACATTTAAGCAT 727
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QY 1132 AAGCTTGGGTACATGGCTGCAATTAATGCTATTCAGAGCAATTCCTTATACGCTAGT 1191
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QY 1483 TTGGATCGGTTCAAAATTTGATGGATTTAGATTTGATGGTGTGACATCAATGATGATATT 1542
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QY 1603 GATGTGATCGTGTGTGTAATCTGATGCTGGTCAACGATCTATTCATGGCTTTTCCCA 1662
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QY 1663 GATGCAATACCATGTTGAGAGTTTACGGGAATGCGGACATTTTGTGATTTCCCGTCCAA 1722
Db 1388 GAAGCAACTGTTGTTGCTGAAGATGTTTCAAGGATGCGGCTGCTTTCGCGGCCAGTTGAT 1447
QY 1723 GAGGGGGTGTGTTGCTTGTACTATCGCTGCTGATATGCAATGCTGTGATAAAGGATGAG 1782
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Db 1568 AACAGAGATATCTGAAATATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1627
QY 1900 GGTGAATAAATACTAGCATCTCTGCTGATGCAAGGATATGATGATGATGATGATGATGATG 1959
Db 1628 GCGGACAAACTATGCAATTTCTCTGATGCAAGGAAATGATGATGATGATGATGATGATG 1687
QY 1960 GATAGACGCTCAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2019
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QY 2020 GTAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2079
Db 1748 ATCAATATGCTTGGAGTGAAGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1807
QY 2080 CTTGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2139
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QY 2140 GGAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2199
Db 1835 GGAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1894
QY 2200 TTAAGATACGTTGGTTCGAAGATTTGACCGGCTTATGATGATGATGATGATGATGATGATG 2259
Db 1895 TTGCGGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1954
QY 2260 GAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2319
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RESULT 13

US-09-257-894-12

; Sequence 12, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lighner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarlan, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2772 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..2580
; US-09-257-894-12

Query Match 23.7%; Score 628.4; DB 4; Length 2772;
Best Local Similarity 59.7%; Pred. No. 9.2e-173;
Matches 1177; Conservative 0; Mismatches 741; Indels 54; Gaps 5;
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RESULT 15

US-09-257-894-25
Sequence 25, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lighner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ. ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

[illegible]

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1317.4	49.8	2418	9	US-09-938-842A-872
4	1290	48.8	2577	9	US-09-938-842A-337
5	1167.2	44.1	3039	10	US-09-792-127-3
6	1166.6	44.1	2559	10	US-09-792-127-1
7	578.2	21.9	2994	9	US-10-084-817-92
8	576.6	21.8	2955	9	US-09-918-624B-30
9	576.6	21.8	2955	10	US-09-880-107-2148
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11	136	5.1	604	10	US-09-925-300-453
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Sequence 111, App
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Sequence 22972, A
Sequence 1384, Ap
Sequence 19524, A
Sequence 25517, A

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ALIGNMENTS

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; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
; US-10-254-534-1

Query Match          97.5%; Score 2581; DB 9; Length 3074;
Best local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 301 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 360
DB 489 GTAGATAGTTCAACAATGGAACACGCTAGCCAGATTAAAACTGAGAACGATGACGTTGAG 548

QY 361 CCCTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTGTCCTTCATCACACAACTA 420
DB 549 CCCTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTGTCCTTCATCACACAACTA 608

QY 421 CACAGAGCTGTTAACTGGAGGACTCTAAACATTAATCTCTGAGACAAATTAAT 480
DB 609 CACAGAGCTGTTAACTGGAGGACTCTAAACATTAATCTCTGAGACAAATTAAT 668

QY 481 GATGAATCTGATAGGATCAGAGAGGGGATCCCTCCAGCTGGACCTTGGTTCAGAAGATT 540
DB 669 GATGAATCTGATAGGATCAGAGAGGGGATCCCTCCAGCTGGACCTTGGTTCAGAAGATT 728

QY 541 TATGAATAACCCCTTTTTCACAAACTATCGTCAACACCTTGTATACAGGTATTCACAG 600
DB 729 TATGAATAACCCCTTTTTCACAAACTATCGTCAACACCTTGTATACAGGTATTCACAG 788

QY 601 TACAAGAACTGAGGGAGCAATTGACAAAGTATGAGGGTGTGTTGGAAGCCCTTTTCTCGT 660
; 789 TACAAGAACTGAGGGAGCAATTGACAAAGTATGAGGGTGTGTTGGAAGCCCTTTTCTCGT 848
; 661 GGTATGAAAAAATGGTTCCTAGTCTAGTACAGGTATCACTTACCGTGGTGGCT 720
; 849 GGTATGAAAAAATGGTTCCTAGTCTAGTACAGGTATCACTTACCGTGGTGGCT 908
; 721 CTGGTCCCGCAGTCAGCTGCCCTCATTGGAGATTCAACAATTTGGGACGCAAAATGCTGAC 780
; 909 CTTGGTCCCGCAGTCAGCTGCCCTCATTGGAGATTCAACAATTTGGGACGCAAAATGCTGAC 968
; 781 ATTATGACTCGGAATGAATTTGGTCTGGAGATTTCCTGCCAAATTAATGCTGAGTGT 840
; 969 ATTATGACTCGGAATGAATTTGGTCTGGAGATTTCCTGCCAAATTAATGCTGAGTGT 1028
; 841 TCTCCTGCAATTCCTCATGCTCCAGAGTGAAGATAGTATGGACACTCCATCATGAGTGT 900
; 1029 TCTCCTGCAATTCCTCATGCTCCAGAGTGAAGATAGTATGGACACTCCATCATGAGTGT 1088
; 901 AAGGATTCCTATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCCTGATGAATTCCTATAT 960
; 1089 AAGGATTCCTATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCCTGATGAATTCCTATAT 1148
; 961 AATGGAATACATATATGATCCACCGAAGAGAGAGGTATATCTTCCAAACCCACGCGCA 1020
; 1149 AATGGAATATATATGATCCACCGAAGAGAGAGGTATATCTTCCAAACCCACGCGCA 1208
; 1021 AAGAAACCAAAAGTCCGTGAGAATATATGAATCTCATATTTGAATGAGTAGTCCGAGGCT 1080
; 1209 AAGAAACCAAAAGTCCGTGAGAATATATGAATCTCATATTTGAATGAGTAGTCCGAGGCT 1268
; 1081 AAAATTAACATACAGTGAATTTTGAAGATGAAGTCTTCTCCTGCATAAAAAGACTGGG 1140
; 1269 AAAATTAACATACAGTGAATTTTGAAGATGAAGTCTTCTCCTGCATAAAAAGACTGGG 1328
; 1141 TACAATCGGCTGCAAAATTTGGCTATTCAAGAGCATCTTATTAAGCTAGTCTTGGTAT 1200
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; 1449 TTGATGATGAAGCTCATGAGTAGAGTAATTTGTTCTCTCATGGACATGTTTCACAGCAT 1508
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; 1509 GCATCAATAATATCTTTAGATGGACTGAACATGTTGACTGCACCGATAGTGTACTTT 1568
; 1381 CACTCTGGAGCTCGTGGTTATPCTATTGGATGGGATTCGCCCTCTTTAACTATGGAAC 1440
; 1569 CACTCTGGAGCTCGTGGTTATPCTATTGGATGGGATTCGCCCTCTTTAACTATGGAAC 1628
; 1441 TGGAGGACTTACTTAGTATCTTCTCTCAATCCGAGATGGTGTGGATCCCTTCAAAATTT 1500
; 1629 TGGAGGACTTACTTAGTATCTTCTCTCAATCCGAGATGGTGTGGATCCCTTCAAAATTT 1668
; 1501 GATGGAATTTAGATTTGATGGTGTGACATCAATGATGATATATTCACCGAGGATATCGGTG 1560
; 1689 GATGGAATTTAGATTTGATGGTGTGACATCAATGATGATATATTCACCGAGGATATCGGTG 1748
; 1561 GGATTCAGTGGAACTACGAGGAATATCTTGGATTCGCAACTGATGATGGATGCTGTGTG 1620
; 1749 GGATTCAGTGGAACTACGAGGAATATCTTGGATTCGCAACTGATGATGGATGCTGTGTG 1808
; 1621 TATCTGATGCTGGTCAAGATCTTATTCATGCGCTTTTCCAGATGCAATTAACCATTTGT 1680
; 1809 TATCTGATGCTGGTCAAGATCTTATTCATGCGCTTTTCCAGATGCAATTAACCATTTGT 1868
; 1681 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTCCAGAGGGGGTGTGGCTTT 1740
; 1869 GAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTCCAGAGGGGGTGTGGCTTT 1840
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Db 1869 GAAGATGTTAGCGAATCCGACATTTTNTATTCCTCGTTCAAGATGGGGTGTGGCTTT 1928
Qy 1741 GACTATCGCTGCATATGSCAATTCCTGATATAAAGGATAGTTGCTCAAGAAACGGGAT 1800
Db 1929 GACTATCGCTGCATATGSCAATTCCTGATATAAAGGATAGTTGCTCAAGAAACGGGAT 1988
Qy 1801 GAGGATGGAGTGGGTGATATGTTTCATACACTGCACAAATAGAAAGATGTCGGAAAG 1860
Db 1989 GAGGATGGAGTGGGTGATATGTTTCATACACTGCACAAATAGAAAGATGTCGGAAAG 2048
Qy 1861 TGTGTTTCATACACTGAAAGTGCATGATCAAGCTCTAGTCGGTGTAAACATATAGCAATC 1920
Db 2049 TGTGTTTCATACACTGAAAGTGCATGATCAAGCTCTAGTCGGTGTAAACATATAGCAATC 2108
Qy 1921 TGGCTGATGGAACAGGATATGATGATTTATGCTCTGGATAGACCGTCAACATCATTA 1980
Db 2109 TGGCTGATGGAACAGGATATGATGATTTATGCTCTGGATAGACCGTCAACATCATTA 2168
Qy 1981 ATAGATCGTGGATAGCAATTCACAAGATGATTAAGGCTTGTAACTATGGGATTAGGAGGA 2040
Db 2169 ATAGATCGTGGATAGCAATTCACAAGATGATTAAGGCTTGTAACTATGGGATTAGGAGGA 2228
Qy 2041 GAAGGTTACCTAATTTTCATGGGAAATGAATTCGGCCACCTGAGTGGATGATTCCT 2100
Db 2229 GAAGGTTACCTAATTTTCATGGGAAATGAATTCGGCCACCTGAGTGGATGATTCCT 2288
Qy 2101 AGGCTCAACAACACCTCTCTGATGGCTCAGTATCCCGGAAACCAATTCAGTTATGAT 2160
Db 2289 AGGCTCAACAACACCTCTCTGATGGCTCAGTATCCCGGAAACCAATTCAGTTATGAT 2348
Qy 2161 AAATGACAGCGGAGATTGACCTGGGAGATGCAGAAATTAAGATACCGTGGGTGCAA 2220
Db 2349 AAATGACAGCGGAGATTGACCTGGGAGATGCAGAAATTAAGATACCGTGGGTGCAA 2408
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Db 2409 GAATTTGACCGGCTATGACGATTCCTTGAAGATAAATATGATTTATGACTTCAGAACAC 2468
Qy 2281 CAGTTATATACAGAAAGGATGAGGAGATAGGATGATTTGATTTGAAAAGGAAACCTA 2340
Db 2469 CAGTTATATACAGAAAGGATGAGGAGATAGGATGATTTGATTTGAAAAGGAAACCTA 2528
Qy 2341 GTTTTGTCTTTTAAATTTTCACTGSCACAAAAGTATTTCAGACTATCCGATAGCTGCTG 2400
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Db 2589 AAGCTTGAATAACAGGTTGCTTGGACTCAGATCCACCTTTTGGTGGCTTCGGG 2648
Qy 2461 AGAATTGATCATATATGCGGAATATTTCCACCTTTGAAGGATGGTATGATGATCCCTCGT 2520
Db 2649 AGAATTGATCATATATGCGGAATATTTCCACCTTTGAAGGATGGTATGATGATCCCTCGT 2708
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Db 2709 TCAATTTGTTGATGACCTTGTAAACAGCAGTGGTGTATGCACCTAGTAGAGCAAGAA 2768
Qy 2581 GAAGAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
Db 2769 GAAGAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2822

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RESULT 2

US-10-254-534-3

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; Sequence 3, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: LARSK, Lars

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; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PC/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-10-254-534-3

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Query Match 51.8%; Score 1369.8; DB 9; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 819 TCIGCCAAATAATGTGGATGGTTCTCTCGCAATTCCTCATGGTCCAGAGTGAAGATACG 878
Db 1 TCIGCCAAATAATGTGGATGGTTCTCTCGCAATTCCTCATGGTCCAGAGTGAAGATACG 60
Qy 879 TATGCACATCCATCAGTGTGAAGATTCATTCCTGCTTGGATCACTACTCTTTACA 938
Db 61 TATGCACATCCATCAGTGTGAAGATTCATTCCTGCTTGGATCACTACTCTTTACA 120
Qy 939 GCTTCTGTGAAATCCATATATATGAATATATATATATATATATATATATATATATATAT 998
Db 121 GCTTCTGTGAAATCCATATATATGAATATATATATATATATATATATATATATATATAT 180
Qy 999 TATCTTCCACACCCAGCGGCAAGAAACCAAGTCCGTGAGATATATATATATATATATAT 1058
Db 181 TATCTTCCACACCCAGCGGCAAGAAACCAAGTCCGTGAGATATATATATATATATATAT 240
Qy 1059 TGAATGAGTAGTCCGAGGCTTAAATTAATCATAGTGAATTTAGATGAAGTTCT 1118
Db 241 TGAATGAGTAGTCCGAGGCTTAAATTAATCATAGTGAATTTAGATGAAGTTCT 300
Qy 1119 TCCTCGCATAAAAAGCTTGGGTACAAATGGCTGCAAAATATGCTATTCAAGAGCATTC 1178
Db 301 TCCTCGCATAAAAAGCTTGGGTACAAATGGCTGCAAAATATGCTATTCAAGAGCATTC 360

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816 TCCAGAGAGGAGAGTATGTTTCAAACTCTCAACCAAGAGACCTAAGTCGCTAAG 875
1041 AATATATCAATCTCATATTTGAATAGTAGTCCCGAGCGCTAAAATTAAGTCATACGTGAA 1100
876 GATTATTAAGACACATGTTGGCATAGTAGCAGCGAACCAATAGTCAATAGTATGCTAA 935
1101 TTTTAGAGATCAAGTCTTCTCTCGCATAAATAAAAGCTTGGGTACATCGCTGCAAAATAT 1160
936 CTTTAGAGATGATGTTCTTCCCGCATCAAAAGCTTGGATATAAAGTGTTCAAATAT 995
1161 GGCATTAACAGACATCTTATTAAGCTAGTTTGGTTATCATGTCACAAATTTTGTTC 1220
996 GGCATTAACAGACATCTTATTAAGCTAGTTTGGTTATCATGTCACAAATTTTGTTC 1055
1221 ACCAAGCAGCGTTTTCGAGCGCCGAGGACCTTAAGTCTTTGATGATGAAGCTCATGA 1280
1056 CCCAAGCAGTCTGCTGGGACCCGAGAGAACTAAAATCACTAGATAGAGTCCAGCA 1115
1281 GCTAGGAATGTTTCTCTCATGGACATGTTTCAAGCCATGTCATCAATATATCTTTAGA 1340
1116 GTTAGGCTGTAGTCTGATGATATCGTTTCATAGCCATGCTTCAAAAACACATTTGA 1175
1341 TGGACTGAACATGTTTGACATCCACCGATGTTTACTTTCACCTCGGAGCTCGTGTTA 1400
1176 TGGACTGAACATGTTTGATGGAAGTATGCTCACTATTTTCACTCTGACCTCGGGGATA 1235
1401 TCATTGATCTGGGATTCGCGCTTAACTATGGAACCTGGAGCTAGTATGATATCT 1460
1236 CCAATGATGTTGGATTCAGGACTTTTCAATTAATGAGGAGCTGGGAAGTATACGATATCI 1295
1461 TCTCTCAAAATCGGAGATGGTGGTGGATCGGTTCAAAATTTGATGATTTAGATTTGATGG 1520
1296 CTTTCAAAATCGGAGTGGTGGTGGATGAGATCAAGCTTCAAGGATTTAGATTTGATGG 1355
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1641 TCTTATTCATGGCTTTTCCAGATGCAATTAACATTTGATGGAATGATCTGGAATGCTC 1700
1476 TATGATTCATGGCTTACCTTACCTGAAGGATTAACGTTGTTGAGATCTTATGTTATGCC 1535
1701 GACATTTTGTATCCCGTCAAGAGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1760
1536 AACATTTCTGATTCCTCTGCAAGATGTTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1595
1761 AATGCTGTATAACGGATTCAGTTGCTCAAGAAACGGATTCAGATTTGGAGATGGTGGTGA 1820
1596 CATAGCTGATAGTGGATGAAATGCTCAAGAGAGAGATGAAGACTGGCAATGGGCGCA 1655
1821 TATGTTTCATCACTGACAAATAGAAGATGGTGGGAAAGTGTGTTTCATACGCTGAAG 1880
1656 CATCATTTACACACTTTACCAACAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1715
1881 TCAATGATCAAGCTCTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1940
1716 TCAGATCAAGCTCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1775
1941 GTATGATTTATGGCTGAGATAGACCGTCAACATCAATTAATAGATCGTGGGATAGCAT 2000
1776 GTATGATTTATGGCTGAGATAGACCGTCAACATCAATTAATAGATCGTGGGATAGCAT 1835
2001 GCACAAAGATGATGAGCTGTAATGATGGATGAGGAGAGAGGTGATCTTAAATTTTCA 2060
1836 GCACAAATGATGAGCTGTAATGATGGATGAGGAGAGAGGTGATCTTAAATTTTCA 1895
2061 GGAATGATGAGCTGAGCTGAGTGGATGATTTCCCTAGGGCTGAACAAACACCTCTC 2120
1896 GGAACAGGATGAGCTGAGCTGAGTGGATGATTTTCCAGAGGCGGAGCAGCTCTTTC 1955

2121 TGATGGCTCAGTAATCCCGAAACCAATTCAGTTATGATTAATGCAGACGAGATTGA 2180
1956 TGATGGTAGCTGATTCCTGCAACAATTCAGTTATGATTAATGCAGACGAGATTGA 2015
2181 CTTGGAGATGAGTAATTTAAGATACCGTGGGTTGCAAGAAATTTGATGAGGCAATGA 2240
2016 TCTTGGGATGAGTAATTTAAGATACCGTGGGTTGCAAGAAATTTGATGAGGCAATGA 2075
2241 GTATCTTGAAGATTAATTTAAGATACCGTGGGTTGCAAGAAATTTGATGAGGCAATGA 2300
2076 ACATCTTGAAGATTAATTTAAGATACCGTGGGTTGCAAGAAATTTGATGAGGCAATGA 2135
2301 TGAAGGATAGGATGATTTGATTTGAAAAAGAAACCTAGTTTGTCTTTAATTTTCA 2360
2136 CGAAGCAGATAGATTAATTTGATTTGAAAAAGAAAGGTGATCTGCTTTTAACTTTCA 2195
2361 CTGACAAAAAGCTTATCAGACTATCGATAGCTGCTGAGCTTGAAGCTTGAATAATACAGGT 2420
2196 CTGGACACGACGCTACITTTGATTTCCGATTTGGTTCCTCAAGCTTGAATAATACAGGT 2255
2421 TGCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATTTGATTAATACAGGT 2480
2256 CGTATTTGACCTGCGACGATCTCTTTTGGTGGATTAATAGGCTTCGATCGCAAGGCGA 2315
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2316 GTACTTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2375
2541 TTGTAACACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2579
2376 GTGTAGAACCCCGTGGTTTATGCTTTAGCAAAACACCA 2414

RESULT 4

US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Query Match 48.8%; Score 1290; DB 9; Length 2577;
Best local similarity 76.1%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 500; Indels 0; Gaps 0;

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Db 443 AGAGGAAGATTCCACCTCCCTGGAGATGGGAAGAAATATATGATGATGATGATGATGATG 502
QY 563 CAAACTATCGTCAACACTTGTATACAGGTTTACAGATGATGGCAGTACAGAAACTCAGGAGCAA 622
Db 503 ACAGTATCTGATCATCTTGATACCGATATGGCAGTACAGAAACTCAGGAGAA 562

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QY 803 GTGCTGGGAGATTTTCTGCCAAATATGTTGATGTTGTTCTTCCCTGCAATTCCTCATGGT 862
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Db 1343 ATTGGATGTTGGATTTCCGCTCTTAACTATGAAAGCTGGAGGTTACTTAGGATCTTC 1402
QY 1463 TCTCAATGCGAGATGTTGGTGGTGGTTCATTAATTTGATGATGATTTAGATTTGATGGT 1522
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Db 1823 ATGATCAAGCTTCTTGGGACAAACGATAGCTTTCTGCTTATGGATAGGACATGT 1882
QY 1943 ATGATTTATGCTCTGGATAGACCGTCAACATCATTAATAGATGCTGGGATAGCATTCG 2002
Db 1883 ATGATTTATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1942
QY 2003 ACAAGATGATTTAGGCTTTGTAATATGAGGATTTAGGAGGAGAGGATTAATTTTCAATG 2062
Db 1943 ACAAAATGATCCGCTCATTTACGATGGATGGGTTGGGAGAAAGGATACCTCAATTTCAATG 2002
QY 2063 GAAATGATTCGGCCACCTCAGTGGATGATTTCCCTAGGCTGAAACACACCTCTCTG 2122
Db 2003 GAAACGAATTTGGACACCCAGATGGATGGATTTCCCAAGGACCGACCGACCTTCTG 2062
QY 2123 ATGCTCAGTATCCCGGAAACCAATTCAGTTATGATTAATGATGAGAGGAGATTTGACC 2182
Db 2063 ATGCAAGTCTATCCCTGGGATTAATGCTAGTATGATTAATGCTAGTGGTGGTGGTGG 2122
QY 2183 TGGGAGATGCAAGATTTTAAAGATACCGTGGGTTGCAAGATTTGACCGGCTATGCAAT 2242
Db 2123 TGGGAGATGCAAGATTTTAAAGATACCGTGGGTTGCAAGATTTGATCGGCAATGCAAA 2182
QY 2243 ATCTTGAAGATTAATATCAGTTTATGACTTCAGAACCCAGTTCATATCAGCAAGAGATG 2302
Db 2183 ATCTAGAGGACCTATGTTTTCATGACTTCAGACACCAAGTTCATATCAGCAAGAGATG 2242
QY 2303 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2362
Db 2243 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2302
QY 2363 GGACAAAAGCTATTCAGACTATCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2422
Db 2303 GGACCAACAGTTACTCTGACTACCGTATCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2362
QY 2423 CTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGATTCATATGATGCGGAT 2482
Db 2363 TTTTGGACTCTGATAACTCTTTATTTGGAGCTTCAACCGCTAGATGACTCCGCGGAGT 2422
QY 2483 ATTTTCACTTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2542
Db 2423 TTTTCACTCTGATGGAAGGACGACGATAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2482
QY 2543 GTAAACAGCAGTGGTCTATGCACTAGTAGCAAGAAAGAGAGAGAGAGAGAGAGAGAG 2592
Db 2483 GCAGAACCGCTGATGTTTACGCTGAGTATGATGATGATGATGATGATGATGATGATGAA 2532

RESULT 5

US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US2002002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIB
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23

1585 TCGGGCATCCTGAATGGATAGACTTTTCAAGAGGCCCAACAGTACTTCCAAAGTGGTAAGT 1644
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2132 TAATCCCGGAAACCAATTCAGTTATGATAAATGACAGCGAGATTTGACCTGGGAGATG 2191
2191
1645 TCATCCCGGAAACCAACAGATTCAGCAAAATGCGGTGGAAGATTTGACCTGGGTGATG 1704
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2192 CAGAATATTTAAGATACCGTGGTGGTGAAGAAATTTGACCGGCTATGAGTATCTTGAAG 2251
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1705 CAGAAATTTCTTAGGTATCATGTATGACAGCAATTTGATCAGCAATGCAATCTTGAGG 1764
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2252 AFAAATATGAGTTTATGACTTCAGAACACCACTTCATATCAGAAAGGATGAGGAGATA 2311
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1765 AAAAATATGTTTATGACATCAGACCAACCACTAGCTATCTCGAAACATGAGGAAGATA 1824
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2312 GGATGATGTTATTTGAAAAGAAACCTAGTTTGTGCTTAAATTTTCACTGGACAAAAA 2371
2371
1825 AGGATGATCGTGTGTTGAAAAGGGGACTTGGTATTTGTGTTCACTTCCACTGGAGTAGTA 1884
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2372 GCTATTCAGACTATTCGCATAGCTTGCCTGAAGCCTGGAAATACAAAGTTGCTTGGACT 2431
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1885 GCTATTTCCGACTACCGGTGCGCTCTTTAAAGCCTGGGAAGTACAAAGTGGTCTTAGACT 1944
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2432 CAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCAATATCCGAATATTTCACT 2491
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2004
2492 TTGAAGGATGTTATGATGATGCTGCTCTGCTTCAATTTATGTTGTTATGCTTGTAAACAG 2551
2551
2005 CTGACTGCCACATGACAAAGGCCCAATTCATTCGATGTTACACTCCTTAGCAGAACCT 2064
2064
2552 CAGTGGCTATGCTAGTACGAAAGGAGAAAGAAAGAAAGAAAG 2596
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2065 GTGTGTCTATGCTCCATGAACATAACAGCAAGTGCAGCATACG 2109
2109

RESULT 7

US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 92
; LENGTH: 2994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CHI
US-10-084-817-92

Query Match 21.9%; Score 578.2; DB 9; Length 2994;
Best Local Similarity 57.5%; Pred. No. 6.2e-149;
Matches 1164; Conservative 0; Mismatches 813; Indels 48; Gaps 5;

QY 544 GAAATAGACCCCTTTTGACAAACTATGTCACACACCTTGATTAACAGTATTCACAGTAC 603
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DB 215 GAGATCGACCCGTACTTTGAAGCCCTAGCCCGTGGACITTCACGCGCAGGATTAAGCAGTTT 274
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QY 604 AAGAACTAGGGAGGCAATTGACAGTATGAGGCTGGTTTGGAGGCTTTTTCGTGGT 663
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DB 275 AGCCAAATTTTGAAGAACATTTGGAGAAATGAAGGTGGTATTTGATAAGTTTTCAGAGCG 334
334

QY 664 TATGAAAAATGGGTTTTCACITCGTACTGCTACAGGTATACACTTTACCCT---GAGTGGCT 720
720
DB 335 TATGAATCATTTGGCGTCCACAGATGCTGTGATGGTGTGTTATFACTGCAAGAAATGGCC 394
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QY 721 CTTGGTCCAGTCACTGCCCTCATTTGGAGATTTCAACAATTTGGACGCAAAATGCTGAC 780
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DB 395 CCGGAGCAGAGGAGGATTTTCTACTGGAGATTTTAAATGGTGGAAATCCATTTTCGTAC 454
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QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAAAATATATGGATGGT 840
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DB 455 CCATACAAAAAAGTGGATTTGAAATGGAGCTGTATATCCCAACAAGAGATATAA 514
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QY 841 TCTCCTGCAATTTCTCATGTTGGTCCAGAGTACAGTACAGTATGAGCACTCCATCAGGTG-- 898
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DB 515 TCTGTACTGCTGCTCATGGATCCAAATTTAAAGGTAGTTATTTACTAGTAAAGCGGAGAG 574
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DB 575 AATCTGTATCGTATTTTCACTGGGCAAGATGTTGGTTCGTGAAGGTGATATGTAAT 634
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DB 635 TATGATGATACACTGGGATCC-----AGAACACTCATATCAGTTTAAGCATTTCCACA 688
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DB 689 CCAAGAAACCAAGTCCGCTGAGATATATGAAATCTCATTTGGAAATTTCTTCCCATGAA 748
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QY 1078 CCTAAATTAACATCACTACCTGGAATTTTAGAGATGAAGTTCTTCTCGCATATAAAAGCTT 1137
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QY 1558 GTGGATTCAGTGGAACTACAGGAATCTTTTGGACTGCGCAACTGATGATGATGATGAT 1617
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DB 1229 CAAGGTTTCTCAGGTGATTAAGTGAATTTTCGGACTACAGTACAGTACAGTACAGTAC 1288
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QY 1618 GTGATCTGATGCTGGTCAACAGTCTTATTCATGGCTTTTCCAGATGCAATTAACAT 1677
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QY 1678 GGTGAAGATTTAGCGGAATCCGACATTTTCTATTCCTCCCAAGAGGGGGTGTGGC 1737
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DB 1349 GCTGAGGATGATCAGGAATGCCAGCTCTGTGCTCTCCAAATTTCCAGAGGGGGTGGT 1408
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1794

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Db 1409 TTTGACATATCGACTAGCCATGGCAATTCACAGATAAGTGGATTCAGCTACTTAAAGAGTTT 1468
Qy 1795 CGGATGAGGATGGAGAGTGGGTGATATTTGTTCAATACATGACATAAGAGATGGTGC 1854
Db 1469 AAAGATGAAGCTGGAACATGGGGATATATATACACGCTTCACAAACAGCGCTACCTT 1528
Qy 1855 GAAAGTGTGTTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
Db 1529 GAAAGTGCAATGCTTATGACAGAGCCATGATCAGGCATGTTGGGGATAAGTCGCTG 1598
Qy 1915 GCATTCGTGCTGATGGAAGAGATATATGATGATTTATGGCTCTGGATAGACCGCTCAACA 1974
Db 1589 GCATTTGGTGTGATGGATGCGGAATGTATACAAACATGATGCTCTGACCTCTTTACT 1648
Qy 1975 TCATTATAGATCGTGGATAGCATTCGACAGATGATAGGCTGTGAACCTATGGGATTA 2034
Db 1649 CCAGTTATGATCGTGGAAATACAGCTTCATAAAATGATGACATACCATGGGCTT 1708
Qy 2035 GGAGGAGAGGTCACCTAAATTTTCATGGGAAATGAATTCGGCCACCCCTGAGTGGATGAT 2094
Db 1709 GGTGGAGAGGCTATCTCAATTCATGGTAAATGAATTTGGGCATCCCTGAATGCTTAGAC 1758
Qy 2095 TTCCTAGGGCTGAACACACCTCTCTGATGGCTCAGTAATCCCGGAAACCAATTCAGT 2154
Db 1769 TTCACAGAGAAA-----GGAAATAAATCAGAGT 1795
Qy 2155 TATGATAAATCAGACGAGATTTGACCTGGGAGATGAGAAATATTTAAGATACCGTGGG 2214
Db 1796 TACCATATGCGCAGCGGAGCTTTCATTTAACTGACGACGACCTTCTTCGTACTAAGTTC 1855
Qy 2215 TTGCAAGAAATTTGACCGGCTATGACGATATCTTCAAGATAAATATGAGTTTATGACTTCA 2274
Db 1856 CTAATAATTTTGACAGGATATGAATAGATTTGGAAGAAATATGTTGGCTTGCAGCT 1915
Qy 2275 GAACACAGATTCATATCAGAAAGGATGACGAGATAGGAGATGATGATTTGAAAGGA 2334
Db 1916 CCACAGGCTACGTGAGTGAAGAAACATGAAGGCAATAGATCATGTCCTTTTGAAGACA 1975
Qy 2335 AACCTAGTTTTGCTTAAATTTTCACTGGCAAAAGCTATTCAGACTATCGGATAGCC 2394
Db 1976 GGTCTTCTTTTCATTTTCACTTCCATCCACAGAGAGCTACACTGACTACCGATTGGA 2035
Qy 2395 TGCCTGAAGCCTGGAAATAACAAGTGGCTTGGACACAGATGATCCACTTTTGGTGGC 2454
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Qy 2455 TTCGGGAGAAATGATCAATGCGGAATATTTCACTTTGAAGGATGCTATGATGATGCT 2514
Db 2096 CATCAGAGACTGGACACGACCTGACTTTTTTTCTGAGGCTTTTGAACATAATGGGCGT 2155
Qy 2515 CCTCGTTCAATATGGTGTATGACCTTGTAAAACAGAGTGGTC 2559
Db 2156 CCTATTCTCTTTTGGTGATACATCCAGAGAGATGGCCCTCATC 2200
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RESULT 8

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US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
; FILE REFERENCE: PA-0033 US
; CURRENT APPLICATION NUMBER: US/09/918,624B
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2955
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

Query Match      21.8%; Score 576.6; DB 9; Length 2955;
Best Local Similarity 57.4%; Pred. No. 1.7e-148;
Matches 1163; Conservative 0; Mismatches 814; Indels 48; Gaps 5;

Qy 544 GAAATAGACCCCTTTTTCACAAAATATCTCGTCAACACTTGTATGATACAGTATTCACAGTAC 603
Db 187 GAGATCGACCCGCTACTTTGAAGCCCTTACGCCCTGGACCTCCAGCGCAGGTATAAGCAGTTT 246
Qy 604 AAGAACTAGGGAGGCAATTGACAAAGTATGAGGTGCTTTGGAGGCTTTTCTCGTGGT 663
Db 247 AGCCAAATTTGAAGACATTTGGAGAAATGAAGTGGTATGATAGATTTTCCAGAGGC 306
Qy 664 TATGAAAAATTTGGTTTTCACCTGCTAGTCTCAGAGTATCATTACCTGTT--GAGTGGGCT 720
Db 307 TATGAATCATTTGGCGTCCACAGATGCTGCTGATGGTGTATATCTCCAAAAGAAATGGGCC 366
Qy 721 CTTGTCGCCAGTCACTGCTCTCATTTGGAGATTTCAACAAATGGGACGCAAAATCTCGAC 780
Db 367 CCGGAGCAGAGAGGATTTTCTTACTGGAGATTTAAGGTTTGAATCCCATTTTCGTAC 426
Qy 781 ATTATGACTCGGAATGAATTTGGTCTCTGGGAGATTTTCTGCCCCAAATAATGTTGATGGT 840
Db 427 CCATACAAAAAACTGGATATGGAATGGGAGCTGATATCCCAACCAAGCAGATAAA 486
Qy 841 TCTCCTGCAATTCCTCATGTTGGTCCAGAGTGAAGTACGTATGAGACATCCATCAGCTG-- 898
Db 487 TCTGTACTCGTGCCTCATGGAATCCAAATTAAGGTAGTATTACTAGTAAAGCGGAGAG 546
Qy 899 -TTAAGGATTCATTCCTGCTGGATCACTACTCTTTTACAGCTTCTCTGATGAAATTCGA 957
Db 547 ATCTGTATGCTATTTACCGTGGGCAAGATATGTTGGTTTCGTAAGGTGATTAATGTGAAT 606
Qy 958 TATATGGAATACATTAATGATCCACCGCAAGAGAGAGAGTATATCTTCCACACCCACGG 1017
Db 607 TATGATTGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCATTTCCAGA 660
Qy 1018 CCAAGAAACCAACTCCCTGAGATATATGAACTCATATGTTGGAATGAGTAGTCCGGAG 1077
Db 661 CCAAGAAAGCCACGGAGTCTAAGAAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
Qy 1078 CCTAAATTAACCTCATAGTGAATTTTGAAGATGAAGTCTCTCCCTCGCATATAAAAGCTT 1137
Db 721 GAAAAGTAGCTTCTTTAATAACATTTTACATGCAATGTACTACCAAGATCAAGGCCCT 780
Qy 1138 GGGTACAATGCGCTGCAAAATATAGCTATTTCAAGAGCATTCCTATTAGCTAGTTTGGT 1197
Db 781 GGATCAACTGCTCAGTTGATGGCAATCATGAGCATGCTTACTATGCCAGCTTTGGT 840
Qy 1198 TATCATGTCACAAATTTTTCACCAACGACCCGCTTTGGAAACCCGACACCTTAAG 1257
Db 841 TACCAATCAACAAGCTTCTTTGACGCTCCACCGGTTATGGAAACCTTGAAGAGCTTACAA 900
Qy 1258 TCTTTGATTTGATAAGCTCATGAGCTAGGAATTTGTTCTCTCATGACATTTGTTCCACAGC 1317
Db 901 GAACTGGTAGACACAGCTCATTTCCATGGGTATCATAGTCTCTTAGATGTGTACACAGC 960
Qy 1318 CATGATCAAAATTAATCTTTAGATGACATGAACATGTTGATGCTGACCGATAGTTGTTAC 1377
Db 961 CATGCTTCAAAAAATTCAGCAGATGGAATGGAATGATTTGATGGGACAGATTCCTTGTTAT 1020
Qy 1378 TTTCACTCTGAGGCTGCTGGTTTATCATTTGGAATGTTGGGATTCCTGCTTTAACTATGGA 1437
Db 1021 TTTCAATCTGGACCTAGAGGAGCTCATGATCTTTGGGATGAGAGATGTTTCCCTACTCC 1080
Qy 1438 AACTGGAGGTACTTAGGTATCTTCTCTCAAAATGGAGATGCTGTTGGTGGATTCGTTCAAA 1497
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Db 1081 AGCTGGGAAGTTTAAAGATTCCTCTGTCACAAATAAGATGGTGGTGGAGAATATCGC 1140
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Db 1141 TTTGATGATTTGATGGTGTGATGGTGTGATGATGATGATGATGATGATGATGATGATG 1200
QY 1558 GTGGGATTCACGTGGGAACATACAGGAATGATTTGGACTCGCACTGCGAATGATGATGATG 1617
Db 1201 CAGGTCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1618 GTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
Db 1261 ACTTACCTCATGTTGGCAATCATTTGGTGTACACGTGTGTCGGATCTATATACAAATA 1320
QY 1678 GTGGAAGATGTTAGCGGAATGCGGACATTTGATGATGATGATGATGATGATGATGATG 1737
Db 1321 GCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1738 TTTGACTATCGGCTCATATGCAATGCTGATGATGATGATGATGATGATGATGATGATG 1794
Db 1381 TTTGACTATCGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1440
QY 1795 CGGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1854
Db 1441 AAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY 1855 GAAAGATGTTTATAGCTGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1914
Db 1501 GAAAGATGTTTATAGCTGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1915 GCATTTCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1974
Db 1561 GCATTTCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1975 TCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2034
Db 1621 CCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 2035 GGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2094
Db 1681 GTTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 2095 TTCCCTAGGCTGAACAACACCTCTGATGCTCAGTAAATCCCGGAAACCAATTCAGT 2154
Db 1741 TTCCCAAGAAA-----GGAAATAGAGAGT 1767
QY 2155 TATGATAATGACAGCGAGATTTGACCTGGGAGATGAGATAATTTAAGATACCGTGGG 2214
Db 1768 TACCATTTGCGAGCGGCGAGTTTCATTTAACTGACGAGACCTTCTTCGCTACAGTTC 1827
QY 2215 TTGCAAGAAATGACCGGCTATGAGTATCTTGAAGATAAATATGATGATGATGATGATG 2274
Db 1828 CTAAATAATTTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1887
QY 2275 GAACACCAAGTTTATCATACGAAAGATGAAGGAGATAGGATGATGATGATGATGATGATG 2334
Db 1888 CCACAGGCTACGTGAGTGAAGACATGAAGCATGAAGCATGAAGCATGAAGCATGAAGCAT 1947
QY 2335 AACCTAGTTTGTCTTAAATTTTCACTGGCAAAAAGCTATTCAGACTATGCGATAGCC 2394
Db 1948 GGTCTCTCTTCAATTTTCACTTCCATCCAAAGCAAGAGCTACACATGACTACCGAGTTGA 2007
QY 2395 TGCCCTGAAGCTGGAAATACAGGTTGCCCTGGACTCAGATGATGATGATGATGATGATG 2454
Db 2008 ACAGACTTGGCAGGGAATCAAAATTCGTAGATTCAGATGATGATGATGATGATGATGATG 2067
QY 2455 TTCCGGGAATGATCATAATGCCGAATATTTCACTTTTGAAGGATGATGATGATGATGATG 2514
Db 2068 CATCAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAATAGGCGT 2127
QY 2515 CCTCGTTCAATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2559
Db 2128 CCTTATCTCTTTTGGTGTACATTCGAAGCAGAGTGGCCCTCATC 2172

RESULT 9

US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2148
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

Query Match

Best Local Similarity 21.8%; Score 576.6; DB 10; Length 2955;

Matches 1163; Conservative 0; Mismatches 814; Indels 48; Gaps 5;

QY 544 GAAATAGACCCCTTTTGACAAATATCGTCAACACCTTGATTACAGGTATTCACAGTAC 603
Db 187 GAGATCGACCCGTACTTGTAGCCCTGACCGGTGGAGCTTCCGCGCAGGTATAGCAGTTT 246
QY 604 AAGAACTGAGGAGGCAATGACAAGTATGAGGGTGGTGGAGCCCTTTTCGTGTT 663
Db 247 AGCCAAATTTTGAAGAACATTTGAGAAATGAGGTGGTATGATAAGTTTTCCAGAGGC 306
QY 664 TATGAAAAATGGTTTCACTCGTAGTGTCTACAGGTATCACTTACCGT---GAGTGGGT 720
Db 307 TATGAATCATTTTGGGTCCACAGATGTGCTGATGGTGTATATATCCCAAGAAATGGGCG 366
QY 721 CTGTGTCACCTGACCTGCTCAATTTGAGATTTTCAACAAATTTGGACCAATGCTGAC 780
Db 367 CCGGAGCAGAGGAGTCTTCTACTGGAGATTTTAAAGTTGGATCCATTTTCGTAC 426
QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATATATGAGTGT 840
Db 427 CCATACAAAAAATGATTTATGAAAATGGAGCTGATATCCCAAGCAGATAAA 486
QY 841 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGTACGTATGGACACTCCATCAGGTG-- 898
Db 487 TCTGTACTGTCCTCATGGATCCAAATTAAGAGTAGTTATTACTAGTAAAGCAGAGAG 546
QY 899 -TTAAGGATTCCTCTGCTGATCAACTACTCTTTACAGCTTCTGATGAAATTCGA 957
Db 547 ATCTGTATCGTATTTTCCCGTGGCAAGATATGTTCTGTAAGGTGATATATGTAAT 506
QY 958 TATAATGGAATACATATGATCCACCGAAGAGAGAGATATATCTTCCACACCCACGG 1017
Db 607 TATGATTGGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCATTC 660
QY 1018 CCAAGAAACCAAACTGCTGATGATATATGATCTCATATTTGGAATGAGTGTAGTGGAG 1077
Db 661 CCAAGAAACCAAGAGTCTAAGAAATTTATGAATCTCATGTGGAAATTTCTCCCATGAA 720
QY 1078 CCTAAATTAACATCACTGATGATTTTATGAGATGAGTTCTTCTCTCGCATAAAGCTT 1137
Db 721 GGAAGAGTAGCTTCTTATTAACATTTTATCATGCAATGTACTACCAAGAAATCAAGCCTT 780

QY 1138 GGTACAAATGCGCTGCAAAATATATGGCTATATCAAGAGCAATCTTATTACGCTAGTTTGGT 1197
Db 781 GGATACAACTGCATTCAGTTGATGCAATCATGAGCATGCTTACTATGCCAGCTTGGT 840
QY 1198 TATCATGTCACAAATTTTTCACCAAGAGCGCGTTTGGAAACCGCGAGCACCTTAAG 1257
Db 841 TACCAAAATCAAAAGCTCTTTCGAGCTTCCAGCGGTTTGAAGAACCTGGAAGAGTACAA 900
QY 1258 TCTTTGATGTATAAGCTCATGAGCTAGGATTTGTTCTTCATGAGCAATGTTTCACAGC 1317
Db 901 GAACCTGGTAGACACAGCTCAITCCATGGTATCATAGTCCCTTAGATGTGTACACAGC 960
QY 1318 CATGATCAAAATATCTTAGATGAGTCAATGATGTTGACTGCAACGATAGTTGTTAC 1377
Db 961 CATGCTTCAAAAATATACGACAGATGATTAATGTTTGTGGACAGATCCCTGTTAT 1020
QY 1378 TTCTACTCTGGAGCTCGGTGTTATCATTTGGATGTGGATTCGCGCTCTTAACTATGA 1437
Db 1021 TTTCTATCTGGACCTTAGAGGACTCATGATCTTGGGATAGCAGATTTGTTGCCFACCTC 1080
QY 1438 AACTGGGAGTACTTAGTATCTTCTCTCAATGGAGATGGTGTGGATGCGTTCAAA 1497
Db 1081 AGCTGGGAAGTTTAAAGATCTCTCTGTCAAACATPAAGATGGTGTGGAAGATATCGC 1140
QY 1498 TTTGATGATTTAGATTTGATGCTGCTGACATCAATGATGTATATTCACACGGATATCG 1557
Db 1141 TTTGATGATTTGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1200
QY 1558 GTGGGATCTACTGGGAACCTACGAGGAATCTTTGGACTCGCAACTGATGTGATGCTGT 1617
Db 1201 CAAGTCTTCTCAGTGATTCAGTGAATATTTCCGACACAGATGATGATGATGATGATG 1260
QY 1618 GTGATCTGATGCTGGTCAACGATCTTATTAATGAGGCTTTTCCAGATGCAATTAACAT 1677
Db 1261 ACTTACCTCATGTTGGCAATCATTTGCTTCAACGCTGTGTCCGATTTCTATAAATA 1320
QY 1678 GGTGAGATGTTAGCGGAATGCGGACATTTGTATTCGGTCCACAGAGGGGTGTGGC 1737
Db 1321 GCTGAGATGATATCAGGAATGCCAGCTCTGTGCTCTCCAAATTTCCAGGGGGGGGTGT 1380
QY 1738 TTTGACTCTGGCTGATATGCAATTCGTATAACGATGATGATGCTCA- --AGAAA 1794
Db 1381 TTTGACTATCGACTAGCCATGCAATTCAGATAGTGTGATTCAGTACTTAAAGATTT 1440
QY 1795 CGGATGAGGATGAGAGTGGGTGATATTTGTCATACACTGACAAATAGAGATGGTGC 1854
Db 1441 AAAGATGAAGCTGGAACATGGCGATATAGTATACAGCTCACAAACAGGGGCTACCTT 1500
QY 1855 GAAAGTGTGTTTCATACGCTCAAAATCATGATCAGCTAGTCTGATGATGATGATGAT 1914
Db 1501 GAAAGTGTGTTTCATGAGAGGCTATGATGAGGATGATGATGATGATGATGATGATGAT 1560
QY 1915 GCATTCGGCTGATGACAAAGATATGATGATTTATGGCTCTGGATAGACCGTCAACA 1974
Db 1561 GCATTTGTTGATGATGCGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1975 TCATTAATAGATGTTGGATGACATTCGACAGATGATGATGATGATGATGATGATGATGAT 2034
Db 1621 CCAGTATATGATGCTGGAATACAGCTTCATAAATGATTCGACTCATTCAGCATGGGCT 1680
QY 2035 GCAGGAGAGGTACTTAATTTTCATGGAATGAATTCGGCCACCCCTGAGTGGATGAT 2094
Db 1681 GGTGAGAGGCTATCTCAATTTTCATGGGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 2095 TTCCCTAGGCTGAAACAACACCTCTCTGATGCTCAGTAATCCCGGAAACCAATTCAGT 2154
Db 1741 TTCCCAAGAAA- -----GGAATAATCAGAGT 1767
QY 2155 TATGATAATGACAGACGGAGATTTGACCTGGGAGATGAGATATTTAAGATFACCGTGG 2214
Db 1768 TACCATTATGCGCGGCGAGTTTCATTTAACTGACGACGACCTTCTTCGCTTACAGTTC 1827
QY 2215 TTGCAAGATTTTGACCGGCTATGACGATCTTGAGATATGATGATGATGATGATGATGAT 2274

Db 1828 CTAAATAATTTTACAGGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1887
QY 2275 GAACACCACTTCATATCACGAAGGATGAAGGATGAGTATGATGATGATGATGATGATGAT 2334
Db 1888 CCACAGGCTAGCTGAGTGAAGAAACATGAAGCAATAGATCATTCCTTTTGAAGAGCA 1947
QY 2335 AACCTAGTTTTCCTTTTAAATTTTCACTGGACAAAGATGATTCAGACATTCGATAGCC 2394
Db 1948 GGTCTTCTTTTTCATTTTCACTTCCATCCAAAGAGCTACACTGACTACCGAGTTGA 2007
QY 2395 TCCCTGAAGCTGGAAATACAAAGTTGCTTGGACTGAGATGATTCAGACATTCGATAGCC 2454
Db 2008 ACAGCATTTGCCAGGAAATTCAAAATTTGCTAGATTCAGATGCGCGGAATATGAGGG 2067
QY 2455 TTCGGGAGAAATTCATATAATCCGAATATTTCACTTTTGAAGGATGATGATGATGATGAT 2514
Db 2068 CATCAGACACTGGACACAGCACTGACTTTTTCCTGAGGCTTTTGAACATATGCGCT 2127
QY 2515 COTCTTCAATTTATGCTGATGACCTTGTAAACAGCAGTGGTC 2559
Db 2128 CCTATCTCTTTTGTGTACATTCACAGCAGATGGCCCTCATC 2172

RESULT 10
US-09-770-149-955/c
; Sequence 955, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Any
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-955

Query Match 9.7%; Score 257.8; DB 10; Length 602;
Best Local Similarity 75.1%; Pred. No. 9.3e-61;
Matches 322; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 2151 CAGTTATGATATAATTCAGACGAGATTTGACCTGGCAGATGATGATGATGATGATGATGAT 2210
Db 602 CAGTTATGATATAATTCAGACGAGATTTGATCTGGGATGAGATGATGATGATGATGATGAT 543
QY 2211 TCGGGTGCAGAAATTTGACCGGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 2270

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Db 542 CGGACTACAAGATTGATCAGCAATGCAACATCTTGAAGAGAAATACGGTTTATGAC 483
QY 2271 TTCAGACACAGATTTCATATCAGCAAGAGATGAGGATAGGATGATGATTGATAAA 2330
Db 482 TTCGGAGACCAATTCATATCAGCAAGAGATGAGGATAGGATGATGATTGATAAA 423
QY 2331 AGGAACACTACTTTTTCCTTAATTTTCACTGGCAAAAGCTATTCAGACTATCGCAT 2390
Db 422 AGGTGACTGCTCTTGTCTTAATTTTCACTGGCAAAAGCTATTCAGACTATTCAGCAT 363
QY 2391 AGCCTGCTGAAGCTGGAAATACAGGTTTGCCTTGGACACAGATGATCCTTTTGG 2450
Db 362 TGGTTCCTCCAGCCTGGAAATATAGATCGTATTTGGACTCGGAGATCCTCTTGG 303
QY 2451 TGGCTTCGGGAGATTCATATATGCGGATATTTTCCCTTGAAGATGGTATGATGA 2510
Db 302 TGGATTCAAATAGGCTCGATCGCAAGGCGAGACTTTCACITATGATGCTTATAGGACA 243
QY 2511 TCGTCCCTCGTTCAATTAATGTTGATGCAACCTTGTAAACAGCAGTGGTCTATGACTAGT 2570
Db 242 ACGACCTGCTCCTTCATGCTGTTATGCAACCGGTAGAACCCGCGTGTATGCTTTAGC 183
QY 2571 AGACAAGA 2579
Db 182 AAACACGA 174

RESULT 11
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (517)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (567)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453
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Query Match 5.1%; Score 136; DB 10; Length 604;
Best Local Similarity 58.8%; Pred. No. 4.6e-27;
Matches 254; Conservative 1; Mismatches 17; Indels 6; Gaps 1;

QY 903 GGATTCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCATATAA 962
Db 47 GTATCGATTTCACCGTGGCAAGATGTTGGTTCGTGAAGGTGATAATGGAATTATGA 106
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QY 963 TGGAAATACATATGATCCACCCGAAAGAGAGAGAGATATATCTTCCAAACACCCAGGCCAAA 1022
Db 107 TTGGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCATTTCCAGACAAA 160
QY 1023 GAAACCAAGTCGCTGAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGCCCTAA 1082
Db 161 GAAGCCAGGAGCTTAAGAAATTTAATCTCATCTGGAATTTCTTCCCATGAAGGAAA 220
QY 1083 AATTAACCTACACGCTGAATTTTAGAGATGAAGTCTTCTCGCATATAAAAGCTTGGGTA 1142
Db 221 AGTACCTCTTATAAACAATTTTACATGCAATGATACCAAGAAATCAAGAGCCTTGGATA 280
QY 1143 CAATCGGCTGCAAAATATATGGCTATTTCAAGAGCAATTTTATACGCTAGTATTTGGTATCA 1202
Db 281 CAACATGATTCAGTTGATGGCAATCATGAGCATGCTTACTATGCGAGCTTTGGTTTACCA 340
QY 1203 TGTCAAAATTTTTTGCACCAAGCAGCGGTTTTTGAAGCCCGCAGGACCTTAAGTCTTT 1262
Db 341 AATCAAGCTTCTTTTGCAGCTTCCAGCGCTTATGGAACACCTGAAGAGCTACAAAGAACT 400
QY 1263 GATTGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGGACATTTTCACAGCCATGC 1322
Db 401 GGTAGACACAGCTCATTTTCATGGGTATCATAGTCTCTTAGATGGTACAGCCATGC 460
QY 1323 ATCAATTAATAC 1334
Db 461 TTCAAAAAATTC 472
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RESULT 12
US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-893
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Query Match 4.3%; Score 114.6; DB 10; Length 441;
Best Local Similarity 67.2%; Pred. No. 3.1e-21;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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410	Db	CCGGGACGAGAAGAGTTTTTCTTACTGGAGATTTTAACTGGTTGGAAATCCATTTTCGTAC	351
781	QY	ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTTCGCAATAATATGGATGGT	840
350	Db	CCATACAAAACCTGGATTATGGAATAATGGAGCTGTATATCCACCAGAGCAATAAA	291
841	QY	TCCTCCGCAATTCCTCATGGGTCAGAGTCCAGAGTGAAGATACGTATGACACTCCATCAGTGG--	898
290	Db	TCGTACTCTGGCTCATGTGATCCAAATTAAGGTATGTTATTACTAGTAAAGCGGAGAG	231
899	QY	-TTAAGGATCCATTCTCTGCTGGATCAACTACTCTTTACAGCTCTCTCGATGAAATCCCA	957
230	Db	ATCTTGATCGTATTTTACCGCTGGCGAAGATGTGGTTCGTGAAGTGATAATGTGAAT	171
958	QY	TATAATGGGAATACATATATGATCCACCGAAGAGGAGAGGTATATCTTCCAACACCCACGG	1017
170	Db	TATGATTGGATACACATGGGATCC-----AGAACCTCATATGAGTTTATAGCATTCGGGA	117
1018	QY	CCAAAGAAACCAAGTCGTGAGAATATATCAATCTCATATTTGAATGAGTAGTCCGGAG	1077
116	Db	CCAAAGAAGCCACGGAGTCTAAGAAATTTATGAATCTCATCTGCGGAATTTCTTCCCATGAA	57
1078	QY	CCATAAATTAACATACAGTGAATTTTATGAGATGAGAGTTCTTCTCGCATATAAA	1131
56	Db	GGAAAGCTAGCTCTTTATAAACAATTTTACATGCAATGTAATGTAACAGAAATCAAA	3

RESULT 1A

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QY      1078  CCTTAAATTAACCAACGACGAAATTTTAGAGATGAAGTCTTCTTCGCATAAAA 1131
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Db      56  GGAAGACTAGCTCTTTATAAACATTTTACATGCAATGTACTACCAAGATCAAA 3
      |||  |||  |||||  |||  |||  |||  |||  |||

RESULT 14
US-09-922-217-304/c
; Sequence 304, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-304

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	Query Match	4.0%;	Score 104.8;	DB 10;	Length 601;
	Best Local Similarity	52.3%;	Pred. No. 1.9e-18;		
	Matches 310;	Conservative 0;	Mismatches 272;	Indels 12;	Gaps 3;
QY	544	GAATAGAGCCCCCTTTTGACAAACTATCGHCACACCTTCGATTACAGGTATTCACAGTAC	603		
Db	590	GAGATGACGGGTACTTTGAAGCCCTCCTACGCCGTGGACTTCGAGCGCAGGTATAAGCACTTT	531		
QY	604	AAGAAACTGAGGAGGCAATTTGACAAGTATGAGGGTGGTTTGGCAAGCCCTTTCTCGTGGT	663		
Db	530	AGCCAAATTTTGAAGACAATTTGAGAGAAATGAGGTGGTATTGATGACTTTTCCAGAGGC	471		
QY	664	TATGAAAAAATGGGTTTCACTCGTACTGCTAGGTGCACAGGTATCACTTACCGT---	720		
Db	470	TATGAATCATTTGGCGTCCACAGATGCTGATGGTGGTTTATCTACGAAAGAAATGGGCC	411		

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QY 721 CTGGTCCAGTCAGTCGCCCTCATTCGAGATTTCAACAATTGGGACGCAATGCTGAC 780
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 CCGGAGCAGAGAGAGTTTCTTACTGGAGATTTTAATGGTTGGAATCCCATTTTCGTAC 351
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 ATTATGACCGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGGATGCT 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 CCAATACAAAACATGGAATATGGAATAATGGGAGCTGTATATCCCAACCAAGCAGATRAA 291
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGAGACACTCCATCAGGTG-- 898
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 TCTGTACTCGTCCCTCATGATCCAAATTAAGGTAGTTATTACTAGTAAAGCGGAGAG 231
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 899 -TTAAGGATTCATTCTCTGGATCAACTACTCTTTACAGCTTCTCTGATGAAATTCGA 957
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 ATCTTGTATCGTATTTTCCACCCGGAAGAGAGGTATATCTTCCAAACACCCACCG 1017
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 958 TATAATGAATACATTTATGATCCACCCGGAAGAGAGGTATATCTTCCAAACACCCACCG 1017
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 TATGATGGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCAATTCGGA 117
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1018 CCAAGAAACCAAGTCCGCTGAGATATATGAACTCATATTTGGGAATGAGTAGTCCGGAG 1077
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 CCAAGAGCCAGGAGTCTAAGAAATTTATGAATCTCATGTGGGAATTTCTCCCATGAA 57
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1078 CCTAAATTAACCTACATGAGTGAATTTAGAGATGAAGTTCTTCTCGCATAAAA 1131
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 GGAAAGTAGCTTCTTTAACAATTTTACATGCAATGTACTACCAAGAATCAAA 3
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15

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US-09-833-263-304/c
; Sequence 304, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-304
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Query Match 4.0%; Score 104.8; DB 10; Length 601;
Best Local Similarity 52.2%; Pred. No. 1.9e-18;
Matches 310; Conservative 0; Mismatches 272; Indels 12; Gaps 3;

QY 544 GAAATAGACCCCTTTGACAAACATATCGTCAACACCTTGATTACAGGTATTACAGTAC 603
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 GAGATCGACCGGTACTTGAAGCCCTACCCCGTGGACTTCCAGCGAGGTATAGCAGTTT 531
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 604 AAGAACTGAGGAGCAATTGACAAATGATAGGCTGGTTTGGAGCCCTTTCTCGTGT 663
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 530 AGCCAAATTTGAAGAACATTTGGAGAAATGAAGTGGTATTGATAAGTTTCCAGAGGC 471
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 664 TATGAAAAATGGTTTCACTCGTAGTGTACAGGTATACATACCGT---GAGTGGGCT 720
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 470 TATGATCATTTGGCGTCCACAGATGTCTGTGGTTTATCTGCAAGAATGGGCC 411
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 CTGGTCCAGTCAGTCGCCCTCATTCGAGATTTCAACAATTGGGACGCAATGCTGAC 780
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 CCGGAGCAGAGAGAGTTTCTTACTGGAGATTTTAATGGTTGGAATCCCATTTTCGTAC 351
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGCTGATGT 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: July 5, 2003, 20:29:57
Job time : 428.708 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:27:32 ; Search time 3588.65 Seconds

(without alignments)

11941.316 Million cell updates/sec

Title: US-10-056-454A-14_COPY_145_2790

Perfect score: 2646

Sequence: 1 ATGGTGATACACTCTGG.....AAGTAGTAGTAGAGAGAA 2646

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177.6	44.5	2766	11 AY109521	AY109521 Zea mays
2	1122.6	42.4	2732	11 AY109532	AY109532 Zea mays
3	615.8	23.3	3012	11 AY105679	AY105679 Zea mays
4	564.4	21.3	2738	11 AK009815	AK009815 Mus muscu
5	482.2	18.2	728	14 BU008463	BU008463 QGH7K17.Y
6	473	17.9	713	14 BQ986883	BQ986883 QGF10L08.

7	436.2	16.5	689	13	BI308555	BI308555 EST529965
8	436	16.5	801	10	BE195628	BE195628 HVSMEH008
9	424.2	16.0	678	10	AV393010	AV393010 AV939010
10	414.6	15.7	731	10	BE602527	BE602527 HVSMEH009
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12	406.2	15.4	573	13	BM526229	BM526229 sal38f02
13	397.6	15.0	825	12	BF065047	BF065047 HV_CEB002
14	393.2	14.9	695	14	BQ240494	BQ240494 TaEO5016F
15	385.4	14.6	621	12	BG521671	BG521671 13-3 Stev
16	384	14.5	650	10	BE427534	BE427534 PSR7153 I
17	381.4	14.4	646	9	AU238577	AU238577 AU238577
18	377.6	14.3	651	12	BG526727	BG526727 63-11 Ste
19	376.6	14.2	639	10	AQ065909	AQ065909 687002G09
20	372.8	14.1	569	10	AV442128	AV442128 AV442128
21	372.4	14.1	571	13	BI699680	BI699680 sal25909
22	369.6	14.0	576	10	AW244197	AW244197 687050F06
23	367.8	13.9	571	13	BI469105	BI469105 sal07e09
24	366.6	13.9	560	14	BM885252	BM885252 sal97a08
25	366.6	13.9	575	13	BI425610	BI425610 sal69a11
26	361.4	13.7	589	10	AW596011	AW596011 si96a03.Y
27	360.6	13.6	588	9	AJ432814	AJ432814 AJ432814
28	358.6	13.6	582	13	BM309136	BM309136 sak55b02
29	351.4	13.3	656	9	AI487345	AI487345 EST245667
30	349	13.2	592	13	BJ268430	BJ268430 BJ268430
31	344.4	13.0	556	10	AV913706	AV913706 AV913706
32	343.6	13.0	602	12	BG524041	BG524041 38-25 Ste
33	342.4	12.9	704	14	BU008407	BU008407 QGH7104.Y
34	342	12.9	592	10	BE402623	BE402623 CSB009H05
35	342	12.9	592	14	BQ608128	BQ608128 BRY_4030
36	340	12.8	516	14	BQ253050	BQ253050 sao05e05
37	337.2	12.7	569	13	BJ233506	BJ233506 RJ233506
38	336.8	12.7	761	13	BM411030	BM411030 EST585357
39	332.8	12.6	568	14	BQ240653	BQ240653 TaEO5014F
40	327.8	12.4	509	12	BG651974	BG651974 sad72d10
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ALIGNMENTS

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DEFINITION Zea mays CL1245_1 mRNA sequence.
ACCESSION AY109521
VERSION AY109521.1 GI:21213273
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays

REFERENCE
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2766)
AUTHORS Coe,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

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mapping Project			
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Matches 1486; Conservative 0; Mismatches 612; Indels 0;

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Db

RESULT 5
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LOCUS

DEFINITION

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BU008463 mRNA sequence.

ACCESSION
BU008463

VERSION

KEYWORDS

SOURCE

ORGANISM

Lactuca sativa.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

1 (bases 1 to 728)

REFERENCE

AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Javelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.

TITLE

Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aasmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig6851, see http://cgdb.ucdavis.edu/
for details.

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FEATURES

Location/Qualifiers

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source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
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BASE COUNT 227 a 133 c 149 g 218 t 1 others

ORIGIN

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Best Local Similarity 78.8%; Pred. No. 2.8e-99;
Matches 574; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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Q9F10L08, mRNA sequence.

ACCESSION BQ986883
VERSION BQ986883.1
KEYWORDS EST.
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ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

REFERENCE 1 (bases 1 to 713)
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevillier, P., Ziegler, J., Ellison,
P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL http://compgenomics.ucdavis.edu/
COMMENT unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Asmudson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig6851, see http://cgdb.ucdavis.edu/
for details.

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FEATURES
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Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUE-flowers post-fertilized
TAG_SEQ-TGCCATCGG"

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ORIGIN

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Matches 563; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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976 GATCCACCCGAGAGGAGAGGTATATCTTCCAAACACCCAGCCGCAAAAGCAAGTCG 1035
301 GATCCACCCGAGAGGAGAGGTATATCTTCCAAACACCCAGCCGCAAAAGCAAGTCG 360
1036 CTGACAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1095
361 CTGACAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
1096 GTGAATTTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1155
421 GTGAATTTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1156 ATTATGGCTATTTCAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1215
481 ATCATGGCTATTTCAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 540
1216 TTTGCACCAAGCAGCGGTTTGGAGCGCCGACGACCTTAACTCTTGTGATGATGATGAT 1275
541 TTTGCACCAAGCAGCGGTTTGGAGCGCCGACGACCTTAACTCTTGTGATGATGATGAT 600
1276 CATGAGCTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1335
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[illegible]

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/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_lib="HVSMEH0089p20f"
/hvcdna0009 (5 to 45 DAP)
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/Note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a 146 c 198 g 236 t      1 others
ORIGIN
Query Match      16.5%; Score 436; DB 10; Length 801;
Best Local Similarity 76.1%; Pred. No. 9.6e-89;
Matches 549; Conservative 0; Mismatches 171; Indels 1; Gaps 1;
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D      1706 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1765 GCTGATAACGGATGTAGTTGCTCAAGAACGGGATGAGGATGAGGATGGGATGAT 1824
D      1766 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1825 GTTCATACACTGACATACAGATGCTCGAAGAGTGTTTCATACGCTGAAGTCAT 1884
D      1826 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1885 GATCAAGCTCTAGTCGGTGTAAACTATAGCATTTGGCTGTGATGGACAGGATATGAT 1944
D      1886 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1945 GATTTTATGGCTCGGATAGACCTGCAACATCATTAATAGATCGTGGGATGACATTCGAC 2004
D      1946 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      2005 AAGATGATAGGCTGTGAATCATGGATTAGGAGAGAGGTTACCTAAATTTTCATGGGA 2064
D      2006 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      2065 AATGAATCGGCCACCTGAGTGGATTGATTCCTAGGCGGTGACACACACTCTCTGAT 2124
D      2066 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      422 AATGAGTTGGGCTCTGATGATGATGATTTTCCAGGGGTCGCGANACTCTTCCAACC 481
D      423 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      2125 GGCTCAGTAATCCCGGNAACCAATTCAGTTATGATAATGACAGCGAGATTTGACCTG 2184
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/organism="Hordeum vulgare"
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/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/Note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      220 a 146 c 198 g 236 t      1 others
ORIGIN
Query Match      16.0%; Score 424.2; DB 10; Length 678;
Best Local Similarity 77.7%; Pred. No. 4.6e-86;
Matches 524; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
QY      697 GGTATCACTTACCGTG-ACGTGGCTCTTGGTCCCGACGTCAGTCGCCCTCAATGGAGATT 755
D      698 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      756 CAACAATGGGACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTGGAGAT 815
D      757 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      816 TTTTCTGCCAAATAATGGATGGTTCCTCGCAATTCCTATGGTCCAGAGTGAAGAT 875
D      817 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      125 TTCTCTCCCTAACAAATGCTGATGGATCCCTCTATTCTCTATGCTCAGGTGAAGAT 184
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Db      482 GCGAAGTTCTCCTGGCAATACAAATAGTTATGATAAATGCCCGTAAATTTGATCTT 541
QY      2185 GGAGATGCGACAATATTTAAGATACCGTGGGTTTGCAGAATAATTGACCGGCTATFGCAGAT 2244
D      2186 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D      542 GGAGATGCGAGATTCTTAGATATCTGGAATGCAAGAGTTCGATCAGGCAATGCCCAT 601
QY      2245 CTTGAAGATAAATATAGTTTATGACTTCAGAACACAGCTTCATATCAGCAAGAGTGA 2304
D      2246 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D      602 CTTGAGGAAAAAATAGGTTTATGACATCTGACACCACTATCTTTCTCGAAACTTGAG 661
QY      2305 GGAGATGAGTATGTTGT-ATTTCAGAAAGAAACCTAGTTTGTCTTTAAATTTCACTG 2363
D      2306 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D      662 GAAGATAAGTGAACATCTTTTGAAGAGGAAATTTGGTATTTTGTTCACATTTCCCTG 721
QY      2364 G 2364
D      722 G 722

RESULT 9
AV939010      678 bp      mRNA      linear      EST 18-JAN-2002
LOCUS      AV939010
DEFINITION      AV939010 K. Sato unpublished cDNA library, strain H602 adult,
                        heading stage top three leaves Hordeum vulgare subsp. spontaneum
                        cDNA clone bah20e24 5', mRNA sequence.
ACCESSION      AV939010
VERSION      AV939010.1 GI:18234807
KEYWORDS      EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
ORGANISM      Hordeum vulgare subsp. spontaneum
                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                        ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 678)
AUTHORS      Sato, K., Saisho, D. and Takeda, K.
TITLE      Barley EST sequencing project in NIG and Okayama Univ
COMMENT      Unpublished (2002)
                        Contact: Tadashi Shin-i
                        Center For Genetic Resource Information
                        National Institute of Genetics
                        1111 Yata, Mishima, Shizuoka 411-8540, Japan
                        Tel: 81-559-81-6856
                        Fax: 81-559-81-6855
                        Email: tshini@genes.nig.ac.jp.
                        Location/Qualifiers
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1..678
/organism="Hordeum vulgare subsp. spontaneum"
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/clone="bah20e24"
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/dev_stage="adult, heading stage"
193 a 135 c 154 g 194 t 2 others
BASE COUNT
ORIGIN
Query Match      16.0%; Score 424.2; DB 10; Length 678;
Best Local Similarity 77.7%; Pred. No. 4.6e-86;
Matches 524; Conservative 0; Mismatches 149; Indels 1; Gaps 1;
QY      697 GGTATCACTTACCGTG-ACGTGGCTCTTGGTCCCGACGTCAGTCGCCCTCAATGGAGATT 755
D      698 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      756 CAACAATGGGACGCAAAATGCTGACATTATGACTCGGAATGAATTTGGTGTGGAGAT 815
D      757 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      816 TTTTCTGCCAAATAATGGATGGTTCCTCGCAATTCCTATGGTCCAGAGTGAAGAT 875
D      817 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      125 TTCTCTCCCTAACAAATGCTGATGGATCCCTCTATTCTCTATGCTCAGGTGAAGAT 184
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Db 485 AAGAGTGTGTTACTTAAGTGAAGATCATGATCAAGCACTTGTGGAGACAAGACATATGC 544
QY 1917 ATTCTGGCTGATGCGACAGGATATCATGATTTATGGCTCTGGATAGACCGTCAACATC 1976
Db 545 ATTCTGGTGTGATGCGACAGGATATGATGATTTATGGCTCTGAGCGGACCTTCGACACC 504
QY 1977 ATTAATAGATCTGGGATAGCATTCACAAAGATGATAGGCTTTGTAACATATGGGATAGG 2036
Db 605 TAAATGATGATCGGGAATAGCACTGCATATAAATGATAGATATACATAATGSCINTAGG 664
QY 2037 AGGAGAAGGTACCTAAATTTTCATGGGAATGAATTCGCCACCTCGAGTGGATGATTT 2096
Db 665 AGGAGAGGGTTATCTTAACCTTTATGGGAATGAGTTCCGGCATCTCTGAAATGGATAGACTN 724
QY 2097 CCTAG 2102
Db 725 TCCAAG 730

RESULT 11
BU005876
LOCUS
DEFINITION
QGG9F08-yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGG9F08, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU005876 717 bp mRNA linear EST 22-AUG-2002
QGG9F08-yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGG9F08, mRNA sequence.
EST.
Lactuca sativa.
Lactuca sativa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 717)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig6851, see http://cgdb.ucdavis.edu/
for details.
Plate: QGG9 row: F column: 08.

FEATURES
source

1..717
/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGG9F08"
/lab_host="E.coli"
/note="Vector: pBRCDNASFIAB: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUE-germinating seeds
TAG_SEQ-TCTGTCGGG"
233 a 122 c 155 g 206 t 1 others

Query Match 15.4%; Score 407; DB 14; Length 717;
Best Local Similarity 74.7%; Pred. No. 3.8e-82;
Matches 523; Conservative 0; Mismatches 176; Indels 1; Gaps 1;
QY 462 TTCTGAAGACAAATTTATTCATGAATCTGATAGATCAGAGAGGGGATCCCTCCACC 521
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QY 522 TGACATTGGTCAGAAATTTATGAAATAGACCCCTTTTGACAAATATCGTCAACACCT 581
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QY 702 CACTTACCGTACGTGGCTCTTGGTGCCAGTCCAGCTGCGCTCATTTGGAGATTCACAA 761
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QY 762 TTGGAGCGCAATGCTGACATTTAGCTCGGAATGAATTTGGTCTCTGGAGATTTTCT 821
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QY 822 GCCAAATTAATGCTGCTCTGCAATTCCTCATGCTGGTCCAGATGAAGATACGTAT 881
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QY 882 GGACATCCATCAGTGTGTTAAGGATTCCTGCTGGATCAATCTCTTACAGCT 941
Db 439 GGATACCCATCTGGCATTTAAAGACTCGATCTGCTGGATCAAGTTTTCAGTACAGC 498
QY 942 TCCTGATGAATTCATATATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
Db 499 ACCTGGTTCAGATTCCTTATATGATGATGATGATGATGATGATGATGATGATGAT 558
QY 1002 CTTCCAAACACCCAGCGGCAAAAGCAAAAGTCCGCTGAGATATATGATGATGATGAT 1061
Db 559 GTTTCACATCCAGACACCAAGAGCCGAATCTCTTANGATTATGAGGCACATGTGGG 618
QY 1062 AATCAGTAGTCCGGAGCCCTAAATTAATCTATAGTGAATTTAGAGATGAAGTCTTCC 1121
Db 619 AATCAGTAGTACGGAACCAATGGATCACACGTATGCTAACTTTAGACAGATGTTCTCC 678
QY 1122 TCGCATRAAAGCTTGGTACAAATGGCTGCAAAATATG 1161
Db 679 TCGCATRAAAGAA-CTCGGTTTACAATGCGATTCAAATCAIG 717

RESULT 12
BM526229
LOCUS
DEFINITION
BM526229 sal38f02.y1 Gm-cl059 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl059-4491 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM526229 573 bp mRNA linear EST 19-FEB-2002
sal38f02.y1 Gm-cl059 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl059-4491 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
PRECURSOR ;, mRNA sequence.
BM526229 GI:18731047
EST.
Glycine max
soybean.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 573)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers

Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Research	1980, Vol. 83, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Research	1980, Vol. 83, No. 3, pp. 21-30
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 4, pp. 31-40
5. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 5, pp. 41-50
6. The Impact of Socioeconomic Status on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 6, pp. 51-60
7. The Importance of Teacher Education	Journal of Educational Research	1980, Vol. 83, No. 7, pp. 61-70
8. The Effect of Teacher Training on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 8, pp. 71-80
9. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 9, pp. 81-90
10. The Impact of Socioeconomic Status on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 10, pp. 91-100

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63110
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1. 573

FEATURES SOUTH

1. 573
1. 573/Quarrels
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/db_xref="taxon:3847"
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/clone_lib="Gm-ci059"
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/lab_host="DHI0B"
/note="Vector: pBluescript II SK+; Site-1: EcoRI; Site-2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of P1648916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
169 a 110 c 126 g 167t 1 others

Query Match 15.4%; Score 406.2; DB 13; Length 573;
Best Local Similarity 81.8%; Pred. No. 5.7e-82;
Matches 468; Conservative 0; Mismatches 104; Indels 0.

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QY	121	CCGAGCCAAAATCAATCAATATGTCAATTTTAGAGATGATGACTGGCTCGCATAAA	180
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QY	1132	AAGCTTGGGTACAAATCGGCTGCAAAATATGGCTATTCAAGAGCAATCTTATTACGCTAGT	1191
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QY	181	AGGCTTGGGTATTAATGCTGTCCAGATATGGCTATCCAAAGAACATCTTATTATGCCAGC	240
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QY	1192	TTTGGTTATCATGTCACAAATTTTTTGCACCACAGCAGCCGTTTGGAGCGCCGACGAC	1251
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QY	241	TTTGGGTACCATGTTTACAAATTTCTTTTGACCTTAGCAGCGGCAATTTGGAATCCAGAGAA	300
Db			
QY	1252	CTTAAAGTCTTTGATGATAAAGCTCATAGCTAGGAAATTTGTTTCTCATGGACATTTGT	1311
Db			
QY	301	CTTAAAGTCTCTGATAGACAGAGCCCATGAATGACTGGGTCCTGCTGTCTGATGATATTGTA	360
Db			
QY	1312	CACAGCCATGCATCAATTAATACTTTAGATGAGACTGAACAATGTTTGCATGCCCGATAGT	1371
Db			
QY	361	CACAGCCATGCATCAAAATAATACATTGATGGCTGAACATGTTTGATGGAATCTGATGT	420
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QY 2242 TAATCTGAAGATAAATAGAGTTTATGACTTCAGAACACAGCTCATATCACGAAGAGAT 2301
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445 CACTTGAGGAATAATGAGTTTATGACATCTGAGCACCAGTAGTTTCACGGAAACAT 504
QY 2302 GAGGAGATAGGATGATTGTTGAAAAAGAAACCTAGTTTGTCTTTAAATTTTAC 2361
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505 GAGGAATAGGATGATCACTTCGAAAGAGGAGATTGGTAATTTGTTTCACATTTCCAC 564
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565 TGGAGCANTAGCTTTTGTGATACCGTGTGGTGTTCACAGCCTGAGAAAGTAGCAAGGTG 624
QY 2422 GCCTTGGACACAGATGATCAGCTTTTGGTGGCTGCGGAGAAATGATCATATGCCGAA 2481
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625 GCCTTGGACCTCCAGCATGACCTCTTGGTGGATTCAGCAGGCTTGATCATGATGTCGAC 684
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Db |||||
685 TACTTAC 692

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RESULT 15

BG521671

LOCUS DEFINITION

13-3 Stevia field grown leaf cDNA Stevia rebaudiana CDNA 5', mRNA
sequence.

ACCESSION

BG521671

VERSION

BG521671.1

KEYWORDS

EST.

SOURCE

Stevia rebaudiana.

ORGANISM

Stevia rebaudiana

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..621

/organism="Stevia rebaudiana"

/strain="751/1501"

/cultivar="Landrace"

/db_xref="taxon:55670"

/clone_lib="Stevia field grown leaf cDNA"

/tissue_type="leaf"

/dev_stage="field grown, mid-size"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This

cDNA library was constructed from polyA+ enriched mRNA

from field grown leaves. Mid-size actively growing leaves

were collected and pooled from several plants and frozen

immediately after harvesting in liquid nitrogen. The cDNA

was prepared using an XhoI-poly(dT) linker-primer. An

EcoRI adapter was ligated to the blunt end cDNA and the

products were digested with EcoRI and XhoI enabling

directional cloning into the lambda ZAP Express vector.

The library was amplified using the host strain XL1-Blue

MRF'. Mass excision of the library was performed to

obtain pBK-CMV phagemid clones in the host strain XL0LR.

Single pass DNA sequencing was performed using the T3

promoter primer: 5' ATTAACCTCCTCAAAAGGGA 3'. This library

was constructed by Alex Richman."

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BASE COUNT 169 a 91 c 162 g 198 t 1 others
ORIGIN
Query Match 14.6%; Score 395.4; DB 12; Length 621;
Best Local Similarity 78.8%; Pred. No. 3.le-77;
Matches 472; Conservative 0; Mismatches 126; Indels 1; Gaps 1;
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422 TTTAAGGCAATGATAGACCATGCTCTCTTATAGATCGCGTATTTGCTATTCATATAA 481
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Search completed: July 5, 2003, 20:10:07

Job time : 3606.65 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 00:19:16 ; Search time 5591 Seconds
(without alignments)
4341.216 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882
Perfect score: 4465
Sequence: 1 EKSSYNSEPRSTVAASGV.....EEEEEEVAAVEVVVEE 834

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4465	100.0	3033	6	A58164
3	4372.5	97.9	2523	8	STU011889
4	4358.5	97.6	2578	6	A58169
5	4339	97.2	2493	8	STSBEI1
6	4334	97.1	2576	6	A58166
7	4320	96.8	3074	6	ARL23355
8	4297	96.2	2982	8	STU011886
9	4274	95.7	2563	6	AX256072
10	4269	95.6	3003	6	A58162
11	4268.5	95.6	3231	6	A58168
12	4225	94.6	2529	6	A58167
13	4220.5	94.5	2955	8	STU011885
14	4161.5	93.2	2975	6	A58163
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25	3239	72.5	3015	6	E14723
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31	3149	70.5	2853	8	TAU66376
32	3136	70.2	2726	8	AF338432
33	3130.5	70.1	2554	8	AF064560
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35	3092	69.2	2918	6	RICBCE3
36	3021.5	67.7	2725	6	AR106495
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ALIGNMENTS

RESULT 1

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LOCUS Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
DEFINITION A-6.
ACCESSION AJ011890.1 GI:4584512
VERSION SBEII gene; starch branching enzyme II.
KEYWORDS Solanum tuberosum
SOURCE Solanum tuberosum
ORGANISM
REFERENCE
AUTHORS Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
TITLE A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2992)
AUTHORS Jobling, S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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Score: 4465.00 Matches: 834
Percent: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

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ACCESSION A58164
VERSION A58164.1 GI:3713889
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
CDS
BASE COUNT 900 a 553 c 712 g 868 t
ORIGIN
Alignment Scores:
Pred. No.:
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US-10-056-454A-15_COPY_49_882 (1-834) x A58164 (1-3033)

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VERSION AJ011889.1 GI:4584510
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SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum.

REFERENCE
AUTHORS Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
TITLE A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
AUTHORS Jobling, S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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AUTHORS Cooke, D., Debet, M., Gidley, M.J., Jobling, S.A., Safford, R.,
Sidebottom, Christopher, M. and Westcott, R.J.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 2493)
Larsson,C.T.A.
Direct Submission
Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
Research, Genetic Center, Swedish University of Agricultural
Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
2 (bases 1 to 2493)
Larsson,C.T., Khosnoodi,J., Ek,B., Rask,L. and Larsson,H.
Molecular cloning and characterization of starch-branching enzyme
II from potato
Plant Mol. Biol. 37 (3), 505-511 (1998)
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VERSION A58166.1 GI:3713891
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ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2576)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.

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DB 1804 GATCAAGCTCTAGTCGGTGATAAACTATAGCAITCTGCTGCTGACGACAGGATATGAT 1863
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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1924 AAGATGATTAGCTTGTAACTATGGATTAGGAGAGAGGCTAAATTTTCATGGGA 1983
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741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
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RESULT 2

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DEFINITION  Sequence 1 from patent US 6169226.
ACCESSION   ARI23355
VERSION     ARI23355.1  GI:14108321
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.

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REFERENCE

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1 (bases 1 to 3074)
Ek,B., Krosnoodi,J., Larsson,C.-T., Larsson,H. and Rask,L.
Starch branching enzyme II of potato
JOURNAL     Patent: US 6169226-A 1 02-JAN-2001;
FEATURES    location/Qualifiers
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BASE COUNT

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Alignment Scores:

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Pred. No.: 0
Score: 4320.00
Percent Similarity: 97.96%
Best Local Similarity: 97.36%
Query Match: 96.75%
DB: 6

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Length: 3074
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Conservative: 5
Mismatches: 13
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US-10-056-454a-15_COPY_49_882 (1-834) x ARI23355 (1-3074)

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693 AGGGCATCCCTCCACCTGGAGCTTGTGAGAAGATTATGAATAGACCCCTTTTGACA 752
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see result 3
res 1
date
too late


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DEFINITION A-4.
ACCESSION AJ011888
VERSION AJ011888.1 GI:4584508
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SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum.
REFERENCE 1 (bases 1 to 2982)
AUTHORS Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
TITLE A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
AUTHORS Jobling,S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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ORIGIN

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Best Local Similarity: 96.52% Mismatches: 17
Query Match: 96.24% Indels: 4
Dbs: 8 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x STU011888 (1-2982)

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ACCESSION A58162
VERSION A58162.1 GI:3713887
KEYWORDS
SOURCE unidentified.
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REFERENCE 1 (bases 1 to 3003)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 12 07-NOV-1996;
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QY	41	GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis	60	Db	1307	TATTCAGAGCAGCATCTTATTAAGTATGTTTGGTATCATGTACAAAATTTTTTTCACC	1366
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QY	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320	Db	2087	TGATTTTATGGCTCTGGATAGCCGTCAACATCATTAATAGATCTGGGTGATGATATACA	2146
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				Db	2147	CAAGATGATTAGGCTTGTAACTATGGGATAGGAGGAGAGGGTACCTAAATTTTCATGGG	2206
				QY	640	yAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAs	660
				Db	2207	AAATGAATTCGGCCACCCCTGAGTGGATTCCTCCCTAGGCTGAACAACACCTCTCTGA	2266
				QY	660	pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgGlyPheAspLe	680
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QY	421	TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu	440
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DB	1692	TCAAAATCGAGATGGTGGTTGGATGAGTGCAAATTTTCRTGGATTTAGATTTGATGGHGTG	1751
QY	461	ThrSerMetMetTyrIleHisHisGlyLeuSerValcIlyPheThrGlyAsnTyrGluGlu	480
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QY	481	TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu	500
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STU011885
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ACCESSION AJ011885
VERSION AJ011885.1 GI:4584502
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2955)
Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M., Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II.
JOURNAL unpublished
REFERENCE 2 (bases 1 to 2955)
AUTHORS Jobling, S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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VERSION A58163.1 GI:3713888
KEYWORDS
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ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2975)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
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AB071286
LOCUS
DEFINITION
Ipomoea batatas SBE II mRNA for starch branching enzyme II,
complete cds.
ACCESSION
AB071286
VERSION
AB071286.1 GI:15553090
KEYWORDS
SOURCE
Ipomoea batatas (cultivar:Kokei 14) cDNA to mRNA.
ORGANISM
Ipomoea batatas
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
REFERENCE
1 Kimura,T. and Saito,A.
Ipomoea batatas mRNA for starch branching enzyme II
Unpublished
2 (bases 1 to 3123)
REFERENCE
Kimura,T. and Saito,A.
Direct Submission
Submitted (08-SEP-2001) Takashi Kimura, National Agricultural
Research Center for Kyushu Okinawa Region; 2421 Suya, Nishigoshi,
Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp,
Tel:81-96-242-1150)
FEATURES
Location/Qualifiers
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Alignment Scores:
Pred. No.: 2,99e-264 Length: 3123
Score: 3535.50 Matches: 645
Percent Similarity: 88.14% Conservative: 76

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Best Local Similarity: 78.85% Mismatches: 96
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DB: 8 Gaps: 1

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Search completed: July 6, 2003, 04:49:04
Job time : 5762 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 00:16:41; Search time 469 Seconds
(without alignments)
4004.620 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882

Perfect score: 4465

Sequence: 1 EKSSYNSEFRPSTVAASGV.....EEEEEEVAEEVVVEE 834

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-De=N_Geneseq_101002 -QPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOALIGN=200 -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4465	100.0	3033	17	AAT42630	Class A starch bra
2	4358.5	97.6	2578	17	AAT42631	Class A starch bra
3	4329	97.0	3074	18	AAT69587	Potato starch bra
4	4322	96.8	2576	17	AAT42636	Class A starch bra
5	4274	95.7	2563	23	ABK50301	Potato cDNA encodi
6	4269	95.6	3003	17	AAT42634	Class A starch bra
7	4268.5	95.6	3231	17	AAT42632	Class A starch bra
8	4229	94.7	2531	17	AAT17267	Class A starch bra
9	4218	94.5	2529	17	AAT42635	Class A starch bra
10	4155.5	93.1	2975	17	AAT42637	Class A starch bra
11	3363	75.3	3090	19	AAV38720	Full length cassav
12	3281.5	73.5	2913	19	AAV38719	Full length cassav
13	3269	73.2	2715	21	AAV05639	Arabidopsis thalia
14	3239	72.5	3015	21	AAV05639	Nucleotide sequenc
15	3136	70.2	2726	22	AAH78337	Rice type IV starc
16	3096	69.3	2919	15	AAQ73750	Rice starch branch
17	3037	68.0	3039	24	ABK15494	Wheat starch bran
18	3030.5	67.9	2640	19	AAV70961	DNA encoding maize
19	3026.5	67.8	2665	18	AAV69729	Plasmid pBE240 ins
20	3026	67.8	2968	22	AAH78342	Nucleotide sequenc
21	3021.5	67.7	2725	19	AAV29757	Zea mays starch br
22	2676.5	59.9	2087	18	AAV69737	Corn starch branch
23	2669.5	59.8	2165	18	AAV69736	Corn starch branch
24	2628	58.9	2307	21	AAZ99938	DNA encoding part
25	2221.5	49.8	1919	19	AAV38722	cDNA encoding star
26	2165	48.5	3128	16	AAT00774	Potato starch bran
27	2147	48.1	4563	22	AAF30910	Wheat starch bran
28	2139.5	47.9	2733	15	AAQ62135	Rice starch branch
29	2130.5	47.7	2733	15	AAQ54674	Rice starch branch
30	2107	47.2	2565	18	AAV69752	Corn starch branch
31	2107	47.2	2763	18	AAV29758	Zea mays starch br
32	2104	47.1	2781	18	AAV69747	Corn starch branch
33	2104	47.1	2771	13	AAQ24257	Branching enzyme D
34	2104	47.1	2772	18	AAV69740	Plasmid pB65 inse
35	2100	47.0	2687	20	AAV34646	WSBE I-D4 cDNA seq
36	2098.5	47.0	2909	13	AAQ27778	Potato amylose-amy
37	2058	46.1	2899	22	AAH02926	Human shear stress
38	2058	46.1	2955	24	ABN95650	Gene #2148 used to
39	2058	46.1	3075	24	AAV94880	Human DNA sequence
40	2052	46.0	2713	19	AAV70962	DNA encoding maize
41	1914.5	42.9	3753	23	ABK50305	Red alga DNA encod
42	1899	42.5	2598	23	ABL07067	Drosophila melanog
43	1866	41.8	1452	21	AAV36957	Arabidopsis thalia
44	1828.5	41.0	4147	21	AAV83166	Glycogen branching
45	1805	40.4	6556	23	ABL07066	Drosophila melanog

ALIGNMENTS

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XX AC
XX AC
DT 25-FEB-1997 (first entry)
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DE DE
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.
XX XX
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FT /*tag= b
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XX 03-MAY-1996; 96WO-GH01075.
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XX 05-MAY-1995; 95GB-0009229.
XX
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
XX Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX P-PSDB; AAW06399.
XX
XX New potato plant starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Claim 28-30; Page 42-46; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX
XX Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;
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Alignment Scores:
Pred. No.: 0 Length: 3033
Score: 4465.00 Matches: 834
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerSerSerLeuThrGlySer 80
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QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGlnGluGlyLysLeuGluGlu 100
DB 529 GTTGAAGAGCTGGATTTTGTCTCATCTACAACTACAAGAAGTGTAAACTGGAGGAG 588
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QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 709 AACTATCGTCAACACCTTGAATTACAGGTATTCACAGTACAAAGAACTGAGGGAGCAATT 766
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DB 769 GACAAGTATGAGGTGGTGGAAAGCTTTTCGTTGGTTATGAAAAAATGGGTTTCACT 828
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QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
DB 889 ATTGGAGATTTCACAAATTTGGGACCGCAAAATCGTACATTAATGACTCGGAATGTTGT 948
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
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QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
DB 1009 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAAGATTCCATCTCTGCTTGGATC 1068
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DB 1429 GGAATCTGTTCTCATGGACATTTGTCACAGCCATGCAATCAATATATCTTTAGATGGA 1488
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1489 CTGAACATGTTGACTGCACCGATAGTTGTTACTTTCATCTGAGGCTCGTGGTTATCAT 1548
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
DB 1549 TGGATGTGGGATTTCCCGCTTTTAACTATGAAACTGGGAGGTACTTAGTATCTTCTC 1608
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
DB 1609 TCAATCGGAGATGGTGGTGCATGCGTCAAATTTGATGGATTAGATTGATGGTGTG 1668
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1669 ACATCAATGATGATATTCACCGGATTTATCGTGGGATTCATCTGAGGAACTACGAGGAA 1728
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAspLeu 500
DB 1729 TACTTTGGACTCGCAACTGATGTGGTGTCTGTTGATCTGATGCTGGTGCACGATCTT 1788
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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Db 1789 ATTCTATGGCTTTTCCCATGATCAATTACCAATGGTGAAGATGTTAGCGGAATGCCGACA 1848
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1849 TTTTGTATTCCTCCAGAGGGGGTGGCTTGTGACTATCGCTGTCATATGCAAT 1908
QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTyrArgValGlyAspIle 560
Db 1909 GCTGATAAACGATAGTTCCTCAAGAAACGGATGAGGATTCGAGAGTGGGTCAAT 1968
QY 561 ValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHis 580
Db 1969 GTTCATACACTGACAAATAGAGATGGTCGAAAAGTGTGTTTCATACGCTCAAGTCA 2028
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyr 600
Db 2029 GATCAAGCTTAGTCGGTGATAAAACATATAGCATTCGGCTGATGGACAAAGATATGAT 2088
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 2089 GATTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGATAGCATTCGAC 2148
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPhemetyly 640
Db 2149 AAGAAGTATAGGCTGTAACTATATGGGATTAGGAGGAAGGGTACCTAAATTTTCATGGA 2208
QY 641 AsnGluPheGlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 2209 AATGAATTCGCCACCTGAGTGGATGATTTCCCTAGGGCTGAACACACCTCTCGAT 2268
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgGlyPheAspLeu 680
Db 2269 GGCTCAGTAATCCCGGAACCAATTCAGTTATGATTAATGCACGCGAGATTTGACCTG 2328
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db 2329 GGAGATGCAGAAATTAAGATACCGTGGTTCGAAAGATTTGACCGGCTATGCAAT 2388
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 2389 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCGATTCATATCAGCAAGGATGAA 2448
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTyr 740
Db 2449 GGAGATAGGATGATGTTATTTGAAAAGGAACCTAGTTTTCCTTTAATTTTCACTGG 2508
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2509 ACAAAGCTATTTCAGACTATCCATAGCCTGCTGAAGCCTGGAATAACAAGTTGCC 2568
QY 761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2569 TGGACTCAGATGATCCACTTTTGGTGCTTCGGGAGAAATGATCAATATGCCGAAT 2628
QY 781 PheThrPheGluGlyTyrPyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2629 TTCACCTTTGAGGATGATGATGATCGCTCGTTCAATTTATGTTGATGACCTTGT 2688
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
Db 2689 AAAACAGCAGTGGTCTATCCTAGTAGACAAGAAGAAGAAGAAGAAGAAGAAGA 2748
QY 821 GluGluValAlaAlaValGluGluValValValValValValValValValVal 834
Db 2749 GAAGAGTAGCAGCAGTAGAAGTAGTAGTAGAAGAAGAAGA 2790

RESULT 2
AAT42631
ID AAT42631 standard; DNA; 2578 Bp.
XX
AC AAT42631;
XX
DT 25-FEB-1997 (first entry)

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XX Class A starch branching enzyme (psbe2con.seq - clone psJ90).
DE Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.
XX
FH Key Location/Qualifiers
CDS 24..2567 /*tag= a
FT sig_peptide 24..56
FT /*tag= b
FT mat_peptide 57..2564 /*tag= c
XX
PN WO9634968-A2.
XX
XX 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
DR WPI; 1996-506170/50.
DR P-PSDB; AAW06400.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
PS Claim 32; Page 55-56; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
SQ Sequence 2578 Bp; 770 A; 462 C; 616 G; 730 T; 0 other;
XX
Alignment Scores:
Pred. No.: 0 Length: 2578
Score: 4358.50 Matches: 817
Percent Similarity: 98.56% Conservative: 5
Best Local Similarity: 97.96% Mismatches: 11
Query Match: 97.61% Indels: 1
DB: 17 Gaps: 1
XX
US-10-056-454A-15_COPY_49_882 (1-834) x AAT42631 (1-2578)
QY 1 GluLysSerSerTyrAsnSerSerGluPheArgProSerThrValAlaSerGlyLysVal 20
Db 66 GAAAGAGCTTCTTACAAATTCGAAATCCGACCTTCTACAGTTCGACGATCGGGAAGTC 125
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
Db 126 CTGTGCTGGAACCCAGAGTAGTATGCTCTCATCTCAACAAACCAATTTGATTCAC 185
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
Db 186 GAGACATCTCCAGAAATTTCCCGACGATCAACTGATGATAGTAGTTCACAAATGGAAC 245
QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
Db 246 GCTAGCCAGATTAAACCTGAGAACGATGACGTTGAGCCGTCAGTATCTTACAGGA 305
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGluGlu 100

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306 GTTGAAGAGCTGGATTTGCTTCATCACTACAACACTACAAGAGGTGGTAACTGGAGGAG 365
101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
366 TCTAAACATTAATAACTTCTGAAGAGACAATTAATGATGAATCTGATGATCAGAGAG 425
121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
426 AGGGGATCCCTCCACCTGGACTTGTCTCAGCAAGATTATGAATAGACCCCTTTTGACA 485
141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAAGAACTGAGGGAGGCAATT 545
161 AspLysTyrGluGlyLeuAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
546 GACAAGTATGAGGTGGTGGAGCTTTTCGCGGTATGAAAAAATGGGTTCACCT 605
181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeu 200
606 CGTAGTGCTACAGTATCACTTACCGTGAAGTGGCTCCTGGTGCCTCAGCTGCCTC 665
201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
666 ATTGGAGATTCAACAATGGGAGCGCAATGCTGACATATGACTCGGAATGAATTTGGT 725
221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
726 GTCTGGGAGATTTCTGCGCAATAATGTGGATGTTCTCTCGAATTCCTCATGGTCC 785
241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
786 AGAGTGAAGATACGTATGGACACTCCATCAGTGTGTTAAGGATTCATTCCTCGTGGATC 845
261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
846 AACTACTCTTCACAGCTTCTGATGAATATCCATATATGGAATATATATGATCCACCC 905
281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
906 GAAGAGGAGAGGATATCTTCCAAACCCACCGCGCAAGAAACCAAGTCGCTGAGAATA 965
301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
966 TATGAATCTCAATATGGAATGAGTAGTCCGAGCGCTAAATTAATCTCATAGCTGAATTT 1025
321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
1026 AGAGTGAAGTCTTCTCGCATAAAAGCTTGGTACAAATGGGTGCAAAATATATGCT 1085
341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
1086 ATTCAGAGCATCTTATATGCTAGTTTGGTTATCATGTCACAAATTTTTCACCA 1145
361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
1146 AGCAGCGCTTTTGAAGCGCGAGACCTTAAGTCTTTGATGTATAAGCTCATGAGCTA 1205
381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
1206 GGAATGTGTCTCATGGACATTTTCACGCCATGATCAAAATATACCTTTAGATGGA 1265
401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
1266 CTGAACATGTTTGAAGCGCACCGATGTGTATCTTCACTCTGGAGCTCGTGGTTATCAT 1325
421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
1326 TGGATGTGGGATTCGCGCTTTTAACTATGGAACCTGGGAGTACTTAGGTATCTTCTC 1385
441 SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
1396 TCAATGCGAGATGGTGTGGATGAGTTCATTAATTTGATGATTTAGATTTGATGGTGIG 1445

461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
1446 ACATCAATGATGATACTCACCACGGATTATCGTGGGATTCTACTGGGAACCTACAGGAA 1505
481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
1506 TACTTTGGACTCGCACTGATGTGGATGCTTGTGTATCTGATGCTGGTCAAGATCTT 1565
501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
1566 ATTATGGGCTTTTCCAGATGCAATTACCATTGGTCAAGATGTTAGCGGAATCCGACA 1625
521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
1626 TTTTGTATCCCGTTCAGATGGGGTGTGGCTTTGACTATCGCTGCATATGGCAATT 1685
541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
1686 GCTGATAAATGGATGTAGTTGCTCAAGAAACGGGATGAGGATTGGAGTGGGTGATAT 1745
561 ValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHis 580
1746 GTTCATACACTGACAAATAGAGATGGTCGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1805
581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyr 600
1806 GATCAAGCTCAGTGGTGTATAAATATAGCATTTCTGGCTGATGGACAGGATATGAT 1865
601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
1866 GATTTATGGCTCTGGATAGACCGCAACATCATTAATAGATCTGGGATGACATGGAC 1925
621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly 640
1926 AAGATGATTAGCTTGTAACTATGGGATTAGGAGAGAGGATACCTAAATTTGATGGGA 1985
641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
1986 AATGAATTCGGCCACCTTGAGTGGATTGATTCCTAGGGCTGAACACACCTCTCTCAT 2045
661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
2046 GACTCAGTAATTCGCGAACCACATTCAGTATGATAAATGCAGACGGAGATTGACCTG 2105
681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
2106 GGAGATGCAGAAATATTAAGATACCGTGGGTGCAAGAAATTTGACGGGCTATGCAGTAT 2165
701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
2166 CTTGAAGATAAATATGACTTTATGACTTCAGAACACCACTTCATATCAGAAAGATGAA 2225
721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
2226 GGAGATAGATGATTTGATTTGAAAAGAAACCTAGTTTTCCTTTTAAATTTTTCACCTG 2285
741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
2286 ACAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAAGCTGGAATAATACAAAGTTGCC 2345
761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
2346 TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAATGATGATCAATGCGCAATAT 2405
781 PheThrPheGluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
2406 TTCACCTTTGAAGGATGATGATGATCGTCTCTCGTCAATATATGCTATGCTACCTTGT 2465
801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
2466 AGAACAGCAGTGTCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAA 2522

QY 821 GluGluValAlaAlaValGluGluValValGluGluGlu 834
Db 2523 GAAGAAGTAGCAGTAGTAGAAGAGTAGTAGTAGAAGAAGAA 2564

RESULT 3

AAT69587
ID AAT69587 standard; cDNA; 3074 BP.
XX
AC AAT69587;

XX 26-AUG-1997 (first entry)

XX Potato starch branching enzyme II gene (beII).

XX Starch branching enzyme II; beII gene; potato; transgenic plant;
XX amylopectin; amylose; starch; ss.

XX Solanum tuberosum.

XX Key Location/Qualifiers
XX CDS 189..2825
XX FT /*tag= a

XX sig_peptide 189..332
XX FT /*tag= b

XX mat_peptide 333..2822
XX FT /*tag= c

XX W09720040-A1.

XX 05-JUN-1997.

XX 28-NOV-1996; 96WO-SE01558.

XX 19-APR-1996; 96SE-0001506.
XX 29-NOV-1995; 95SE-0004272.

XX (EKBB/) EK B.

XX (KHOS/) KHOSNOODI J.

XX (LARS/) LARSSON C.

XX (LARS/) LARSSON H.

XX (RASK/) RASK L.

XX (AMYL-) AMYLOGENE HB.

XX Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;

XX WPI; 1997-310596/28.
XX P-PSDB; AAW19113.

XX Isolated potato starch branching enzyme II - useful for altering
XX degree of amylopectin branching and amylopectin/amylose ratio in
XX potato starch

XX Claim 4: Page 12-15; 24pp; English.

XX A cDNA clone (AAT69587) codes for potato starch branching enzyme II
XX (BEII) (AAW19113). It was isolated from potato tuber cDNA by PCR
XX amplification using primers (AAT69588-89) based on tryptic peptides
XX of isolated BEII; the 5' and 3' ends of the sequence were detd. by
XX RACE. A vector comprising the whole or a functional active part of
XX the isolated sequence (sense or antisense), plus regulatory
XX sequences active in potato, can be used to produce transgenic
XX potatoe. The starch obtd. from such plants will show a changed
XX pattern of amylopectin branching and an altered amylopectin/amylose
XX ratio.

XX Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other;

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4329.00 Matches: 814
Percent Similarity: 98.08% Conservative: 4
Best Local Similarity: 97.60% Mismatches: 12
Query Match: 96.95% Indels: 4

DB:	18	Gaps:	1
US-10-056-454A-15_COPY_49_882 (1-834) x AAT69587 (1-3074)			
QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20			
Db 333 GAAAGTCTCTTACAAATCCGAAATCCCGACTTCTACAGTTGACATCGGGAAGTC 392			
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGluPheGluPheThr 40			
Db 393 CTGTGCTGGAACCCAGAGTATAGTCTTCACTCACTCAACAGACCAATTTAGTTCAC 452			
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60			
Db 453 GAGACATCTCCAGAAAATTCGCCAGCATCACTGATGATAGTAGTTCAACAATGCAACAC 512			
QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer 80			
Db 513 GCTAGCCAGATTAACAACTGAGAACGATGACGTTGAGCGCTCAAGTGATCTTACAGAAAT 572			
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGluGlu 100			
Db 573 GTTGAAGAGCTGGATTTTGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACT 632			
QY 101 SerLysThrLeuAsnThrSerGluThrIleLeuAspGluSerAspArgIleArgGlu 120			
Db 633 TCTAAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 692			
QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140			
Db 693 AGGGGCACTCCCTCCAGCTGGACTGGTTCAGAGAAATTAAGAAATAGAGCCCTTTTGACA 752			
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160			
Db 753 AACTATCGTCAACACCTTGATTACAGGTATTTCACAGTACAGAACTAGAGGAGCAATT 812			
QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180			
Db 813 GACAAGTATGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 872			
QY 181 ArgSerAlaThrGlyIleThrTyrArgGlnTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200			
Db 873 CGTAGTGTACAGGTATCACTTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 932			
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220			
Db 933 ATTGAGATTTCACAAATTTGGAGCAATGCTCACATTTATGACTCGCAATGAATTGGT 992			
QY 221 ValTrpGlnIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySer 240			
Db 993 GTCGGGAGATTTTTCGCCAAATAATGTGATGGTCTCTCTGCAATTCCTCATGGTCC 1052			
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260			
Db 1053 AGAGTGAAGATAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 1112			
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280			
Db 1113 AACTACTCTTTACAGCTTCTCTGATGAATTTCCATAAATGAATATATATATATATATAT 1172			
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300			
Db 1173 GAGAGGAGAGGTATATCTTCCCAACACCCAGCCCAAGCAAGCAAGCAAGCAAGCAAG 1232			
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320			
Db 1233 TATGAATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1292			
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340			
Db 1293 AGAGATGAAGTCTTCTCTCGCATAAAGAGCTTGGGTACAAATCGGTGCAAAATATGGCT 1352			
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360			

Db 1353 ATTCAAGAGCAATCTTATTATGCTAGTTTGGTTATCATGCTCAAAATTTTTTNGCACCA 1412
QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuLeuLeuLeuLeuLeuLeuLeu 380
Db 1413 AGCAGCGCTTTTGGAAACCCGACGACCTTAAGCTTTTGATTAAGATCATGAGCTA 1472
QY 381 GlyLeuValLeuLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db 1473 GGAATTTGTTCTCATGGACATGTTTCACAGCATGCAATCAAAATAATCTTTAGATGGA 1532
QY 401 LeuAsnMetPheAspCysThrAspSerCysThrPheHisSerGlyAlaArgGlyTyrHis 420
Db 1533 CTGAACATGTTTGAGGSCACAGATAGTTGTTTACTTTCACCTCGAGCTCGTGGTTATCAT 1592
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuLeuArgTyrLeuLeu 440
Db 1593 TGGATGCGGATTCGCCCTCTTTAATATGGAACCTGGAGGTACTTAGGTATCTCTC 1652
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db 1653 TCAAAATCGAGATGGTGGTGGATGAGTTCAAATTTGATGATTTAGATTGAGGTGTG 1712
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db 1713 ACATCAATGATGATATCTACCCACCGGATTTATCGGTGGGATTCAGTGGGAACCTACGAGAA 1772
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAspLeu 500
Db 1773 TACTTTGGACTCGCAATGATGGATGCTGTGTGTATCTGATCGCTGGTCAACGATCTT 1832
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1833 ATTCATGGGCTTTTCCAGATGCAATTAACATTTGGTGAAGATTTAGCGGAATCCGACA 1892
QY 521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1893 TTTTNTATCCCGTCAAGATGGGGGTGTGGCTTTGACTATCGCTGCATATGGCAAT 1952
QY 541 AlaAspLysArgIleGluLeuLeuLysArgAspGluAspTrpArgValGlyAspIle 560
Db 1953 GCTGATAAATGGATGTAGTGTCTCAAGAAAGCGGATGAGGATGGAGGTGGGTGATAT 2012
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db 2013 GTTCATACACGACAAATAGAGATGTCGGAAGTGTGTTTCAACGCTGAAAGTCAT 2072
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db 2073 GATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGGCTGATGGCAAGGATATGAT 2132
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 2133 GATTTTATGGCTCTGGATAGACCCATCAATCAATATAGATCGTGGATAGCAATGGAC 2192
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
Db 2193 AAGATGATAGGCTTTGAACTATGGGATTAGGAGGAAGGGTACCTAAATTTTCATGGCA 2252
QY 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 2253 AATGAATTCGGCCCACTGAGTGGATGATTTCCCTAGGGCTGAACACACCTCTCTCAT 2312
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
Db 2313 GGCTCAGTAATTCGCGGAACCAATTCAGTTATGATAATCGACACGAGATTTGACCTG 2372
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db 2373 GGAGATGCAGAAATATTAAGATACCGTGGTGTGAAGAAATTTGACCGGGCTATGCAGTAT 2432
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720

Db 2433 CTTGAAGATAAATATGATGATTATGACTTCAGAACACCCAGTTTCATATCAGAAAGATGAA 2492
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Db 2493 GGAGATAGGATGATTTGATTTGAAAAAGGAACCTAGTTTGTCTTAAATTTTCACTGG 2552
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2553 ACAAAAAGCTATTTCAGACTATCGCATAGGCTGCTGAAGCTGGAAAAATACAAGGTGCC 2612
QY 761 LeuAspSerAspAspProLeuPheGlyClyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2613 TTGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATAATGCCGAATAT 2672
QY 781 PheThrPheGluGlyTyrTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2673 TTCACCTTTGAGAGTGGTATGATGATCGTCTCGTTCATTAATATGGTGTATGSCACCTAGT 2732
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
Db 2733 AGAACAGCAGTGGTCTATGCTAGTACACAAA-----GAAGAAGAAGAGAA 2780
QY 821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
Db 2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAGAA 2822
RESULT 4
AAT42636
ID AAT42636 standard; DNA; 2576 BP.
XX
AC AAT42636;
DT
XX 03-MAR-1997 (first entry)
DE Class A starch branching enzyme (86con.seq) cloned in QE32.
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX WO9634968-A2.
PD 07-NOV-1996.
PF 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX (NATIT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
PA Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
PS Example 1; Page 49-51; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 2576
Score: 4322.00 Matches: 816
Percent Similarity: 98.44% Conservative: 5

QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
 DB 2164 CTTGAGATAAATATGAGTTTATGACTTCAGAACACCACTTCATATCAGAAAGGATGA 2223
 QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
 DB 2224 GGAGATGAGTATGTTATGTAAGAAAGAAAGAACTAGTTTCTCTTTAAITTTCACTGG 2283
 QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
 DB 2284 ACAAAAAGGTATTCAGACTATCGCATAGGCTGCTGAAGCTGGAAGAAATACAAGGTGGC 2343
 QY 761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
 DB 2344 TTGGACTCAGATCATCCACTTTTGGTGGCTTCGGGAGAAATTCATCATATGCGGAATAT 2403
 QY 781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
 DB 2404 TTCACCTTTGAAGATGGTATGATGATCGTCTCGTTCAATTATGGTGTATGCACCTTGT 2463
 QY 801 LysThrAlaValIleValTyrAlaLeuValAspLysGluGluGluGluGluGlu 820
 DB 2464 AGAACAGCAGTGTCTCATGCTAGTACAGCAAA---GAAGAAGAAGAAGAAGAA 2520
 QY 821 GluGluValAlaAlaValGluGluValValValValGluGlu 834
 DB 2521 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562

RESULT 5

ABK50301
 ID ABK50301 standard; cDNA; 2563 BP.

AC ABK50301;

DT 15-JUL-2002 (first entry)

XX Potato cDNA encoding starch branching enzyme, SBE II.

XX Potato; starch branching enzyme; SBE II; glucan branching enzyme;

KW GBE; ss; gene; plant; transgenic; antisense; food industry;

KW paper industry; chemical industry.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FT 3. 2552

FT /*tag= a

FT /product= "SBE II"

FT /partial

FT /note= "No start codon shown"

XX GB2360521-A.

XX 26-SEP-2001.

XX 20-MAR-2000; 2000GB-0006733.

XX 20-MAR-2000; 2000GB-0006733.

XX (DANI-) DANISCO AS.

XX Poulsen P, Sorensen IS;

XX WPI; 2001-650142/75.

DR P-PSDB; AAU80169.

XX New transformed plants with reduced endogenous starch branching enzyme

PT and heterologous glucan branching enzyme activities, useful for

PT producing starch with improved properties, which is in the food, paper

PT and chemical industries -

XX Example 1; Page 31-35; 61pp; English.

PS

XX

CC The invention relates to a transformed organism, preferably a transformed
 CC plant, having a reduced endogenous starch branching enzyme (SBE)
 CC activity, and having a heterologous glucan branching enzyme (GBE)
 CC activity. The reduced SBE activity is effected via expression of a
 CC nucleotide sequence that is antisense to at least part of a SBE exon.
 CC Also included are a method of producing starch with altered
 CC characteristics comprising (a) providing a plant having reduced
 CC endogenous SBE activity, and having heterologous GBE activity
 CC from the plant; starch obtainable from the transformed plant; and
 CC a nucleic acid construct system capable of directing the expression
 CC of all or part of one or more antisense SBE exons and optionally one or
 CC more heterologous GBE. The transformed plants are useful for producing
 CC starch with modified and improved properties, which is an important raw
 CC material and used in the food, paper and chemical industries. The
 CC present sequence encodes Potato SBE II, used to make transgenic plants of
 CC the invention.

XX Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

Alignment Scores:

Preq. No.: 0 Length: 2563
 Score: 4274.00 Matches: 802
 Percent Similarity: 97.58% Conservative: 6
 Best Local Similarity: 96.86% Mismatches: 14
 Query Match: 95.72% Indels: 6
 DB: 23 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x ABK50301 (1-2563)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
 DB 81 GAAAAGCTCTTACAAATCCGAATCCGACCTTCTACAGTTGAGCATCGGGAAAGTC 140
 QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerSerThrAspGlnPheGluPheThr 40
 DB 141 CTGTGCTGGACCCAGAGTAGCTCTCTCACTCCACAGACCACTTCAACAAATGGATTACT 200
 QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
 DB 201 GAGACATCTCCAGAAATTTCCAGCATCACTGATGATAGATATTTCAACAAATGGAACAC 260
 QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerSerLeuThrGlySer 80
 DB 261 GCTAGCCAGATTAATAACTGAGACGATGACCTTCCAGCGCTCACTGATCTTACAGGAAGT 320
 QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGluGlu 100
 DB 321 GTTGAGAGCTGGATTTTGGTTCATCACTACACTACAGAGGTGGTAAACTGGAGAG 380
 QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
 DB 381 TCTAAACATTAATAACTTTTGAAGAGACAAATTTATGATGAATCTGATAGGATCAGAGAG 440
 QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
 DB 441 AGGGGCATCCCTCCACCTGGACTTGGTCAGAGAGATTTATGAAATAGACCCCTTTTGACA 500
 QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
 DB 501 AACTATCGTCAACACCTTGTATCAGGTATTCACAGTACACAGAACTGAGGAGGCAATT 560
 QY 161 AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
 DB 561 GACAAATGATGAGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACT 620
 QY 181 ArgSerAlaThrGlyIleThrTyrArgGluThrAlaLeuGluAlaGlnSerAlaAlaLeu 200
 DB 621 CGTAGTGTACAGGTATCATTACCGTGAGTGGCTCTCTGGTGGCCAGTCACTGGCCCTC 680
 QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
 DB 681 ATTGGAGATTTCAACAATTGGACGCAATGCTGACATTTATGACTCGGAATGAATTTGGT 740

PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
DR
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 38-39; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
XX Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 0 Length: 3003
Score: 4269.00 Matches: 804
Percent Similarity: 97.25% Conservative: 8
Best Local Similarity: 96.29% Mismatches: 18
Query Match: 95.61% Indels: 5
DB: 17 Gaps: 1

US-10-056-454a-15_COPY_49_882 (1-834) x AAT42634 (1-3003)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaLaserGlyLysVal 20
DB 287 GAAAGTCTCTTACAAATCCGAATCCGACCTTCACAAATTCAGCATCGGGAAATC 346

QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerSerThrAspGlnPheGluPheThr 40
DB 347 CTTGTGCTGGAAATCCAGAGTGATAGTCTCTCATCCATCAACAGATCAATTTGAGTTGCT 406

QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 407 GAGACATCTCCAGAAATCCCGACGATCACTGATGATGATGATGATGATGATGATGATGAT 466

QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerSerSerSerSerThrGlySer 80
DB 467 GCTAGCCAGATTAAACTGGAACGATGACGTTGAGCGGTCAGTGATCTTACAGGAAT 526

QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyLysLeuGluGlu 100
DB 527 GTTGAAGAGCTGGATTGCTTCATCACTACAACTACAAAGGTTGTAACACTGGAGGAG 586

QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
DB 587 TCTAAACATTAATTAATCTCTGAGAGACAAATTAATGATGATGATGATGATGATGATGATGAT 646

QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGlnLeuLeuAspProLeuLeuThr 140
DB 647 AGGGCATCCCTCCACCTGACCTGGTCAGAAAGATTATGAAATAGACCCCTTTTGACA 706

QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 707 AACTATGTCACACCTTGATTACAGTATTCAGTATTCAGTATTCAGTATTCAGTATTCAGTATTC 766

QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 767 GACAAGTATGAGGGTGGTTGGAGACCTTTTCTGCTGTTATGAAAGAAATGGGTTTCACT 826

QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
DB 827 CGTAGTCTACAGGTATCACTTACCGTAGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 886

QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220

DB 887 ATTGGGATTTCAACAATTTGGGACGCAAAATGCTGACTTTTATGATCGCAATGAATTTGGT 946
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
DB 947 GCTGAGAGATTTTCTGCCAAATAATGIGATGGTTCCTCTGCAATCTCAAGGTCC 1006
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
DB 1007 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCATCTGCTGCTGATC 1066
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
DB 1067 AACTACTCTTTACAGCTTCTGATGAATTCATATAATGAATATATATGATGATCCACC 1126
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
DB 1127 GAAGAGGAGAGTATATCTTCCACACCCACGCCCAAGAACCAATCGGTCAGAGAATA 1186
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysLysIleAsnSerTyrValAsnPhe 320
DB 1187 TATGAATCTCATATTTGGAATGAGTAGTCGGAGCTAAATTAACCTCATACGTGAATTTT 1246
QY 321 ArgAspGluValLeuProArgIle-LysLysLeuGlyTyrAsnAlaLeuGlnIleMetAl 340
DB 1247 AGAGATGAAGTCTTCTCTGCATAAAAAGCTTGGGTACATCGGTCGCAATATAGGC 1306
QY 340 alleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPr 360
DB 1307 TATCAAGACATCTTATATGCTAGTTTGGTATCATGTCACAAATTTTTCACACC 1366
QY 360 oSerSerArgPheGlyThrProAspAspLeuLysSerLeuLysLysAlaHisGluLe 380
DB 1367 AAGCAGCGCTTTTGGAAACGCGACGACCTTAAGTCTTTGATGATGAAGCTCAAGCT 1426
QY 380 uGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThrLeuAspGl 400
DB 1427 AGGAATTTGTTCTCATGGACATGTTTCACAGCCATGATCAATTAATATCTTTAGATGG 1486
QY 400 yLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHi 420
DB 1487 ACTGAACATGTTTGCAGCGCACAGATAGTTGTTACTTTTCTGAGCTGAGCTGCTATCA 1546
QY 420 sTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLe 440
DB 1547 TTGATGTTGGGATTTCCGCCCTTTAACTATGGAACCTGGAGGTACTTAGTATCTTCT 1606
QY 440 uSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVa 460
DB 1607 CTCAAATGCGAGATGGTGGTGGATGAGTTCAAAATTTGATGATTTAGATTTGATGGTGT 1666
QY 460 lThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGl 480
DB 1667 GACATCAATGATGTTACTACCACCGGATTTACGGTGGATTCCTCTGGAACACTACGAGA 1726
QY 480 uTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLe 500
DB 1727 ATACTTTGGACTCCCACTGATGAGTGGATGCTGTGTGTTATCTGATCTGCTGCTGCTGCT 1786
QY 500 uIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProTh 520
DB 1787 TATTCATCGGCTTTTCCAGATGCAATTTACCAATTTGGTGAAGATGTTACGGAATCCGAC 1846
QY 520 rPheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
DB 1847 ATTTTGTCTTCCGTTCAAGATGGGGTGTGGCTTTGACTATCGGCTGATATGGAAT 1906
QY 540 eAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIl 560
DB 1907 TGTGATAAATTTGATTTGCTCAAGAAACGGGATGAGATTTGGAGAGTGGGTGATAT 1966
QY 560 eValHisThrLeuThrAsnArgTyrTrpSerGluLysCysValSerTyrAlaGluSerHi 580

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Db 1967 TGTTCAATACACTGACAAATAGAGATGGTCGGAAAAAGTGTCTTTCATACGCTGAAAGTCA 2026
Qy 580 sAspGlnAlaLeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTy 600
Db 2027 TGATCAAGCTCTAGTCGGTGAATAAATAGCAATAGCAATCTGGCTGATGGACAAAGGATATGTA 2086
Qy 600 rAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHi 620
Db 2087 TGAATTTAAGCTCTGATAGACCGCTCAACATCATTAATAGATCTGGGATAGCATATACA 2146
Qy 620 sLysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 640
Db 2147 CAAGATGATTAGGCTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 2206
Qy 640 YAsnGluPheGlyHisProGluThrIleAspPheProArgAlaGluGlnHisLeuSerAs 660
Db 2207 AATGATATCGGCACCTCGAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 2266
Qy 660 pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLe 680
Db 2267 TGGCTCAGTAAATCCAGAAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATG 2326
Qy 680 uGlyAspAlaGluThrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTy 700
Db 2327 GGGAGATGCGAATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCACTA 2386
Qy 700 rLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspG1 720
Db 2387 TCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCACTTCATATACGAAAGGATGA 2446
Qy 720 uGlyAspArgMetIleValPheGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 740
Db 2447 AGGAGATAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2506
Qy 740 pThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAl 760
Db 2507 GACAAAGAGCTATTCAGACTATCCGATATCCGATATCCGATATCCGATATCCGATATCCG 2566
Qy 760 aLeuAspSerAspAspProLeuPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 780
Db 2567 CTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATATCCGAAATA 2626
Qy 780 rPheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCy 800
Db 2627 TTTCACTTTGAAGAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2686
Qy 800 sLysThrAlaValValTyrAlaLeuValAspLysGlyGluGluGluGluGluGluGluGlu 820
Db 2687 TAGAAGCAGGTGGTCTATGCACCTAGTAGACAAA-----GAAGAAGAAGAAGA 2734
Qy 820 uGluGluValAlaAlaValGluGluValValValValValValValValValValValVal 834
Db 2735 AGAAGAAGTAGCAGTAGTAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2777
```

RESULT 7

AA142632

ID AA142632 standard; DNA; 3231 bp.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

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XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

Class A starch branching enzyme (psbe2con.seq).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

amylose; viscosity; potato; ss.

Solanum tuberosum.

Key Location/Qualifiers

45..3200

/*tag= a

/note= "claim 34"

FT

FT

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CDS 228..2855

/*tag= c

W09634968-A2.

07-NOV-1996.

03-MAY-1996;

96WO-GB01075.

10-APR-1996;

96GB-0007409.

05-MAY-1995;

95GB-0009229.

(NATI) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

Sidebottom CM, Westcott RJ;

WPI; 1996-506170/50.

New potato plant starch having high amylose content - also class A

starch branching enzyme and corresp. DNA to alter the viscosity of

starch; for use in food, biodegradable products, adhesives, etc..

Claim 31, 34; Page 53-55; 142pp; English.

Class A starch branching enzyme (SBE) has been obtained from

potatoes. In class A SBE mols., a flexible N-terminal domain,

is found, which is not found in class B mols.

The same sequence is given in Figure 8, however, nucleotides

1-44 omitted.

Sequence 3231 BP; 960 A; 577 C; 739 G; 947 T; 8 other;

Alignment Scores:

Pred. No.:	0	Length:	3231
Score:	4268.50	Matches:	802
Percent Similarity:	97.12%	Conservative:	8
Best Local Similarity:	96.16%	Mismatches:	19
Query Match:	95.60%	Indels:	5
DB:	17	Gaps:	1

US-10-056-454A-15_COPY_49_882 (1-834) x AA142632 (1-3231)

```
Qy 1 GluLysSerTyrAsnSerGluPheArgProSerThrValAlaLysSerGlyLysVal 20
Db 372 GAAAGTCTTCTTACGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCC 431
Qy 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerSerSerSerSerSerSerSer 40
Db 432 CTGTGACCTGGATCCAGAGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
Qy 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
Db 492 GAGACAGCICACAGAAAATCCCCAGCAICAACTGATGATGATGATGATGATGATGATGATG 551
Qy 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerSerSerSerSerSer 80
Db 552 GCTAGCCAGATTAAACTGAGAACGATGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 611
Qy 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlnGlnGlnGlnGlnGlnGln 100
Db 612 GTTGAAGAGTTGGATTTTCTTCATCACAACACTACAACACTACAACACTACAACACTACA 671
Qy 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
Db 672 TCTAAACATTAATACTTCTGAGAGACAAATTAATGATGATGATGATGATGATGATGATG 731
Qy 121 ArgGlyIleProProGlyLeuGlnLysIleTyrGluIleAspProLeuLeuThr 140
Db 732 AGGGGCATCCCTCCACCTGACTTGGTCAGAGATTTATGAAATACACCCCTTTTGACA 791
Qy 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
```

Db 792 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAGAAATAGGGAGGCAATT 851
QY 161 AspLysTyrGluGlyClyLeuGluAlaPheSerArgGlyTyrClyLysMetGlyPheThr 180
Db 852 GACAAAGTATGAGGGTGGTTGGAAGCTTTTCGTGGTATGAAAAAATGGGTTCAC 911
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeu 200
Db 912 CGTAGTGTACAGGTATACCTACCGTGAAGTGGCTCTGGTGGCCAGTCAGTGTCTC 971
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
Db 972 ATTGGAGATTTCAACAATGGACGCAAAATGTGACATTAATGACCTCGGAATGAATGGT 1031
QY 221 ValTrpGluIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySer 240
Db 1032 GTCGGGAGATTTTCGCCAAATAATGGAGTGGTTCCTCGCAATTCCTCAAGGTCC 1091
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db 1092 AGAGTAGAGATAGCGATGACACTTCATCAGGTGTTAAGATTCCATTCCTGCTGGATC 1151
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
Db 1152 AACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATATTAATGATCCACCC 1211
QY 281 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
Db 1212 GAGAGAGAGGTATGCTTCCNACCCACGCGCCAAAGAAACCAAGTCGCTGAGAA 1271
QY 301 TyrGluSerHisIleGlyMetSerProGluProLysIleAsnSerTyrValAsnPhe 320
Db 1272 TATGAATCATATTTGGAATGAGTAGTCGCGAGCCCTAAATTAACATACGTGAATTT 1331
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
Db 1332 AGAGATGAAGTCTCTCTCGCATAAAAACCTTGGGTACAAATCGGTGCAAAATATGGCT 1391
QY 341 IleGlnGluHisSerTyrTrpAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
Db 1392 ATTCAGAGCATTTCTATATGCTAGTTTGGTTAATCATGTCACAAATTTTTCACCA 1451
QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db 1452 AGCAGCCGTTTGGAGCGCCGACGCTTAAGTCTTTGATTAAGCTCATGAGCTA 1511
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db 1512 GGAATGTTGTTCTCATGGACATGTTTCAGCCATGATCAAAATAACTTTTAGATGGA 1571
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
Db 1572 CTCAACATGTTTCAGCGCACAGATAGTTGTTACTTTCACICTGGAGCTCGTGTATCAT 1631
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
Db 1632 TGGATGAGGATCCCGCCCTTTAACTATGGAACCTGGGAGGTACTTAGGTATCTCTC 1691
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db 1692 TCAAAATGCGAGATGGTGGTGGATGAGTGCAAAATTTGRTGGATTTAGATTTGATGGTGT 1751
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db 1752 ACATCAATGATGATATCACTACCGCGGATTCATCGTGGGATTCAGTGGAACTACGAGGAA 1811
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db 1812 TACTTTGGATCGCAACTGATGTGTGCTGCCGTGATCTGATCTGCGCAAGCATCTT 1871
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1872 ATTCATGGGCTTTTCCAGATGCAATTAACCAITGGTGAAGATGTTACGGAAATGCCGACA 1931

521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1932 TTTTGTATTCCTCCCTTCAAGATGGGGTGTGGCTTTCACCTATCGGTGCATATGGCAATT 1991
QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db 1992 GCTGATAAAATGGATTTGAGTTGCTCAAGAAACGGGATGAGGATTCGAGAGTGGGTGAT 2051
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db 2052 GTTCATACACTGACAAATAGAGATGGTCGAAAAAGTGTGTTTCATACGCTGAAGTCA 2111
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheThrPheLeuMetAspLysAspMetTyr 600
Db 2112 GATCAAGCTCTAGTCGGTGTATAAACTATAGCATTCCTGCTGTATGGACAAGGATATGTAT 2171
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 2172 GATTTTATGGCTTTGGATAGACGCTCAACATCATTAATAGATCGTGGGATAGCATTCAC 2231
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly 640
Db 2232 AAGATGATAGGCTTGTAACATATGGATATAGGAGGAGAGAGGTACCTTAATTTCAUGGA 2291
QY 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 2292 AATGAATTCGGCCACCCTGAGTGGATTGATTCCTAGGGCTGAACAACACCTCTCTCAT 2351
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgAspPheAspLeu 680
Db 2352 GGCTCAGTAAATCCCGAAACCAATTCAGTATGATAAATGCAGACGGAGATTTGACCTG 2411
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyr 700
Db 2412 GGAGATGCAAAATATTTAAGTACCGTGGTTCAGAAATTTGACCGGCTATGCAGTAT 2471
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 2472 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCACTCATATCAGAAAGGATGAA 2531
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db 2532 GGAGATAGGAGATTTGATTTGAAAAAGGAAACCTAGTTTGTCTTTAATTTTCACTGG 2591
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2592 ACAAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCTGGAATAACAGGTTGCC 2651
QY 761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2652 TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGAGAAATGATCATTAATGCCGAATGT 2711
QY 781 PheThrPheGluGlyTyrTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2712 TTCACCTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2771
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
Db 2772 AGACAGCAGCTGCTTATGCACTAGTAGACAAA -----GAAGAAGAGAA 2816
QY 821 GluGluValAlaAlaValGluGluValValValValValValValValValValVal 834
Db 2817 GAAGAAGTAGCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2858

RESULT 8
AAT17267
ID AAT17267 standard; DNA: 2531 BP.
XX
AC AAT17267;
XX
DT 03-MAR-1997 (first entry)
XX

Class A starch branching enzyme (direct sequencing).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato; ss.

Solanum tuberosum.

W09634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R; Sidebottom CM, Westcott RJ;

WPI: 1996-506170/50.

P-PSDB; AAR93804.

New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.

Example 1; Fig 9; 142pp; English.

Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols. This sequence was obtained by direct sequencing of PCR fragments amplified from first strand cDNA. Nucleotides which could not be unambiguously assigned are indicated using standard IUPAC notation.

Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

Alignment Scores:

Pred. No.: 0 Length: 2531
Score: 4229.00 Matches: 793
Percent Similarity: 96.96% Conservative: 4
Best Local Similarity: 96.47% Mismatches: 25
Query Match: 94.71% Indels: 0
DB: 17 Gaps: 0

US-10-056-454A-15_COPY_49_882 (1-834) x AAT17267 (1-2531)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
DB 59 GAAAGTCCTTACAAATCCGAAATCCGACCTTACAGTTCCAGCATCGGGGAAAGTC 118
QY 21 LeuValProGlyThrGlnSerAspSerSerSerThrAspGlnPheGluPheThr 40
DB 119 CTGTGCTCCGGAAYCCAGAGTAGTACTCTCATCTCATCAACACCAATTTGATTCAC 178
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 179 GAGACATCTCCAGAAATTTCCGACAGTCAACTGATGATAGTATCAACAAATGGAACAC 238
QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer 80
DB 239 GCTAGCCAGATTAATACTGAGACGATGACGTTCAGCCGCTCAAGTGATCTTACAGGA 296
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGlnGlu 100
DB 299 GTTGAAGAGCTGGATTTTCTTCATCCTACATACAACTACAGAGAGTGGTAACTGGAGAG 358
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
DB 359 TCTAAACATTAATACTTCTGAAGAGACAATATTGATGAATCTCTAGGATCAGAGAG 418

QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
DB 419 AGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCCCTTTTGACA 478
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 479 AACTATCGTCAACACCTTGATACAGGTATTACAGTATACAGTAAAGAACTGAGGAGCAATT 538
QY 161 AspLysTyrGluGlyGlyLeuAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 539 GACAAGTATGAGGGTGGTTCGAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACT 598
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
DB 599 CGTAGTCTACAGCTATCACITACCGTACGTGGCTCTCTGTCGCCAGTCAGTCGCCCTC 658
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
DB 659 ATTGGAGATTTCAACAATTTGGGAGCGCAATGCTGACATTATGACTCGGAATGAATTTGGT 718
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
DB 719 GTCTGGGAGATTTTTCGCCAAATAATGATGATGCTCTCTGCAATTCCTCATGGGTCC 778
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
DB 779 AGAGTGAAGATACGATGGACACATCCATCAGGTGTTAAGGATTCATTCCTGCTGGATC 838
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProLysTrpAsnGlyIleHisTyrAspPro 280
DB 839 AACTACTCTTTACAGCTCTCTGATGAATTCATATATATGAATATATATATGATCCACCC 898
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
DB 899 GAAGAGGAGGTATRTCTCCACACCCAGCGCCAAAGAACCAAGTCCCTGAGATA 958
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
DB 959 TATCAATCTCATATTGGAATGAGTAGTCCGAGCGCTAAATTAATCACTCATGCAATTT 1018
QY 321 ArgAspGlnValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
DB 1019 AGAGATGAAGTCTCTCTCGATAAAAAAAGCTTGGGTACATGCGGTGCAATTTATGGCT 1078
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
DB 1079 ATTCAAGAGCATCTTATTTATGCTAGTTTGGTTATCATGTCACAAATTTTTTTCACCA 1138
QY 361 SerSerArgPheGlyThrProAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
DB 1139 AGCAGCGCTTTGAGACGCGCGAGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1198
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
DB 1199 GGAATTTGTTCTCATGGACATGTTTCACAGCATCATCAATAATATCTTTAGATGGA 1258
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1259 CTGAACATGTTTGACGCGCACAGATAGTTGTTACTTTCACCTCTGGAGCTCGGTGTTATCAT 1318
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
DB 1319 TGGATGTGGATTCGCGCTCTTTAACTATGAAAGCTGGGAGGTACTTAGGTATCTCTC 1378
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
DB 1379 TCAATTCGAGATGGGTGGTGGATGAGTTCAAAATTTGATGGATTTAGATTGATGTG 1438
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1439 ACATCAATGATGATATCTACCCACGAGTATTCGGTGGGATTCCTGGGAACACTACGAGAA 1498

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QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
DB 1499 TACTTTGGACTCGCACTGATGGGATGCTGTGTGATCTGATGCTGGTCAACGATCTT 1558
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
DB 1559 AUTCAGGGGCTTTCCAGATGCAATACCATTTGGTGAAGATGTTAGCGGAATGCGGACA 1618
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
DB 1619 TTTTGTATTCCCGGTTCAAGATGGGGTGTGGCTTTGACTATGCGTGCATATGGCAATT 1678
QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
DB 1679 GCTGATAAATGGATTGCTCAAGAAACGGGATGAGGATTTGGAGAGTGGGTGATATT 1738
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
DB 1739 GTTCATACACTGCACAAATAGAGATGGTCGGAAGAGTGTGTTTCATMCGCTGAAGTCAAT 1798
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
DB 1799 GATCAAGCTCTAGTCGGTGATAAACTATAGCATYCTGGCTGATGGACAAGGATATGTAT 1858
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
DB 1859 GATTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCGTGGATAGCATTCAC 1918
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
DB 1919 AAGATGATTAGGCTTGTAACTATCGGATTAGGAGAGAGGTAACCTAAATTTTCATGGGA 1978
QY 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
DB 1979 AATGAATCGCCACCTGAGTGGATGTATTCCTAGGCTGACAAACACCTCTCTGAT 2038
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
DB 2039 GGCTCAGTAATTCGCGAACCATTACAGTTATGATAAATGCAGACGGAGATTGACCTG 2098
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyr 700
DB 2099 GGAGATGCAGAAATTTAAGATACCATGGGTTCAGAAATTTGACCGGGCTATGCAGTAT 2158
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
DB 2159 CTTGAGATAAATATGAGTTTATGACTTCAGAACACCGCTCATATCACAAGAGATGAA 2218
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
DB 2219 GGAGATAGGATGATTGTTTGAARAGGAAACCTAGTTTGTGCTTTAATTTTCACTGG 2278
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
DB 2279 ACAAAATAGCTATTACAGATTCGCATAGGCTGGCTGAAAGCTGGAATAACAGGTTGGC 2338
QY 761 LeuAspSerAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
DB 2339 ITTGACTACAGATATCCACITTTTGGTGGCTTCGGGAGAAATGATCATATATCGCGAATAT 2398
QY 781 PheThrPheGluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
DB 2399 TTCACCTCTGAAGGATCGTATGATGATCGTCYCYCAATTTATGGTGTATGCCACCTAGT 2458
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGlu 820
DB 2459 AGAACAGCATGGTGTATGCTACTAGTACACAAATAGAGNAGNAGGAAGAAGAAAGAACCC 2518
QY 821 GluGlu 822
DB 2519 GNNGAA 2524
```

RESULT 9

```
AAT42637
ID AAT42637 standard; DNA; 2529 BP.
XX
AC AAT42637;
XX
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX
XX 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 51-53; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
SQ Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
```

```
Alignment Scores:
Pred. NO.: 0 Length: 2529
Score: 4218.00 Matches: 790
Percent Similarity: 96.72% Conservative: 5
Best Local Similarity: 96.11% Mismatches: 27
Query Match: 94.47% Indels: 0
DB: 17 Gaps: 0
```

US-10-056-454A-15_COPY_49_882 (1-834) x AAT42637 (1-2529)

```
QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
DB 59 GAAAGAGCTCTTCAATTCGAAATCCGACCTTCTACAGTTGAGCATCGGGAAGTC 118
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
DB 119 CTTGTGCTGGAAYCCAGAGTAGTCCTCATCTCAACAGACCAATTTGAGTTCAT 178
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 179 GAGACATCTCCAGAAAATTCGCCAGCATCAACTGATGATAGTAGTTCAACATGGAACAC 238
QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer 80
DB 239 GCTAGCCAGATTAACCTGAGACGATGACGCTTGAGCGCTCAAGTATCTTACAGGAAT 298
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyLysLeuGluGlu 100
DB 299 GTTGAAGAGCTGGATTTTGTCTCATCACTACAACTACAAAGAGGTGGTAAACTGGAGAG 358
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgGlu 120
```


RESULT 10

AAT42635

ID AAT42635 standard; DNA; 2975 BP.

XX AAT42635;

XX AC AAT42635;

XX DT 03-MAR-1997 (first entry)

XX Class A starch branching enzyme (11con.seq).

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 KW amylose; viscosity; potato; ss.
 XX Solanum tuberosum.

XX PN WO9634968-A2.

XX PD 07-NOV-1996.

XX PF 03-MAY-1996; 96WO-GB01075.

XX PR 10-APR-1996; 96GB-0007409.

XX PR 05-MAY-1995; 95GB-0009229.

XX XX

PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

PI Sidebottom CM, Westcott RJ;

XX WPI; 1996-506170/50.

XX New potato plant starch having high amylose content - also class A
 PT starch branching enzyme and corresp. DNA to alter the viscosity of
 PT starch; for use in food, biodegradable products, adhesives, etc.
 XX Example 1; Page 40-41; 142pp; English.

XX Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE moles, a flexible N-terminal domain,
 CC is found, which is not found in class B moles.
 XX Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 2975
 Score: 4155.50 Matches: 791
 Percent Similarity: 95.79% Conservative: 6
 Best Local Similarity: 95.07% Mismatches: 26
 Query Match: 93.07% Indels: 11
 DB: 17 Gaps: 1

US-10-056-454a-15_COPY_49_882 (1-834) x AAT42635 (1-2975)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
 |||
 DB 289 GAAAGTCTCTTACAAATCCGAATCCGACCTCTACAGTTGCAGCATCGGGGAAAGTC 348
 |||
 QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
 |||
 DB 349 CRTGTGCTGGAAACCCAGAGTGATAGTCTCTATCTCAACAGACCAATTTAGTTCACT 408
 |||
 QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
 |||
 DB 409 GAGACATCTCCAGAAAATCCCCAGCATCAACTGATGATAGATTCAACAAATGGAACAC 458
 |||
 QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerSerSerSerThrGlySer 80
 |||
 DB 469 GCTAGCCAGATTAATAACTGAGAACGATGAGTGTGAGCCGTCAAGTCTTACAGGAAGT 528
 |||
 QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyGlyLysLeuGluGlu 100
 |||
 DB 529 GTTGAGAGCTGGATTTCCTTCATCACTACACTACAGAGGTGGTAACTGGAGGAG 588
 |||

QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
 |||
 DB 589 TCTAAACATTAATAACTTCTGAAGACACAATATTGATGAATCTGATAGATCAGAGAG 648
 |||
 QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
 |||
 DB 649 AGGGCATCCCTCCAGCTGGACTGGTCAGAGATTATGAATAGACCCCTTTTGACA 708
 |||
 QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGluTyrLysLysLeuArgGluAlaIle 160
 |||
 DB 709 AACTATCGTCACACCTTGATTACAGGTATTCACAGTACAGAACTAGAGGAGCAATT 768
 |||
 QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
 |||
 DB 769 GACAAGTATCAGGGTGGTTTGAAGC-TTTTCTCTGGTTATGAAAAATGGGTTTCAC 827
 |||
 QY 181 ArgSerAlaThrGlyIleThrTyrArgGluThrAlaLeuGlyAlaGlnSerAlaLeu 200
 |||
 DB 828 CGTAGTGCTACAGGTATCACTTACCGTGAAGTGGCTCTGCTGCCAGTCCAGTCCCTC 887
 |||
 QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
 |||
 DB 888 ATTGGAGATTTCACCAATTGGGACGCAAAATGCTGACATTAGACTCGGAATGATTGGT 947
 |||
 QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
 |||
 DB 948 GTCCTGGAGATTTTCTGCCAAATAATGTGATGGTTCTCTCTCAATTCCTCATGGTCC 1007
 |||
 QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
 |||
 DB 1008 AGAGTCAAGATAGCTATGGACATCCACTCAGGTGTTAAGATTCCATCTCTGCTGGATC 1067
 |||
 QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
 |||
 DB 1068 AACTACTCTTACAGCTTCTGTGATGAAATTCATATAATGGAATATATATGATCCACCC 1127
 |||
 QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
 |||
 DB 1128 GAAGAGGAGAGGTATATCTTCCACACCCAGCCCAAGAAACCAAGTCCGTCAGAGATA 1187
 |||
 QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysLysIleAsnSerTyrValAsnPhe 320
 |||
 DB 1188 TATGAATCTCATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1247
 |||
 QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
 |||
 DB 1248 AGAGATCAAGTCTTCTCTCCATAAAAAAGCTTGGGTACAAATGCGCTGCGAATTTATG 1307
 |||
 QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
 |||
 DB 1308 ATTCAAGAGCATTTCTTATTATGCTAGTTTGGTTATCATCATCAAAATTTTTCACCA 1367
 |||
 QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
 |||
 DB 1368 AGCAGCGCTTTTGGACGCCGAGACCTTAAGTCTTCGATTGATAAAGCTCAAGCTA 1427
 |||
 QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
 |||
 DB 1428 GGAATGTGTTCTCTCATGGACATCGTTTCACAGCCATGCATCAAAATATACTTTAGAT 1487
 |||
 QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
 |||
 DB 1488 CTGAACATGTTTGACGSCACCGATAGTTTACTTTCACCTCTGAGCTCGGTGTTTATCAT 1547
 |||
 QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
 |||
 DB 1548 TGGAGTGGGATTC-CGCTCTTTAACTATGGAACGAGGAGGTACTTACGTATCTTCTC 1606
 |||
 QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
 |||
 DB 1607 TCAAAATCGAGATGGTGGTGGATGAGTTTCAAAATTTGATGATTTAGATTCGATGGTGTG 1666
 |||

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QY 461 ThrSerMetMetTyrIleHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1667 ACATCAATGATGATATCACTACCAACGGAATTCGGTGGGATTCACCTGGGAACCTACGAGAA 1726
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrIleuMetLeuValAsnAspLeu 500
DB 1727 TACTTTGGAGCTGCACACTGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1786
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
DB 1787 ATTCAATAGGCTTTCCACATGCAATACCATTTGGTGAAGATGTTAGCGGAATGCCGACA 1846
QY 521 PheCysIleProValGluGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
DB 1847 TTTTGTATCCCGTTCCAGATGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1906
QY 541 AlaAspLysArgIleGluLeuLysLysArgAspGluAspTyrArgValGlyAspIle 560
DB 1907 GCTGATAAATGGATTCAGTGTCTCAAGAAACGGGATGAGATGGAGAGTGGGTGATATT 1966
QY 561 ValHisThrLeuThrAsnArgArgTyrPheSerGluLysCysValSerTyrAlaGluSerHis 580
DB 1967 GTTCATACACTGCAATAGAGATGGTCCGAAAGTGTGTTCATACGCTGAAGTCAT 2026
QY 581 AspGluAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyr 600
DB 2027 GATCAAGCTCTAGTGGTGTATAAATATAGCATTTCTGGCTGATGACAGAGATATGTAT 2086
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
DB 2087 GATTTATGGCTCTGATAGACCGCCACATCATTAATAGATCGTGGGATGATGATGCAC 2146
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGluGlyTyrLeuAsnPheMetGly 640
DB 2147 AAGATGATAGGCTTCTAATCTATGGGATAGGAGAGAGGATGCTAAATTTTCATGGGA 2206
QY 641 AsnGluPheGlyHisProGluTyrPheAspPheProArgAlaGluGluHisLeuSerAsp 660
DB 2207 AATGAATTCGGCCACCTCAGTGGATGATTTCCCTNGSGCTGAGCCACACCTTTCGAT 2266
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
DB 2267 GGTCTAGTAATCCCGGAACCAATTCAGTTATGATAAATGACGAGGAGATTTGACCTG 2326
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGluGluPheAspArgProMetGlnTyr 700
DB 2327 GGAGATGACAGATTAATTAAGATACCATGGTTTACAGAAATTTGACTGGGCTATGCAATAT 2386
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
DB 2387 CTTGAGATAAATCAGTTTATGCTTCAGAACACCACTTCATATACGAAAGGATGAA 2446
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheAsnPheHisTyr 740
DB 2447 GGAGATAGGATGATTTATTTGAAGAGGAACCTAGTTTTCGCTCTTTAATTTTCACTGG 2506
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
DB 2507 ACAAATAGCTATTTCAGCATATCCGATAGCTGCCGAGCCCTGGAAATACAGAGTGTCT 2566
QY 761 LeuAspSerAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
DB 2567 TTGCATCATGATCCACTTTTGTGGCTTCGGGAGAAATTCATCAATATGCCGAATAT 2626
QY 781 PheThrPheGluGlyTyrTyrAspArgProArgProArgSerIleMetValTyrAlaProCys 800
DB 2627 TTCACCTCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2686
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
DB 2687 AGAACACGACGTGGTCTATGACCTAGTAGACAAA----- 2719
QY 821 GluGluValAlaAlaValValGluGluValValValGlu 832
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DB 2720 CTAGAAGTAGCAGTAGTAGAAGAACCACCTTGAAGAA 2755
RESULT 11
AAV38720
ID AAV38720 standard; DNA; 3090 BP.
XX AAV38720;
AC AAV38720;
DT 21-SEP-1998 (first entry)
XX Full length cassava tuber cDNA in pSJ146.
DE Starch branching enzyme; SBE; cassava; ss.
XX Manihot esculenta.
OS Location/Qualifiers
FH Key 35..2760
FT misc_feature /*tag= a
FT /*note= "these nycleotides are SBE II sequence, the
FT remainder are derived from the plamsid"
FT CDS 131..2677
FT /*tag= b
FT /*product= SBE II
W09820145-A2.
XX 14-MAY-1998.
XX 04-NOV-1997; 97WO-GB03032.
XX 05-NOV-1996; 96GB-0023095.
PR (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Jobling SA, Safford R;
XX WPI: 1998-286958/25.
DR P-PSDB; AAM62600.
XX Starch branching gene from cassava - useful for producing altered
XX plants giving modified starch
XX Claim 2; Fig 13; 67pp; English.
XX The present sequence encodes starch branching enzyme (SBE) II. It
XX was isolated from cassava tubers. The products can be used for
XX producing plants having altered starch quantities and qualities.
XX They can also be used for producing altered plants such as cassava,
XX banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
XX and rice plants.
XX Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;
SQ Alignment Scores:
Pred. No.: 3,27e-315 Length: 3090
Score: 3363.00 Matches: 618
Percent Similarity: 84.20% Conservative: 75
Best Local Similarity: 75.09% Mismatches: 98
Query Match: 75.32% Indels: 32
DB: 19 Gaps: 4
US-10-056-454a-15_COPY_49_882 (1-834) x AAV38720 (1-3090)
QY 2 LysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeu 21
DB 284 AAGTCTCTCTATGAATCTGACTCTCTCAAAATTAATCTCTCTGATCTGAGAAGTCTT 343
QY 22 ValProGlyThrGlnSerAspSerSerSerSerSerSerSerSerSerSerSerSer 41
DB 344 GTTCTTGATGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
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US-10-056-454A-15 COPY 49 882 (1-834) X AAC45939 (1-2715)

925	Db	GAGCAGGATAAATATGCTTCAACACATCCTCGTCCAAAGAAACCCACATCGCGCGGGAIR	304
301	QY	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320
985	Db	TATGAATCACATGTTGGAAATGAGTAGTACGGACCAACAGATAAATACATATGCCAACTTT	1044
321	QY	ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla	340
1045	Db	AGAGATGATGTACITCCCGGTATAAAAAAGCTAGCGTATAATGCTGTGAGATAAATGGCC	1104
341	QY	IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro	360
1105	Db	ATTCAAGACGATGCGCTACTATGCGAGCTTTGGGTATCATGTGACAAATTTTTCGCACCT	1164
361	QY	SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu	380
1165	Db	AGCAGCGCGTTTGGAAACACTGATGACCTTAATCTTTGATACAAAAGCTCATGAGCTA	1224
381	QY	GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThrLeuAspGly	400
1225	Db	GCTCTGGTGTCTGTATGATATGTGCACAGCCATGATCAAAAACACACACITGGATGGC	1284
401	QY	LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis	420
1285	Db	CTGACATGTTTGATGGTACTGATGGTCAATATTTCCACTCTGGATCGCGTGTATCAT	1344
421	QY	TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu	440
1345	Db	TGGATCTGGGATCTCGTCTTTTCAATTACGGAAGCTGGGAAGTCTTAGGTATCTCTT	1404
441	QY	SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal	460
1405	Db	TCCAACGCGAGATGGTGGCTGGGAAGAATCAAGTTTGATGGGTTCAGATTGTAGTGTG	1464
461	QY	ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrClnGlu	480
1465	Db	ACTTCCATGATGTACACTCATCATGAGTGGAGTGCAGGTTCGAATTTACTGGGAATTA	1524
481	QY	TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu	500
1525	Db	TACTTTGGATATCTACTGATGTGAGCTGTGCTATCAATCAATGCTGGTGAACGATTG	1584
501	QY	IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr	520
1585	Db	ATTCATGGCGTATACCTCGAGCGTATCTTTGTGCGGGAAGATGTTAGCGGATGCCAGCT	1644
521	QY	PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetalAlaIle	540
1645	Db	TTTTCGGTTCCTGTGGAAGACGGTGGTGTGGTTTTGACTACCGTCTACACATGGCAGT	1704
541	QY	AlaAspLysArgIleGluLeuLeuLysArgAspGluAspTyrArgValGlyAspIle	560
1705	Db	GCAGATAAATGGATGTAGCTCTTAAGAAGAGAGACGAGGACTGCCAGTTGTTGATATA	1764
561	QY	ValHisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHis	580
1765	Db	ACTTTCACGCTTACCAACAGGAGTGGGAGAAAAATGTGCTCTATGCAGAGATCAT	1824
581	QY	AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr	600
1825	Db	GATCAAGCCCTTGTGTGGACAAAACGATAGCTTTCTGGCTATGTGATAGGACATGAT	1884
601	QY	AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis	620
1885	Db	GATTTCATGGCGTGTGTATAGACAGGCCACTCCGCGTGTAGACCGTGGGATGTGTTTACAC	1944
621	QY	LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly	640
1945	Db	AAAATGATCCGCTCATTTACGATGGGATTTGGTGGGAAGGATACCTCAATTTTCATGGGA	2004
641	QY	AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGlnHisLeuSerAsp	660
2005	Db	AACGAATTTGGACACCCAGAAATGATGCGACTTCCCAAGGACCGACGACCTTCTCTGAT	2064

PT wheat and barley -
 PS Example 1; Fig 1; 103pp; English.
 XX

CC The present sequence encodes wheat starch branching enzyme 9,
 CC designated BE1a. The specification describes BE1b. BE1b is a
 CC type II starch branching enzyme (SBE). The BE1b nucleic acids may
 CC be used to genetically transform cereal plants such as wheat or
 CC barley and for altering their nutritional content by modulating
 CC the starch biosynthetic pathway to vary levels of amylopectin and/or
 CC amylose produced in the plant.
 XX

SQ Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,62e-293 Length: 2726
 Score: 3136.00 Matches: 577
 Percent Similarity: 81.95% Conservative: 86
 Best Local Similarity: 71.32% Mismatches: 98
 Query Match: 70.24% Indels: 48
 DB: 22 Gaps: 6

US-10-056-454A-15_COPY_49_882 (1-834) x AAH78337 (1-2726)

QY 12 SerThrValAlaAlaSerGlyLysValLeuValProGlyThrGlnSerSerSerSer 31
 DB 127 GCGACGTTCGGGTGTCGCGCGGACCCCTC-----GGTGTGGCGCGCGCGCGGCG 180
 QY 32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
 DB 181 GCGCAACCTGAGAAATACAGATACCTGAA----- 210
 QY 52 AspValAspSerSerThrMetGluHisAlaSerGlnLeuLysThrGluAsnAspVal 71
 DB 211 GACATCGAGAGCAAAACGGCTGAA----- 234
 QY 72 GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerLeuGln 91
 DB 235 -----GTAACATGACGAGGGGGGACTGCAGAA----- 261
 QY 92 LeuGlnGluGlyGlyLysLeuGluSerLysThrLeuAsnThrSerGluGluThrIle 111
 DB 262 -----AACTTGAATCTTCAGAAACCGACTCAAGGCAATTCGGAACAATC 306
 QY 112 IleAspGluSerAspArg---IleArgGlu-----ArgGlyIle 123
 DB 307 ACTGATGGTGTAAACCAAGAGGTAAAGAACTAGTCGTGGGAGAAACCGCGAGTTGTC 366
 QY 124 ProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
 DB 367 CCAAAACCGAGAGTGGCAGAAAATATACGAGATGACCCACGCTGAAAGATTTTCGG 426
 QY 144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLeuArgGluAlaIleAspLysTyr 163
 DB 427 AGCCATCTTGACTACCGATACAGCAATACAGGAGATTCGTGCTGATTGACCAACAT 486
 QY 164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
 DB 487 GAAGGTGGATGGAGCAATTTCTCGTGTATGAAGAGCTGGATTTACCCGCGAGTGTCT 546
 QY 184 ThrGlyIleThrTyrArgGluThrPalalaLeuGlyAlaGlnSerAlaLeuIleGlyAsp 203
 DB 547 GAAGGTATCACTTACCGAGAATGGCTCTGGAGCGCATTTCTGAGCATTTAGTGTGAC 606
 QY 204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
 DB 607 TTCAACAATTTGGAATCGATGACAGATACATGACAGAGATGATTTGTTGGGAG 666
 QY 224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 243
 DB 667 ATTTCCTCCCTAACAAATGCTGATGGATCCCGACTATTCTCTGAGCTCACGGTGAAG 726
 QY 244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263

DB 727 ATACGCGATGATCTCACTCTGGTGAAGGATTCATTTCTCTGGATCAAGTCTCT 786
 QY 264 LeuGlnLeuProAspGluLeuProTyrAsnGlyIleHisTyrAspProGluGluGlu 283
 DB 787 GTGCGAGCTCCAGGTGAATACCATTCATTCATATATATATATATATATATATATAT 846
 QY 284 AsgTyrIlePheGlnHisProArgProLysProLysProLysSerLeuArgIleTyrGluSer 303
 DB 847 AAGTATGCTTCCACATCTCAACCTAAACAGCAGAGCTACTGAGGATTTATGAATCA 906
 QY 304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
 DB 907 CACATTGGAATGAGCAGCCGAGAGATTAATCAATGCTTAATTTAGGATGAG 966
 QY 324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
 DB 967 GTGCTGCCAAGAATTAAGGCTTGATACAATGCAATGCAATGCAATGCAATGCAATGCA 1026
 QY 344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArg 363
 DB 1027 CATTCACTATGCGAGCTTTGGGTACCATGTTACTAATTTTTCACCAAGTAGCCGT 1086
 QY 364 PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 383
 DB 1087 TTTGGAACCTCAGAGGACTTAAATCCCTGATCATAGAGCAGATGAGCTTGGTTGCTT 1146
 QY 384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
 DB 1147 GTTCTTATGATATGTTTCATAGTCAITCATCAATAATAATACCTTGAGCGCTTGAATGT 1206
 QY 404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTyrMetTrp 423
 DB 1207 TTGATGCGACTGATACATTAATCTCCAGGTGCTCCAGTCCCATCATGATGATGTTGG 1266
 QY 424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAla 443
 DB 1267 GATTCGTCTATTCAACTATGGGAGTTGGAGATTTGAGATTTCTTACTGTCAACGCG 1326
 QY 444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
 DB 1327 AGATGGTGGCTTGAAGAATAAAGTTTGAATGATTTGATTTGATGGGTGACCTCATG 1386
 QY 464 MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly 483
 DB 1387 ATGTATACTACCATGATTAACAAATGACATTTACTGGGAACATATGCGAGTATTTTGA 1446
 QY 484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
 DB 1447 TTTGCTACTGATGTTGATGCGGTAGTTTACTTTGATGCTGTGTCACGATCTAATCAAGA 1506
 QY 504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
 DB 1507 CTTATCTCTGATGCTGATTCCTTCATGTTGAAGATGTCAGTGAATGCCACATTTTCATC 1566
 QY 524 ProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543
 DB 1567 CCGTGTCCAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1626
 QY 544 ArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
 DB 1627 TGGATTGAACCTCTCAAGCAAGTCAACCAATCTTGGAAAAATGGGTGGTGGTGGTGGT 1686
 QY 564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
 DB 1687 CTAACAATAAGAGGTGGCTTGAGAAAGTGTGTAATGATGAGAAAGTCATGATCAAGCA 1746
 QY 584 LeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyrAspPheMet 603
 DB 1747 CTACTTGGTGAACAGACTATTCGATTCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1806
 QY 604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623

Mon Jul 7 12:40:56 2003

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Db      1807 GCCTGGANAGGCTTCAACTCCCTCGCATTCGCTGGCATAGCATTAATAAATGATC 1866
QY      624  ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db      1867 AGGCTTGTCCACATGGGTTAGGTGGTGAAGGCTATCTTAACCTTCATGGGAAATGAGTTT 1926
QY      644  GlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db      1927 GGGCATCTGAATGATAGATTTTCCAGAGGTCGCGAACTCTCCAAACGGGAAAGTT 1986
QY      664  IleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 683
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QY      684  GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
Db      2047 GATTTCTTAGATATCATGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2106
QY      704  LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db      2107 AATATATGGTATTATGACATCTGACATCTGACATCTGACATCTGACATCTGACATCTG 2166
QY      724  MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db      2167 GTGATCACTTCGAAGAGAGAGATTTGGTATTTGTTTCACTTCCACTGAGGCAATAGC 2226
QY      744  TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrIlyValAlaLeuAspSer 763
Db      2227 TTTTGTGACTACCGTGTGGTGTTCAGAGCTGGGAGTACAAAGTGGCTTAGACTCC 2286
QY      764  AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
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QY      784  GluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
Db      2347 GAACATCCGCATGACAAACAGGCGCGCTCTTCTCGGTGTACACTCCGAGCAAGACTGG 2406
QY      804  ValValTyrAlaLeuValAspLysGlu 812
Db      2407 GTCGTGTATGCCCTTACAGAGTAAGAA 2433

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Search completed: July 6, 2003, 03:15:45
Job time : 646 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: July 6, 2003, 02:55:51 ; Search time 100 Seconds
(without alignments)
2557.684 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882
Perfect score: 4465
Sequence: 1 EKSYNSEFRPSTVAASKV.....EEEEEVAAVEVVVEE 834

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US10056454/runat_01072003_145501_8303/app_query.fasta_1.1031
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-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2_6/ptodata/1/ina/6C_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4320	96.8	3074	4	US-09-087-277-1
3	3026.5	67.8	2665	4	US-09-087-277-1
4	3021.5	67.7	2725	3	US-08-941-445A-14
5	2676.5	59.9	2087	4	US-09-257-894-9
6	2669.5	59.8	2165	4	US-09-257-894-8
7	2462	55.1	1393	4	US-09-087-277-3
8	2462	55.1	1393	4	US-09-087-277-3
9	2165	48.5	3128	3	US-08-716-449-1
10	2107	47.2	2565	4	US-09-257-894-24
11	2107	47.2	2763	3	US-08-941-445A-16
12	2104	47.1	2487	4	US-09-257-894-19

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20	522.5	11.7	2426	4	US-08-528-0260-3
21	516.5	11.6	4411529	4	US-09-103-840A-1
22	507.5	11.4	4403765	4	US-09-103-840A-2
23	455.5	10.2	11384	4	US-08-961-527-45
24	261.5	5.9	1680	4	US-09-242-690A-14
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26	241.5	5.4	2712	2	US-08-410-784A-1
27	238	5.3	414	4	US-09-257-894-2
28	233	5.2	1791	1	US-08-399-646-3
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30	233	5.2	1791	2	US-08-961-240-3
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34	233	5.2	2056	2	US-08-961-240-13
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ALIGNMENTS

RESULT 1

US-09-087-277-1
Sequence 1, Application US/09087277B
Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE OF INVENTION: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: beii gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189)..(332)

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FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Alignment Scores:
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Score: 4320.00 Matches: 812
Percent Similarity: 97.96% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 13
Query Match: 96.75% Indels: 4
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Db 393 CTGTGCTGGAAACCCAGAGTGATAGCTCTCTCATCCWCAACAGACCAATTTGAGTTCACT 452
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAlaAspSerSerThrMetGluHis 60
Db 453 GAGACATCTCCAGAAATTCGCCAGCATCACTGATGTAGATAGATTTCAACAAATCGAACAC 512
QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerSerSerSerSerSerSer 80
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QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyLysLeuGluGlu 100
Db 573 GTTGAAGAGCTGGATTTTGTCTCATCACTACAACTACAAAGAGTGGTAAAGTGGAGAG 632
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerArgIleArgGlu 120
Db 633 TCTAAACATTAATTAATCTCGAGAGCAATTAATGATGATCTGATAGATCAGAGAG 692
QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleLeuAspProLeuLeuThr 140
Db 693 AGGGGCACTCCACCTGGAGCTTGTCAGAGAAATTAATGAATAGACCCCTTTTGACA 752
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLeuArgGluAlaIle 160
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181 ArgSerAlaThrGlyIleThrTyrArgGluTupAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
933 ATTGAGATTTCAACAATTTGGGACGCAAAATGCTGACATATGACATCGAATCGAATTTGT 992
221 ValTrpGluIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySer 240
993 GTCTGGAGATTTTCTGCCAAATAATGTGGATGGTCTCCCTGCAATTCCTCATGGGTCC 1052
241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaIlePhe 260
1053 AGAGTGAAGATACGTATGACACTCCATCAGGTGTTAAGGATTCATTCCTGCTGGATC 1112
261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
1113 AACTACTCTTTACAGCTTCTGATGAATTCATATAATGCAATATATATGATGACACCC 1172
281 GluGluGluArgTyrIlePheGlnHisProArgProLysProLysSerLeuArgIle 300
1173 GAAGAGGAGAGGTATATCTTCCAAACACCCCGCCCAAGAACCAANGTCGCTGAGAATA 1232
301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
1233 TATGATCTCATATTGGAATGAGTAGTCGGAGCCTAAATAAATTAACATCATACGTAATTT 1292
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1293 AGAGATGAAGTCTTCTCCGCAATAAAAGCTTGGTACATCGGTCGGAATATGAGT 1352
341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
1353 ATTCAAGAGCATCTTATATATGCTAGTTTGGTTATCATGTCACAAATTTTNGACCA 1412
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1413 AGCAGCCGTTTGAACCCGACGACCTTAAGTCTTTGATGATGAAGCTCATGAGCTA 1472
381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
1473 GGAATTTGTTCTCATGGACATTTGTTACAGCCCATGCATCAAAATAATACATTTAGATG 1532
401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
1533 CTGAACATGTTGACGGCAGACATAGTTGTTACTTCTACTCTGGAGCTCGTGGTTATCAT 1592
421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
1593 TGGATCGGGATTCGCCCTCTTTAACTATGAAACTGGGAGTACTTAGTATCTTCTC 1652
441 SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
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461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
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481 TyrPheGlyLeuAlaThrAspValAlaValValTyrLeuMetLeuValAsnAspLeu 500
1773 TACTTTGGACTCGCAACTGATCTGGATGCTGTGTATCTGATCTGCTGCTGCAACATCTT 1832
501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
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QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTyrArgValGlyAspIle 560
Db 1953 GCTGATAAATGGATGAGTGGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATT 2012
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Db 2133 GATTTTATGGCTCTGGATAGACNTCAACATCAATTAATAGATCGTGGATAGCATTCAC 2192
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly 640
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QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
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RESULT 2

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US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
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; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:berII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
; US-09-658-499-1
Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4320.00 Matches: 812
Percent Similarity: 97.96% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 13
Query Match: 96.75% Indels: 4
DB: 4 Gaps: 1
US-10-056-454a-15_COPY_49_882 (1-834) x US-09-658-499-1 (1-3074)
QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
Db 333 GAAAAGTCTTCTTACATTCGATCCGACCTTCTACAGTTGCAGATCGGGAAAGTC 392
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThr 40
Db 393 CTTGTGCTGGACCCAGAGTGTAGCTCCTCATCTCAACAGACCAATTTGAGTTCACT 452
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerSerThrMetGluHis 60
Db 453 GAGACATCTCCAGAAATATCCCGAGCATCAACTGATGATAGTATGATCAACAATGGAACAC 512
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QY	81	ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyLysLeuGluGlu	100	QY	441	SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal	460
DB	573	GTTGAAGAGCTGGGATTGCTTCATCACTACACTACAGAGGTGGTAACTGGAGGAG	632	DB	1653	TCAATGGCAGATGGTGGTGGATGAGTTCAAATTTGATGGATTAGATTGATGGTGG	1712
QY	101	SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu	120	QY	461	ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu	480
DB	633	CTTAACACATTAAATACTTCTGAAGAGACAATTTATGATGAATCTGATAGGATCAGAGAG	692	DB	1713	ACATCAATGATGATPACTCACCGGATATCGGTGGGATTCACCTGGGAACATACGAGAA	1772
QY	121	ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr	140	QY	481	TyrPheGlyLeuAlaThrAspValAspAlaValTyrLeuMetLeuValAsnAspLeu	500
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DB	753	AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAGAACTCAGGAGGCAATT	812	DB	1833	ATTCATGGGCTTTTCCAGATGCAATACCATTTGGTGAAGATTTAGCGGAATGCCGACA	1892
QY	161	AspTyrGlyGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr	180	QY	521	PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle	540
DB	813	GACAAAGTATGAGGCTGGTTTGAAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACT	872	DB	1893	TTTTNTATCCCGTTCAAGATGGGCTGTGGCTTTGACTATCGGCTGCATATGGCAATT	1952
QY	181	ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyValGluGlnSerAlaLeu	200	QY	541	AlaAspLysArgIleGluLeuLeuLysLysLysArgGluAspTrpArgValGlyAspIle	560
DB	873	CGTAGTGTACAGGTATCACTTACCGTGAGTGGGCTCCGTGGCCAGTCACCTGCCCTC	932	DB	1953	GCTGATAAATGGATTGAGTTGCTCAAGAAACCGGATGAGGATGGAGAGTGGGTATAT	2012
QY	201	IleGlyAspPheAsnAspTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly	220	QY	561	ValHisThrLeuThrAsnArgTyrTrpSerGluLysCysValSerTyrArgLysHis	580
DB	933	ATTGAGATTTCACAAATGGACGCAATGCTGACATTTATGACTCGGAATGAATTTGCT	992	DB	2013	GTTTCATACACTGACAAATAGAGATGGTCGGAAGAGTGTTCATACGCTGAAAGTCAT	2072
QY	221	ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer	240	QY	581	AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr	600
DB	993	GTCGGGAGATTTTCTGCCAAATAATGTGGATGTTCTCTGCAATTCCTCATGGGCTCC	1052	DB	2073	GAACAACCTAGTCGGTGATAAACTATAGCAATTCCTGGTGTGAGAGAGGATATCTAT	2132
QY	241	ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle	260	QY	601	AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis	620
DB	1053	AGAGTGAAGATACGTATGACACTCCATCAGGTGGTAAAGATTCCATTCCTGCTGGATC	1112	DB	2133	GATTTATGGCTCTGATAGACCTCAACATCATTAATAGATCGTGGATAGCATTCGCAC	2192
QY	261	AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro	280	QY	621	LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly	640
DB	1113	AACTACTCTTTACAGCTTCTCATGATAATCCATAATATGGAATATATTATGATCCACCC	1172	DB	2193	AAAGATGANTAGGCTTGTAACATGCGGATAGGAGGAGAGAGGTAACCTAAATTCATGGA	2252
QY	281	GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle	300	QY	641	AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp	660
DB	1173	GAAGAGGAGAGGTATATCTTCCAAACACCCAGCCCAAGAAACCAAGTCGCTGAGAATA	1232	DB	2253	AATGAATTCGGCCACCTCGAGTGGATTTCTCTAGGGCTGAACACACCTCTCTCAT	2312
QY	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320	QY	661	GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu	680
DB	1233	TATGAATCATATGAGATGAGTATCGGAGCCCTAAATTAACCTCATACGTGAATTTT	1292	DB	2313	GGCTCAGTAATTCGGGAAACCAATTCAGTTATGATAAAGCGACACGAGATTGACCTG	2372
QY	321	ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla	340	QY	681	GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr	700
DB	1293	AGAGATGAGTTCTTCTCGCATAAAAAGCTTGGGTACAAATCGGCTGCAAAATATGSGCT	1352	DB	2373	GGAGATCCAGNAATTTAAGATACCGTGGGTTCAGAAATTTGACCGGCTATGACGAT	2432
QY	341	IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro	360	QY	701	LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu	720
DB	1353	ATTCAAGAGCATTTCTATTATGCTAGTTTGGTATCATGCTCAAAATTTTNGCACCA	1412	DB	2433	CTTCAACATAAATATGATTTATGACTTCAGAACACCATTCATATCAGGAAGATGAA	2492
QY	361	SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu	380	QY	721	GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp	740
DB	1413	AGCAGCGCTTTTGGACNCCCGAGGACCTTAAGCTTTGATGATAAAGCTCATGACCTA	1472	DB	2493	GGAGATAGGATGATGTATTTGAAAAAGAAACCTAGTTTGTCTTTAATTTTCACTGG	2552
QY	381	GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly	400	QY	741	ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla	760
DB	1473	GGAATTTCTTCTCATGGACATTTGTCACAGCCATGCATCAAAATAATACTTTAGATGGA	1532	DB	2553	ACAAAAAGCTATTTCAGACTATCGCATAGGCTGCCTGAAGCTGGAAGAAATCAAGGTTGCC	2612
QY	401	LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis	420	QY	761	LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGlnTyr	780
DB	1533	CTGAACATGTTTGACGGCACAGATAGTTGTTTACTTTCCTCCTGAGGCTCGTGGTTATCAT	1592	DB	2613	TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGATGATGATCAATATCCCGAATAT	2672
DB				DB	781	PheThrPheGluGlyTyrTrpTyrAspArgProArgSerIleMetValTyrAlaProCys	800

Db 2673 TTCACCTTGAAGCATGGTATGATGATCGCTCGTTCATTTATGGTATGACCTAGT 2732
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGlu 820
Db 2733 AGACACAGTGGTCTAGTACCTAGTACAAA-----GAAGAAGAAGAA 2780

QY 821 GlnGluValAlaAlaValGluGluValValValValGluGlu 834
Db 2781 GAAGAAGTACACCTAGTAGAGAGTAGTAGTAGAGAA 2822

RESULT 3

US-09-257-894-1

; Sequence 1, Application US/09257894

; Patent No. 6376749

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Klein, Theodore M.

; APPLICANT: Hubbard, Natalie L.

; APPLICANT: Lightner, Jonathan E.

; TITLE OF INVENTION: No. 6376749el Starches via Modification of

; TITLE OF INVENTION: Expression of Starch Biosynthesis

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 95

; SOFTWARE: Version 7.0a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/257,894

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/091,052

; FILING DATE: JUNE 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Majarian, William R.

; REGISTRATION NUMBER: 41,173

; REFERENCE/DOCKET NUMBER: BB-1066-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-992-4926

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2665 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 79..2476

US-09-257-894-1

Alignment Scores:

Pred. No.:

Score: 0

Length: 2665

Matches: 553

Conservative: 75

Best Local Similarity: 83.85%

Mismatch: 100

Query Match: 67.78%

Indels: 21

Gaps: 3

US-10-056-454a-15_COPY_49_882 (1-834) x US-09-257-894-1 (1-2665)

QY

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Db 277 GAGATGATGCGCTCGCATCAAGGCGTGAC----- 306
QY 87 AlaSerSerLeuGlnGluGlnGluGlyClyLysLeuGluGluSerLysThrLeuAsnThr 106
Db 307 -----TCGGCTCAATTCAGTCG-----GATGAACCTGGAGGTACACACATT 348
QY 107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121
Db 349 TCTCAAGAGACACACGTGCGGTGCTGGTGTGCTGCTCAAGCTTCAACAGAGTTGGA 408
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db 409 GTGTGTCCTCCCAAGAGGATGGACAAAAATATTCAGATTGACCCCATGTCGAAGGC 468
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 469 TATAAGTACCATCTTGAGTATCGGTACAGCTCTATAGAAGATCCGTTTCAGACATTGAT 528
QY 162 LysTyrGluGlyLeuGluAlaPheSerArgTyrGluLysMetGlyPheThrArg 181
Db 529 GAACATGAAGGAGGCTTGAAGCCTTCTCCGTAGTTATGAGACATTTGGATTAAAGCC 589
QY 182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeuIle 201
Db 589 AGCGCGGAAGGTATCATCATATCGAAGATGGCTCTCGAGCATTTTCTGCAGCATTTGGT 648
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 649 GGTGACTTCAACAACTGGGATCCAAATGACAGATCGTATGAGCAAAATGAGTTGGTGT 708
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 709 TGGGAAATTTTCTGCTCAACAATGCAGATGGTACATCATCTATTCCTCATGATCCTGT 768
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaIleAsn 261
Db 769 GTAAGGTGAGATGGATATCTCATCAGGATTAAGGATTCATATCCAGCTGGATCAAG 828
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 829 TACTCAGTCAGCCCCCAGGAGAAATACCAATATGATGGGATTTATTATGATCTCCTGAA 888
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db 889 GAGGTAAAGTATGTGTTCAGGATCGCAACCTTAAACGCAAAATCATTCGGATATAT 948
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 949 GAACACATGTCGGAATGATAGTACCGGAAACCGAAGATAACACATATCTAACTTAGG 1008
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db 1009 GATGAAGTCTCCCAAGATAAAAAACITGGATACATGCAATGCGAGTCAAAATATGCAATC 1068
QY 342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
Db 1069 CAAGAGCACTCATATTATGGAAGCTTGGATACCAATGTAACATAATTTTTCGCGCACT 1128
QY 362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db 1129 ACTCGTTTGGTACCCCAAGAGATTGGAAGTCTTTGATTGATAGACATGAGCTTGGT 1188
QY 382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db 1189 TTGCTAGTTCTCAUGATGTGGTGTATAGTATGCGTCAAGTAATACTTCTGGATGGGTG 1248
QY 402 AsnMetPheAspCysThrAspSerCystTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db 1249 AATGGTTTGTATGGTACAGATACACATTACITTCACAGTGGTCCAGTGGCCATCCTAC 1308
QY 422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuSer 441

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Qy 442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db 1369 AATGCTAGATGGTGGCTGAGGAATATAAGTTTGAATGGTTTCCGTTTGTGAGTGGTACC 1428
Qy 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db 1429 TCCATGATGTACACTCACCGGATTAACAATACATTTACGGGAAGCTTCAATGAGAT 1488
Qy 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1489 TTTGGCTTGGCCACCGAGTAGATCCAGTGGTTTACTGCTGGTAAATGATCAAT 1548
Qy 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1549 CATGACATTTATCCTGAGGCTGTACCATTTGTTGAAGATGTTAGTGGAAATGCTACATTT 1608
Qy 522 CysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1609 GCCCTTCCTGTTACGATGGTGGGTAGTGTGTTGACTATCGGATGCATATGGCTGGCT 1668
Qy 542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValcIlyAspIleVal 561
Db 1669 GACAATGGATGACCTTCTCAAGCAAGTGTGAATCTGGAAGTGGTGTATATG 1728
Qy 562 HisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1729 CACACACTGACAAATAGAGGTGGTTAGAGAGTGTGTAACATGCTGAAAGTCATGAT 1788
Qy 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db 1789 CAAGCATAGTCGGGCACAAAGACTATTCGCTTTGGTTGATCGACAAAGATATGATGAT 1848
Qy 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1849 TTCAATGGCCCTCGATAGACTTCAACTCTACCAATGATGTCGGGATGATACATAAAG 1908
Qy 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 641
Db 1909 ATGATTAGACTTATCAATGAGTGTAGGAGGAGGGCTATCTTAAATTCATGGGAAT 1968
Qy 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1969 GAGTTGGACATCCTGAATGATAGATTTTCCAAAGAGTCCGCAAGACTTCCCAAGTGT 2028
Qy 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db 2029 AAGTTTATCCAGGGAATAACAACAGTTATGACAAATGCTGCAAGATTTGACCTGGGT 2088
Qy 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db 2089 GATGACAGACTATCTTAGTATCATGTTGATGCAAGAGTTTGAUCAGGCAATGCAACATCT 2148
Qy 702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db 2149 GACCAAAATATGAATCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAG 2208
Qy 722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db 2209 GATAAGGTGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2268
Qy 742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
Db 2269 AACAGCTATTTGACATACCTGATTTGGTTGCGAAAGCCGTGGGTGTATAGGTGGTCTTG 2328
Qy 762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
Db 2329 GACTCCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCCGAGCCGAGCACTTC 2388
Qy 782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db 2389 ACCGGCGGACTGTTGCGCATGATAATAGGCCATATTCCTCCGTTTATACCAACGACGA

Qy 802 ThrAlaValValTyrAlaLeuValAsp 810
Db 2449 ACATGTGCTGCTATGCTCCAGTGGAG 2475
RESULT 4
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
; US-08-941-445A-14
Alignment Scores:
Pred. No.: 0
Score: 3021.50
Percent Similarity: 83.71%
Best Local Similarity: 73.70%
Query Match: 67.67%
DB: 3
Length: 2725
Matches: 552
Conservative: 75
Mismatch: 101
Indels: 21
Gaps: 3
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Db 319 -----TCGCTCAATTCAGTCG-----GATGAATGGAGGTACACGACATT 360
QY 107 SerGluGluThr-----llelleAspGluSerAspArglleArgGluArg 121
Db 361 TCTGAAGAGACAAACGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 420
QY 122 GlylleProProGluGlyLeuGlyGlnLyslleTyrgluLeuAspProLeuLeuThrAsn 141
Db 421 GTGGTCCCCCAACCAAGCATGATGCAAAAAAATATCCAGATTGACCCCATGTCGAAGGC 480
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 481 TATAAGTACCATTCTTGAGTATCGGTACAGCCCTATAGAGAATCCGTTTCAGACATTGAT 540
QY 162 LysTyrGluGlyGlyLeuAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 541 GAACATGAAGAGGGCTTGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTAAATGCC 600
QY 182 SerAlaThrGlylleThrTyrArgGluTyrAlaLeuGlyAlaSerAlaAlaLeuIle 201
Db 601 AGCGGGAAGGTATCACATATCGAAGTGGGTCTCTGGAGCATTTTCTGCACCATTTGGTG 660
QY 202 GlyAspPheAsnAsnTyrAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 661 GGTGACGTCAACAACCTGGATCGCAATGCGATCGTATGAGCAAAATGAGTTTGGTGT 720
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 721 TGGGAATTTTCTGCCCTAACATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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Db 841 TACTCAGTGCAGGCCCCAGAGAAATACCATATGATGGATTATATGATCCTCTCTGAA 900
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db 901 GAGTAAAGTATGTCTTCAGGCATGCGCAACCTAAACGACCAAAATCATCTCGGATAT 960
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 961 GAACACATGTCGNAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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Db 1141 AGTCGTTTTGTACCCAGAGATTTGAAGTCTTTGATGATGATGATGATGATGATGATGATGAT 1200
QY 382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
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QY 402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db 1261 AATGGTTTTGATGGTACAGATACATATTTTACAGTGGTCCAGCTGGGCCATCTCTG 1320
QY 422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db 1321 ATGTGGGATCTCGCCTATTAACTATGGGAACCTGGGAAGTTTAAAGATTCTTCTCTCC 1380

QY 442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db 1381 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTCATGGTTCCGTTTGTATGGTGTGACC 1440
QY 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db 1441 TCCATGATGATACATCCACCGGATTACAAGTAACTATTACGGGGAACTTCAATGAGTAT 1500
QY 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1501 TTTGGCTTTGCCACCGAGTAGAGCACTGGTTTACTGTGATGTGGTAAATGATCTAAT 1560
QY 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1561 CATGGACTTATCTCAGGCTGTAACCATTTGGTGAAGATCTAGTGAATGCCATACATT 1620
QY 522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1621 GCCCTTCTCTCAGCATGGTGGGTAGTTTGTACTATCGATCGATGATGGTGTGGCT 1680
QY 542 AspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db 1681 GACAAATGGATTGACCTTCTCAAGCAAGTGTGAACCTTGGAGATGGGTGATTTGTG 1740
QY 562 HisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1741 CACACACTGACAAATAGGAGGTGTAGAGAAGTGTAACTTATGCTGAAAGTCATGAT 1800
QY 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db 1801 CAAAGCATTTAGTCGGCACAAGACTATTGGCTTTGTGTTGATGACAAGATATGTATGAT 1860
QY 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1861 TTTCATGGCCCTCGATAGACCTTCAACTCTACCATTGATCGGGGATACATTTACATTAAG 1920
QY 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsn 641
Db 1921 ATGATTTAGACTTATCAAAATGGTTTGTAGGAGAGAGGGCTATCTTAATTTATGGSAAAT 1980
QY 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1981 GAGTTTGGACATCCCTGAATGGATAGATTTCACAGAGGTCCGCAAGACTTCCAAGTGT 2040
QY 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db 2041 AAGTTTATTTCCAGGGAATAACAACAGTATGACAAATGTCTGCGAAGATTTGACCTGGGT 2100
QY 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db 2101 GATGAGACTATCTTTAGGTATCATGATGATGCAAGAGTTTGTATGATGCAAGCAATCTT 2160
QY 702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db 2161 GAGCAAAATATGATTTATGATCATCATCTGATCACCAGTATTTCCCGGAAACATGAGGAG 2220
QY 722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db 2221 GATAAGGTGATTTGTCGAAAAAGGAGATTTGGTATTTGTGTTTGTCTCACTTCCACGCAAC 2280
QY 742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
Db 2281 AACAGCTATTTTGACTACCGTATTGGTTGTCGAAAGCCTGGGTGTATTAAGGTGGTCTTG 2340
QY 762 AspSerAspProLeuPheGlyPheGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
Db 2341 GACTCCGACGCTGACATATTTGGTGGATTTAGCAGGATFCCATCAGCAGCAGCAGCAGC 2400
QY 782 ThrPheGluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db 2401 ACCGCCGACTCTTCGCTATGATAATAGCCCATTTCACTTCTCGGTTTATACCAAGCAGA 2460

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QY      802 ThrAlaValValTyrAlaLeuValAsp 810
Db      2461 ACATGTGCTGCTATGCTCCAGTGGAG 2487

RESULT 5
US-09-257-894-9
; Sequence 9, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-257-894-9

Alignment Scores:
Pred. No.:      2.8e-289      Length:      2087
Score:          2676.50      Matches:     485
Percent Similarity: 85.12%      Conservative: 64
Best Local Similarity: 75.19%      Mismatches: 75
Query Match:      59.94%      Indels:      21
DB:                4          Gaps:           3

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-9 (1-2087)
QY      67 GluAsnAspValGluProSerAspLeuThrGlySerValGluLeuAspPhe 86
Db      199 GAGAAATGCGCTCCATCAGGGGTGAC-----228
QY      87 AlaSerSerLeuGlnLeuGlnGlyLysLeuGluSerLysThrLeuAsnThr 106
Db      229 -----TCGGCTCAATTCAGTCG-----GATGAATGGAGGTACCAGACATT 270
QY      107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121
Db      271 TCTGAAGAGACAACTGCGGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 330
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QY      122 GlyIleProProGlyLeuGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db      331 GTGFTCCCCCAACGCGATGGACAAAATAATCCAGATTGACCCCATGTGCAAGGC 390
QY      142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db      391 TATAAGTACCATCTTGATATCGGTACAGCCTCTATAGAGAATCCGTTCAGACATGAT 450
QY      162 LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db      451 GAACATGAAGGAGGCTTGGAAAGCCTTCGCCGTAGTTATGAGAAAGTTTGGATTTAATGCC 510
QY      182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db      511 AGCGCGGAAGGTATCACATATCGAGATGGCTCTCGGAGCATTTCTTCGACATTTGTTG 570
QY      202 GlyAspPheAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db      571 GGTGACTTCAACACTGGGATCCAAATGACATGCTATGACAGAAAATGAGTTTGTGTT 630
QY      222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db      631 TGGGAAATTTTCTGCCTAACANTGCGAGATGATACATCACCTATTCTCTCATGATCGT 690
QY      242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db      691 GTAAAGGTGAGATGATGATCTCATCAGGATAAAGGATTCATATCCAGCTGGATCAAG 750
QY      262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db      751 TACTCAGTCAGGCCCCAGGAGAAATACCATATGATGGGATTTATATGATCTCTGAA 810
QY      282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db      811 GAGTTAAAGTATGTGTTCAGGCATCGCAACCTAAACGACCAAAATCATTCGGATATAT 870
QY      302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db      871 GAAACACATGTCGAATGAGTAGCCGGAACCGAAGATAACACATATATAACTTTTGG 930
QY      322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db      931 GATGAGTCTCTCCAGAAATAAAAACITTGATACATCGCAGTGCATAATATGGCAATC 990
QY      342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
Db      991 CAAGACACTCATATATATGGAAGCTTTGGATACCATGTAACATAATTTTTTGGCCAA 1050
QY      362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db      1051 AGTCGTTTGGTACCCAGAAAGATTTGAAGTCTTTGATTGATAGACACATGAGCTTGGT 1110
QY      382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db      1111 TTGCTAGTTCTCATGATGTTGTTTCATAGTCATGTCAGTAACTACTCTGGATGGTTG 1170
QY      402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db      1171 AATGGTTTGTGTTACAGATACACATTACTTTACAGTGGTGGTGGTGGTGGTGGTGGT 1230
QY      422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db      1231 ATCTGGGATTTCTCGCTATTTAACTATGGGAATGGGAAGTTTATAGATTCTCTCTCC 1290
QY      442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db      1291 AATGCTAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1350
QY      462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db      1351 TCCATGATGTACACTCACCAGGATTACAAGTAACTTTACGGGGAACCTTCAATGATGAT 1410
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QY 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1411 TTGGCTTTGCCACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
QY 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1471 CATGACCTTTATCCCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1530
QY 522 CysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1531 GCCCTTCCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
QY 542 AspLysArgIleLeuLeuLysLysArgAspGluAspTyrArgValGlyAspIleVal 561
Db 1591 GACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1650
QY 562 HisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1651 CACACACTGACAAATAGGAGGTGGTGTAGAGAAAGTGTAACTATGCTGAAAGTCATGAT 1710
QY 582 GlnAlaLeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyrAsp 601
Db 1711 CAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1770
QY 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1771 TTCATGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
QY 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 641
Db 1831 ATGATTAGACTATACAAATGGGTTTAGAGAGAGGCTATCTTAATTTTCATGGGAAAT 1890
QY 642 GluPheGlyHisProGluThrIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1891 GAGTTTGACATCCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1950
QY 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGly 681
Db 1951 AAGTTTATCCAGGGAATTAACAAGTATGACAAATGTCGTCGAAGATTGACCTGGGT 2010
QY 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db 2011 GATCAGACTATCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2070
QY 702 GluAspLysTyrGlu 706
Db 2071 GAGCAAAAATGAA 2085
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RESULT 6

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US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-257-894-8
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Alignment Scores:

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Pred. No.: 1,81e-288 Length: 2165
Score: 2669.50 Matches: 484
Percent Similarity: 84.96% Conservative: 64
Best Local Similarity: 75.04% Mismatches: 76
Query Match: 59.79% Indels: 21
DB: 4 Gaps: 3
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US-10-056-454a-15_COPY_49_882 (1-834) x US-09-257-894-8 (1-2165)

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QY 67 GluAsnAspAspValCluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
Db 1889 GAGATGATGGCTCGCATCAAGGGCTGAC----- 1860
QY 87 AlaSerSerLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db 1859 -----TCGGCTCAATTCAGTCG-----GATGAACCTGGAGTACCAGACATT 1818
QY 107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121
Db 1817 TCTGAAGAGACAAACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuAsn 141
Db 1757 GTGGTCCCCCACCACCAAGCATGACAAATAATATCCAGATTGACCCCATGTGCAAGGC 1698
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 1697 TATAAGTACCATCTTGAGTATCGGTACAGCCCTATAGAGAAATCCGTTTCAGACATGTAT 1638
QY 162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 1637 GAACAATGAGGAGGCTTCGAGCCCTCTCCCGTAGTTATGAGAAGTTTGGATTATATGCC 1578
QY 182 SerAlaThrGlyIleThrTyrArgGluTyrAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db 1577 AGCGGGGAAGGTATCACAATCGAGATGGGCTCTGGAGCATTTTCTGCAGCATTTGGTG 1518
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 1517 GGTGACGTCAACACTGGGATCCAAATCGATCGATCGATGACGAAATGAGTTTGGTCTT 1458
QY 222 TrpGluIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 1457 TGGGAATTTTCTGCCTAAACATGACATGATGATGATGATGATGATGATGATGATGATGAT 1398
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db 1397 GTAAAGGTGAGAATGGATATCCATCAGGGATAAAGGATTCANTCCAGCCTGGATCAAG 1338
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Pred. No.: 1,44e-265 Length: 1393
Score: 2462.00 Matches: 454
Percent Similarity: 98.49% Conservative: 3
Best Local Similarity: 97.84% Mismatches: 7
Query Match: 55.14% Indels: 0
DB: 4 Gaps: 0

US-10-056-454a-15_COPY_49_882 (1-834) x US-09-087-277-3 (1-1393)

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QY 226 LeuProAsnAsnValaspGlySerProAlaIleProHisGlySerArgValIleLeuArg 245
Db 2 CWGCCAAATAATGTGGATGCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGT 61
QY 246 MetAspThrProSerGlyValIysAspSerIleProAlaIleProAlaIleProAlaIle 265
Db 62 ATGGACATCCATCAGGTGTTAAGGATTCATCTCTGCTGGATCACTACTCTTTACAG 121
QY 266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGluGluArgTyr 285
Db 122 CTTCTGTAGTAAATCCATATATGAATATATATGATCCACCCGAGAGAGATAT 181
QY 286 IlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIle 305
Db 182 ATCTTCCACACCCCGGCAAGAAACCAAAAGTCGCTGAGATATATGAATCTCATATT 241
QY 306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
Db 242 GGAATGAGTAGTCCGAGGCTAAATTAATCTCATGCTGAATTTTAGAGATGAAGTCTT 301
QY 326 ProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnHisSer 345
Db 302 CCTCGCATAAAAAGCTTGGTACAAATGGGTGCAAAATTTATGCTATTTCAAGAGCATCT 361
QY 346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 365
Db 362 TATTATGCTAGTTTGGTATCATGCTCAAAATTTTTCGCCACCAAGCAGCGTTTGA 421
QY 366 ThrProAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
Db 422 ACNCCCGAGGACCTTAAGTCTTTGATGTATAAGCTCATGAGTAGGAATTTGTGTCTC 481
QY 386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
Db 482 ATGGACATTTTCACAGCCATCATCAATAATACCTTAGATGGAGTGAACATGTTGAC 541
QY 406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSer 425
Db 542 GCACAGATAGTGTACTTTCACTCTGGAGTCTGGTATCATTTGGATGTGGATTC 601
QY 426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp 445
Db 602 CGCCTCTTTAATACTATGGAACCTGGAGGTACTTAGTATCTCTCTCAATCGGAGATGG 661
QY 446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
Db 662 TGGTTGGATGATCTCAAAATTTGATGATTTAGATTTGATGTTGATGATGATGAT 721
QY 466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
Db 722 ACTCACCGAGGATATCGGTGGATTCACCTGGGAACCTACGAGGAATCTTTGGACTCGCA 781
QY 486 ThrAspValAspAlaValIleValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505
Db 782 ACTGATGTGGATGCTGTGTATCTGATGCTGGTCAAGCATCTTATTCATGGGCTTTTC 841
QY 506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
Db 842 CCAGATGCAATTAACCATTTGGTGAAGATGTAGCGGAATGCCGACATTTTNTATTCGGT 901
QY 526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspIleArgIle 545
Db 902 CAAGATGGGGGTGTTGGCTTTGACTATCGGTGCATGCGCATGATGCAATGCTGATAAATGAT 961
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QY 546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
Db 962 GAGTTGCTCAAGAAACGGGATGAGGATTTGGAGATGGGTGATATTTGTTCACTACTGACA 1021
QY 566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
Db 1022 ATAGAGATGGTGGGAAAGTGTGTTTCATACGCTGAAAGTCAIATCAAGCTCTAGTC 1081
QY 586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
Db 1082 GGTGATAAACTATAGCAITCTGCTGATGAGCAAGATATGATGATTTTATGGCTCTG 1141
QY 606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisIysMetIleArgLeu 625
Db 1142 GATAGACCTCAACATCATTAATAGATCGTGGATGATGATGATGATGATGATGATGAT 1201
QY 626 ValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
Db 1202 GTAACCTATGGATTAGAGAGAGAGGATCTAAATTTCAATGGAATGATGATGATGAT 1261
QY 646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
Db 1262 CCTGAGTGGATTCATTTCCCTAGGCTGAACACACCTCTCTCATGGCTCAGTAATTC 1321
QY 666 GlyAsnGluPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
Db 1322 GGAACCAATTCAGTTATGATAAATGCAGCGGAGATTTGACCTGGGAGATGAGATAAT 1381
QY 686 LeuArgTyrArg 689
Db 1382 TTAAGATACCGT 1393
RESULT 8
US-09-658-499-3
: Sequence 3, Application US/09658499
: Patent No. 6469231
: GENERAL INFORMATION:
: APPLICANT: EK, Bo
: APPLICANT: KHOSMOODI, Jamshid
: APPLICANT: LARSSON, Clas-Tomas
: APPLICANT: LARSSON, Hakan
: APPLICANT: RASK, Lars
: TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
: FILE REFERENCE: 003300-486
: CURRENT APPLICATION NUMBER: US/09/658,499
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 09/087,277
: PRIOR FILING DATE: 1998-05-29
: PRIOR APPLICATION NUMBER: PCT/SE96/01558
: PRIOR FILING DATE: 1996-11-28
: PRIOR APPLICATION NUMBER: SE 9504272-7
: PRIOR FILING DATE: 1995-11-29
: PRIOR APPLICATION NUMBER: SE 9601506-0
: PRIOR FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 3
: LENGTH: 1393
: TYPE: DNA
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
: OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
: OTHER INFORMATION: (potato)
: NAME/KEY: CDS
: LOCATION: (2)..(1393)
: NAME/KEY: misc.feature
: LOCATION: (424)..(1150)
: OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
: OTHER INFORMATION: C, G or T.
: NAME/KEY: misc.feature
: LOCATION: (422)..(424)
: OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
```



```

/ REFERENCE/DOCKET NUMBER: 1552
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 368-2400
/ TELEFAX: (416) 363-7246
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3128 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ DESCRIPTION: cDNA encoding starch branching enzyme
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE: clone 1.2.1 and E2
/ ORGANISM: Solanum tuberosum
/ STRAIN: cv desiree
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE: mature tuber
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE:
/ CELL LINE:
/ ORGANELLER:
/ IMMEDIATE SOURCE:
/ LIBRARY: lambda Zap tuber cDNA
/ CLONE: 1.2.1 and E2
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE: open reading frame
/ NAME/KEY: starch branching enzyme
/ LOCATION: 44-2788
/ IDENTIFICATION METHOD: lone ORF with homology to other starch
/ IDENTIFICATION METHOD: branching enzymes
/ OTHER INFORMATION: complements KV832 E. coli glycogen
/ OTHER INFORMATION: branching enzyme mutant
US-08-716-449-1

Alignment Scores:
Pred. No.: 9,74e-232 Length: 3128
Score: 2165.00 Matches: 423
Percent Similarity: 64.73% Conservative: 124
Best Local Similarity: 50.06% Mismatches: 218
Query Match: 48.49% Indels: 80
DB: 3 Gaps: 12

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-716-449-1 (1-3128)

QY 6 AsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeuValProGlyThr 25
DB 95 TCCTCCTCACTAAAGTTCTTCAGGGGCTCTAGAGATAAGATATGTTTCCTCTCAA 154
QY 26 GlnSerAspSerSerSerSerThrAspGlnPheGluPheThrGluThrSerProGlu 45
DB 155 CATAGTACTGACTCAAGTTTGGATCTCAGAACGGTCTTGGGATATTTCTCCACCCA 214
QY 46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
DB 215 AAATCAAGAGTAGAAAAGAT-----GAAAGGATGAAGCACAGTTCAGCTATT-- 262
QY 66 ThrGluAsnAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85
DB 263 -----TCCGCTGTTTGGACCGAT-----GAC 283
QY 86 PheAlaSerSerLeuGlnGluGlyLysLeuGluSerLysThrLeuAsn 105
DB 284 AATTCGACAATGGCACCCCTAGAGGAAGATGCAAGACTGAATAATTGACCTCTAAAT 343
QY 106 ThrSerGluGluThrIleAlaAspGluSerAspArgIleArgGluArgGlyPro 125

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DB 343 ----- 343
QY 126 ProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHis 145
DB 344 -----TTGGATCCAACCTTGGAACTTATCTAGATCAC 376
QY 146 LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly 165
DB 377 TTCAGACACAGAGATGAAGATATGTGGATCAGAAATGCTCATTTGAAATATAGGGA 436
QY 166 GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly 185
DB 437 CCCCTTGAGGAATTGCTCAAGTTATTAAATTTGGATTCAACAGGAAGATGCTTGC 496
QY 186 IleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn 205
DB 497 ATAGTCTATCGTGAATGGCTCTGCTGCTCAGGAAGCAGAAAGTTATTGGCATTTCAAT 556
QY 206 AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe 225
DB 557 GGATGGACGGTTCTTAACACACATGATGAGAGAGGACCACTTTGGTATTGGAGTATGA 616
QY 226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
DB 617 ATTCTCT---GATGTTTCACAGTAAGCCAGTCATCCACAACTCCAGAGTTAAGTTCT 673
QY 246 MetAspThrProSerGlyVal---LysAspSerIleProAlaTrpIleAsnTyrSerLeu 264
DB 674 TTCAAACATGTAATGGAGCTGTGGGTAGATCGTATCCCTGCTGGGATAAAGTATGCCACT 733
QY 265 GlnLeuProAspGluIle-----ProTyrAsnGlyIleHisTyrAspProGluGlu 282
DB 734 GCAGACGCCACAAAGTTTCAGCACCATATGATGTGTCTACTGGGACCCACCACTTCA 793
QY 283 GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu 302
DB 794 GAAAGTACCACCTTCAAAATACCCTCGCCCTCCCAAAACCCGAGCCCAAGATTCACGAA 853
QY 303 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAsp 322
DB 854 GCACATGTGGCATGAGCAGCTCTGAGCCACGCTGTAATTCGTATCGTGTGAGTTCAGAT 913
QY 323 GluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln 342
DB 914 GATGTTTACCTCGGATTAAGCAATAACTATACTATCTGTCAGTGTGATGCCATAAG 973
QY 343 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSer 362
DB 974 GAACATTCCTACTATGATCATTTGGATATCATGTTACAAACTTTTCTGTGAGCAAT 1033
QY 363 ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle 382
DB 1034 AGATATGGAACCCGAGGACCTAAAGTATCTAGATATAAGACATACATAGTGGTGTGA 1093
QY 383 ValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsn 402
DB 1094 CAGGTTCTGGTGGATAGTGTTCACACTATGCCAATATGGGAGGTTCTTCGTTTCCTT 1153
QY 403 MetPheAspCys-----ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyr 419
DB 1154 GSCCTTGATATTGGCCCAAGTCTCAAGAACTCTACTTTTCATGCTGGAGCGAGGTAC 1213
QY 420 HisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeu 439
DB 1214 CATAAGTTGTGGGATAGCAGGCTGTTCAACTATGCCAATATGGGAGGTTCTTCGTTTCCTT 1273
QY 440 LeuSerAsnAlaArgTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGly 459
DB 1274 CTTTCCCACTTGGTGGTGGCTAGAGAGTATAACTTTGACGGATTTCGATTTGATGGA 1333
QY 460 ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGlu 479
DB 1334 ATAACCTTCTGCTGTTTCATCATGGAATCATATGGAATATGGGATTTTACAGGAACATATAT 1393

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QY 480 GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetIeuValAsnAsp 499
Db 1394 GAGTATTTCAGGAGCTACAGATGTTGATGCTGGTCTATTTAATGTTGCCAATAT 1453
QY 500 LeuLeHisGlyLeuPheProAspAlaThrIleGlyGluAspValSerGlyMetPro 519
Db 1454 CTGATTCAAGATTTCCAGACGCAACTGTTAATGCCGAAGATGTTTCTGTTATGCGG 1513
QY 520 ThrPheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAla 539
Db 1514 GGCCATTACCGCCCTGTTCTGAGGAGGAATGTTTGAATACCGCTGCCAATGGCA 1573
QY 540 IleAlaAspLysArgIleGluLeuLeuLys---LysArgAspGluAspTrpArgValGly 558
Db 1574 ATCCAGATAGTGTAGATATTTAAAGATAAGATGATGAAGATGGTCCCAAGAG 1633
QY 559 AspIleValHisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGlu 578
Db 1634 GAAGTAACATCGAGTTTGACAAATAGAGATATACAGAAAGTGTATAGCATATCGGAG 1693
QY 579 SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAsp 598
Db 1694 AGCCATGATCATGCTATGTCGTGACAGACCATGTCATTCTCTAATGACAAAGAG 1753
QY 599 MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla 618
Db 1754 ATGTATTCTGCAATGCTTCTGTCACATGCTTCTCTCTGTTGATCGAGGAATGCG 1813
QY 619 LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPhe 638
Db 1814 CTTCACAGATGATCATTTTTCACAAATGGCCTTGGAGGAGAGGGTACCTCAATTTC 1873
QY 639 MetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeu 658
Db 1874 ATGGTACAGAGTTGGCATCCGAGTGATGATGATGATGATGATGATGATGATGATG 1918
QY 659 SerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPhe 678
Db 1919 -----GAGGGCAATAATGAGCTTATGACAAATGATAGACGCCAGTGG 1960
QY 679 AspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMet 698
Db 1961 AACCTCGCAGATGACGACACTTGATACAACTTATCAATGCAATTTGATAGACTATG 2020
QY 699 GlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLys 718
Db 2021 AATTCGCTCGAAGAAAGTTCTCATTCCTGCATCAGGAACACATAGTAGACGATG 2080
QY 719 AspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPhe 738
Db 2081 GATGATGATAATAAGTTGTGTTTGAACGTGCTGACCTGGTATTTGATTCAACTTC 2140
QY 739 HisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLys 758
Db 2141 CACCAATAACACATACAGAGGGGTATAAAGTTGATGACTTGCACAGGGAAGTACAGA 2200
QY 759 ValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAla 778
Db 2201 GTTGCACTGGCAGTGATGCTTGGGAATTTGTTGGCCATGGAAGAGCTGTTGATGAT 2260
QY 779 GluTyrPheThrPhe-----GluGlyTrpTyrAspAspArg 790
Db 2261 GACCAATTTCACATCACACAGGAATACTGAGTTCAGAAACAAATTTCAATGGTGTG 2320
QY 791 ProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAsp 810
Db 2321 CCAAACTCTCAAGAGTCTGTCTCTCGCGGAACATGTGTGGCTTATACAGATTGAT 2380
QY 811 LysGluGlnGluGluGluGluGluGluGluGluGlu----- 823
Db 2381 GAACGCATGTGAGAAACTGAAGATTACACAGACAGACATTTGTAGTGAGCTACTACCAACA 2440
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QY 824 AlaAlaValGluGlu 828
Db 2441 GCCAATATCGAGAA 2455

RESULT 10
US-09-257-894-24
Sequence 24, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-257-894-24

Alignment Scores:
Pred. No.: 2,16e-225 Length: 2565
Score: 2107.00 Matches: 404
Percent Similarity: 66.33% Conservative: 124
Best Local Similarity: 50.75% Mismatches: 206
Query Match: 47.19% Indels: 62
DB: 4 Gaps: 10

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-24 (1-2565)

QY 43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
Db 16 TCGCGCTCTCTCGCGCGACTCGGCTTCGCGCGCGCGGCTCTGCTCGCATGCT--- 72
QY 63 GlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGlu 82
Db 73 -----GATCGGCGGCAACCGCGGGGATCCCGGGTGGCGGCAATGTG 114
QY 83 GluLeuAspPheAlaSer-----Ser 89
Db 115 CGCCCTGAGTGTGTGTTCTCTCCAGTCACAGGCTCGCCGCTCAGGGGTGCGGAAGTCAAG 174

Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 49...2580
US-09-257-894-12

Alignment Scores:
Pred. No.: 5,34e-225 Length: 2772
Score: 2104.00 Matches: 393
Percent Similarity: 70.60% Conservative: 121
Best Local Similarity: 53.98% Mismatches: 172
Query Match: 47.12% Indels: 42
DB: 4 Gaps: 8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-12 (1-2772)

QY 98 LeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleLeuAspSerArg 117
Db 310 GTGCAAGAAATAAATATGCAACTATGCAACTGCAAGGCGATGTC-----GACCAT 357
QY 118 IleArgGluArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspPro 137
Db 358 CTC-----CCCATATAGCCTGGACCCC 381
QY 138 LeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArg 157
Db 382 AAGCTGGAGATATTCAGGACCATTCAGGTACCGGATGAAAGATTCCTAGACAGAAA 441
QY 158 GluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMet 177
Db 442 GGATCAATTAAGAAAAATGAGGAAGTCTTGAATCTTTTCTAAAGGCTATTTCGAAATTT 501

QY 178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSer 197
Db 502 GGGATTAAATACAAATGAGGATGAACTGTATTCGTGTAATGGSCACCTCTCGCAGAG 561
QY 198 AlaAlaLeuIleGlyAspPheAsnThrTrpAspAlaAsnAlaAspIleMetThrArgAsn 217
Db 562 GCAGAGCTTATTGGTGACTTCAATGACTGGAATGTCAAAGATGAGAGAGGAT 621
QY 218 GluPheGlyValTrpGluIlePheLeuProAsnValAspGlySerProAlaIlePro 237
Db 622 AAATTGGTGTGGTCGATCAAAATTT---GACCATGTCAAAGGAGAACTCCATCCCT 678
QY 238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
Db 679 CACAATCCCAAGTTAAATTTCCGCTTCTACATGCTGGAGTATGGTTCATGCTATCCA 738
QY 258 AlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIle-----ProTyrAsnGlyIle 275
Db 739 GCATTCGATTCGTATGCGACTGTTGATGCTCTAAATTTGGAGCTCCCTATGATGTT 798
QY 276 HisTyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProLysLysPro 295
Db 799 CATTCGGATCCTCCTGCTTCGAAAGGTACACATTTAAGCATCCTCGGCTTCAAGCCT 858
QY 296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
Db 859 GCTGCTCCAGCTATCTATGAGCCCATGTAGTATGATGAGTGTGTAAGAACCCAGCAGTAA 918
QY 316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
Db 919 ACATATAGGAAATTTGCAGACAATGTGTGCACCATACAGAGCAAAATACATACACACA 978
QY 336 LeuGlnIleMetAlaIleGlnHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
Db 979 GTTCAGTTGATGGCAGTATGAGCATTCGTACTATGCTTCTTCGGGTACCATGTGACA 1038
QY 356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLysLysSerLeuLeuAsp 375
Db 1039 AATTTCTTTGGGGTTAGCAGCAGATCAGCAGCACACAGGAGGACCTCAATATCTTTGAT 1098
QY 376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
Db 1099 AAGCACACAGTTTGGGTTTGGAGTCTGTATGATGATGTGTCATAGGCAATGCAAGTAA 1158
QY 396 AsnThrLeuAspGlyLeuAsnMetPheAsp-----CysThrAspSerCysTyrPhe 412
Db 1159 AATGTCACAGATGGTTTAAATGGCTATGATGTTGCACAAAGCACCCACAGTCTATTT 1218
QY 413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
Db 1219 CATCGGGAGATAGAGGTTATCAAAACCTTTGGGATAGTCGGCTGCTTCAACTATGCTAAC 1278
QY 433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTyrTrpLeuAspAlaPheLysPhe 452
Db 1279 TGGAGGCTATTAAGGTTTCTTCTTAACCTGAGATATGTTGCTGATGAATTCATGTT 1338
QY 453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
Db 1339 GATGCTTCCTCCATTTGATGGAGTTACATCAATGCTGATATCATCACCAGGTATCAATCG 1398
QY 473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
Db 1399 GGGTTTACTGGAACACTACAGGAATATTTTCAGTTTGGACACAGAGTGTGGATGCTGTT 1458
QY 493 TyrLeuMetLeuValAsnAspLeuLeHisGlyLeuPheProAspAlaIleThrIleGly 512
Db 1459 TACATGATGCTTGCAGAACCATTTAATGCAGAACTCTTGGCAGAGCAACTGTTGTTGCT 1518
QY 513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyLysPhe 532
Db 1519 GAAGATGTTTCAGGCATGCCGGTCTCTTTCGCCGCCAGTGTGATGAGGTTGGGGTTT 1578

QY 533 AsptyrArgLeuHisMetAlaileAlaAspLysArgIleGluLeuLeuLysLysArgAsp 552
Db 1579 GACTATGCGCTGGCAATGGCTATCCCTGATAGATGATGACTACCTGAAGAATAAGAT 1638
QY 553 Glu---AspTrpArgValGlyAspIleValHisThrLeuThrAsnArgTrpSerGlu 571
Db 1639 GACTCTGAGTGTGATGGTGAATACGATACCTTTGACTAACAGAGATATACCTGAA 1698
QY 572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
Db 1699 AAATGATCGATATGCGAGAGCCATGATGATGATGATGATGATGATGATGATGATGAT 1758
QY 592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
Db 1759 TTTCCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1818
QY 612 LeuIleAspArgGlyIleAlaLeuHisTyrMetIleArgLeuValThrMetGlyLeuGly 631
Db 1819 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1878
QY 632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTyrIleAspPhe 651
Db 1879 GGTGATGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1938
QY 652 ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr 671
Db 1939 CCAAGA-----GAAGGGAACAACCTGGAGCTAT 1965
QY 672 AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu 691
Db 1966 GATAAATGACAGCAGACATGAGGCTTGTGACACTGATCAGCTTGTGATCAGTACAGTAC 2025
QY 692 GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu 711
Db 2026 AATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2085
QY 712 HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn 731
Db 2086 AAGCAGATGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2145
QY 732 LeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCys 751
Db 2146 TTAGTTTGTGTTTCAATTCATCCCAAGAAACTTACGAGGGCTACAAAGTGGATGC 2205
QY 752 LeuLysProGlyLysTyrLysValAlaLeuAspSerAspProLeuPheGlyGlyPhe 771
Db 2206 GATTTGCTGGAAATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2265
QY 772 GlyArgIleAspHisAsnAlaGluTyrPheThrPhe----- 783
Db 2266 GGAAGAGTTGGCCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2325
QY 784 GluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
Db 2326 GAACGAACCTCAACACCGCGGCAACTGTTCAAAGTCTTCTCCGCGCGGACCTGT 2385
QY 804 ValValTyrAlaLeuValAspLys 811
Db 2386 GTGGCTTATACCGGTAGACGAA 2409

RESULT 14

US-08-104-158-1

; Sequence 1, Application US/08104158
; Patent No. 6215042

GENERAL INFORMATION:

; APPLICANT: Willmitzer, Lothar
; APPLICANT: Sonnewald, Uwe
; APPLICANT: Kossmann, Jens
; APPLICANT: Mueller-Roeber, Bernd
; APPLICANT: Vissler, Richard Gerardus Franciscus
; APPLICANT: Jacobsen, Evert
; TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
; CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE

; TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
; AND PLANTS CONTAINING THESE PLASMIDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,158
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP PCT/EP92/00302
; FILING DATE: 11-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 41 04 782.6
; FILING DATE: 13-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-382-0700
; TELEFAX: 212-382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum cv. Desiree
; STRAIN: Desiree
; DEVELOPMENTAL STAGE: growing tuber
; TISSUE TYPE: tuber
; CELL TYPE: total tuber
; IMMEDIATE SOURCE:
; LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1699
; OTHER INFORMATION: /note= "for Branching enzyme I
; OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to
; OTHER INFORMATION: active potato branching enzyme"
; US-08-104-158-1

Alignment Scores:

Pred. No.: 2,39e-224 Length: 2909
Score: 2098.50 Matches: 409
Percent Similarity: 66.00% Conservative: 123
Best Local Similarity: 50.74% Mismatches: 196
Query Match: 47.00% Indels: 78
DB: 4 Gaps: 12

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-104-158-1 (1-2909)

QY 46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
Db 26 TCCACCCCAAAATCAAGAGTTAGAAAAAGATGAAGGATGACAGACAGATTTCAGTATT--- 82
QY 66 ThrGluAsnAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85

Db	83	-----TCGCTGTTTGCACC-----	1034	CATAAGTTGGGATAGCAGCGCTGTTCAACTATPCCCAATTGGGGAGGTTCTTCGTTTCCTT	1093
QY	86	PhaAseSerLeuGlnLeuGlnGluGlyLysLeuGluGluSerLysThrLeuAsn	440	LeuSerAsnAlaArgTrrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGly	459
Db	98	-----GATGACAAATTCGACAATGCGCAATGGCA	1094	CTTTCCAACTTGAGTGGTGGCTAGAAAGACTATAAATCTTTCACCGATTTTCGATTTGATGGA	1153
QY	106	ThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGluArgGlyIleProPro	460	ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGlu	479
Db	119	CCCTTAGAGAGATGTCACACTGAAAT-----	1154	ATAACTTCTATGCTGTATGTTTCATCATGGAATCAATATGGATTTTACAGGAACATAAAT	1213
QY	126	ProGlyLeuGlyGlnLysIleGlyIleAspProLeuLeuThrAsnTyrArgGlnHis	480	GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAsp	499
Db	149	-----ATTGGC-----CTCCTAAATTTGCAATCCAACTTGGAACTTAICTAGATCAC	1214	GAGTATTTCCAGCAGGCTACAGATGTGATGCTGTCTATTTAATGTTGGCCAAATAAT	1273
QY	146	LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly	500	LeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetPro	519
Db	197	TTCAGACACAGATGAAGATATGGTATGAGATGCTCAGAAATGCTATTGAAATAATAGGGA	1274	CTGATTCACAAGATTTTCCAGCAGCAACTGTATTGCTCCCGAAGATGTTCTGCTATGCCG	1333
QY	166	GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly	520	ThrPheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAla	539
Db	257	CCCTTGAGGAATTTGCTCAAGGTTATTAAATTTGGATTCAACAGGGAAGATGGTGC	1334	GGCCTTAGCCGGCCTGTTCTGAGGGGAGGAATTTGTTGATTACCGCTGGCAATGGCA	1393
QY	186	IleThrTyrArgGlnTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn	540	IleAlaAspLysArgIleGluLeuLys---LysArgAspGluAspTrrpArgValGly	558
Db	317	ATAGTCTATCGTGAATGGCTCTGCTGCTCAGGAAGCAGAAGTTATTGGCGATTTCAT	1394	ATCCAGATAAGTGGATAGATTATTAAAGAAATAAGAAATGATGAAGATGCTCCATGAAG	1453
QY	206	AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe	559	AspIleValHisThrLeuThrAsnArgTrrpSerGluLysCysValSerTyrAlaGlu	578
Db	377	GGTAGACCGGTCTCAACCAATGATGAGAGAGACCAGTTTGGTGTGGAGTATTAGA	1454	GAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAGTGTATAGCATATGCCGAG	1513
QY	226	LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg	579	SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAsp	598
Db	437	ATTCCT--GATGTGACAGTAAAGGAGTGTGGTATCGTATCCCTGCTGGATAAAGTATGCCACT	1514	AGCCATGATCAGTCTATTGTGCGTGACAAAGACCATTCATCTCTCTTAATGAACAAGAG	1573
QY	246	MetAspThrProSerGlyVal---LysAspSerIleProAlaTrpIleAsnTyrSerLeu	599	MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla	618
Db	494	TTCAAACTAGTAAATGAGTGTGGTATCGTATCCCTGCTGGATAAAGTATGCCACT	1574	ATGATTCGGCATGCTTCCTTGACAGATGCTTCCTCTGTTGTTGATGCAGAAATGCG	1633
QY	265	GlnLeuProAspGluIle-----ProTyrAsnGlyIleHisTyrAspProGluGlu	619	LeuHisLysMetIleArg-LeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPh	638
Db	554	GCAGAGCCCAAAAGTTTCACACACCATATGATGTGTCTACTGGGACCCACCCACTTCA	1634	CITTCACAAGATGATCCATTTTTCACATGGCTTGGGAGGAGAGGGGTACCTCAATTT	1693
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Db	614	GAAGGTACCCTTCAAAATACCCTCGCCTCCCAAAACCCGAGCCCAAGATCAGAA	1694	CATGGGTACAGATTTGGCCATCCTGAGTGGATTGACTTCCCTAGT-----	1739
QY	303	SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAsp	658	uSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPh	678
Db	674	GCACATGTGGCATGAGCAGCTCTGAGCCACGCTGTAATTCGTATCGTATGTCAGAT	1740	-----GAGGCAATAATTGGAGTTATGACAAATGTAGACGCCAGTG	1780
QY	323	GluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln	678	eAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMe	698
Db	734	GATGTTTACCTCGGATTAAGCAATAACTATAACTGTCCAGTTGATGGCCATAATG	1781	GAACCTCGCAGATAGCGCAACTTGATACAAAGTTTATGATGATGATGATGATGAT	1840
QY	343	GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSer	698	tGlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLy	718
Db	794	GAACATCTTACTATGATCAATTTGGATATCATGTTTACAACTTTTTCCTGTGACCAAT	1841	GAATTCCTCGATGAAGAGTTCTATCTCCATCAGCAAAACACATAGTAGAGCAT	1900
QY	363	ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle	718	sAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPh	738
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Job time : 269 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 03:05:21 ; Search time 337 Seconds

(without alignments)
3863.106 Million cell updates/sec

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Perfect score: 4465

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Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4320	96.8	3074	9	US-10-254-534-1
2	3309.5	74.1	2418	9	US-09-338-842A-872
3	3266	73.1	2577	9	US-09-938-842A-337
4	3037	68.0	3039	10	US-09-792-127-3
					Sequence 1, Appli
					Sequence 872, App
					Sequence 337, App
					Sequence 3, Appli

5	2997	67.1	2559	10	US-09-792-127-1	Sequence 1, Appli
6	2462	55.1	1393	9	US-10-254-534-3	Sequence 3, Appli
7	2058	46.1	2955	9	US-09-918-624B-30	Sequence 30, Appl
8	2058	46.1	2955	10	US-09-880-107-2148	Sequence 2148, Ap
9	2058	46.1	2994	9	US-10-084-817-92	Sequence 92, Appl
c 10	627	14.0	602	10	US-09-770-149-955	Sequence 955, App
11	530.5	11.9	1830121	9	US-10-329-960-1	Sequence 1, Appli
12	513.5	11.5	2193	9	US-09-738-626-1354	Sequence 1354, Ap
c 13	513.5	11.5	3309400	9	US-09-738-626-1	Sequence 1, Appli
14	484.5	10.9	1877	10	US-09-974-300-653	Sequence 653, App
15	463.5	10.4	604	10	US-09-925-300-453	Sequence 453, App
16	453	10.1	2514	9	US-10-156-761-2792	Sequence 2792, Ap
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c 19	419	9.4	601	9	US-10-025-380-304	Sequence 304, App
c 20	419	9.4	601	10	US-09-922-217-304	Sequence 304, App
c 21	419	9.4	601	10	US-09-833-263-304	Sequence 304, App
22	317	7.1	441	10	US-09-770-444-893	Sequence 893, App
23	305.5	6.8	543	10	US-09-815-343-373	Sequence 373, App
24	261.5	5.9	1680	10	US-09-908-855-14	Sequence 14, Appl
25	249.5	5.6	1743	9	US-10-156-761-2147	Sequence 2147, Ap
c 26	247	5.5	310	9	US-10-102-524-1616	Sequence 1616, Ap
27	244.5	5.5	3033	9	US-10-212-219-5	Sequence 5, Appli
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29	240.5	5.4	204	10	US-09-878-574-12567	Sequence 12567, A
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31	226	5.1	661	10	US-09-765-272-77	Sequence 77, Appl
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33	223	5.0	2437	9	US-10-238-091-6	Sequence 6, Appli
34	210.5	4.7	976	10	US-09-765-272-79	Sequence 79, Appl
35	209.5	4.7	576	10	US-09-815-343-924	Sequence 924, App
36	207.5	4.6	2736	10	US-09-833-435A-14	Sequence 14, Appl
37	205	4.6	2106	9	US-10-156-761-2139	Sequence 2139, Ap
38	203	4.5	5058	9	US-09-252-088-22	Sequence 22, Appl
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40	195	4.4	2508	9	US-09-738-626-2305	Sequence 2305, Ap
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42	194	4.3	2997	9	US-10-238-091-2	Sequence 2, Appli
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44	184	4.1	2247	9	US-10-156-761-2776	Sequence 2776, Ap
45	182	4.1	2151	9	US-10-127-032-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown

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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:belII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
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; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
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; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
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; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
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; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
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; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
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; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
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; Query Match: 96.75% Indels: 4
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; QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
; DB 453 GAGACATCTCCAGAAAATTCGCCAGCATCAACTGATGATAGTAGTTCAACAATGGAACAC 512
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; QY 61 AlaSerGlnIleLysThrGluAspAspValGluProSerSerAspLeuThrGlySer 80
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; DB 573 GTTCAAGAGCTGGATTTTTCITCATCTACACTACAAGAGTGGGTAAACTGGAGGAG 632
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; QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
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; QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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; QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480

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; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILLING DATE: 2001-06-22
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; SEQ ID NO 337
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

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Query Match:	73.15%	Indels:
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DB	445	AGGAAGATTCACCTCTCGAGATGGGAAGAGATATGACATTGATCCTATGTTGAAC	504
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DB	505	AGTCATCGTAATCATCTTGATTACCGCATATGGGCAGTACAGAAAACGCGTCGAGAAAT	564
QY	161	AspLysTyrGluGlyGlyLeuGluAlaPheSerArgLysTyrGluLysMetGlyPheThr	180
DB	565	GACAAGAATGAAGTGGTGTGGAGGCAATTTCTCGTGGTTATGAAATATTTGGCITCACT	624
QY	181	ArgSerAlaThrGlyIleThrTyrArgGluTyrAlaLeuGlyAlaGlnSerAlaAlaLeu	200
DB	625	CGAAGCCCACTGGTATCATCTACCGGGAATGGGCACCGGAGCTAAGSCAGCATCACTG	684
QY	201	IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly	220
DB	685	ATCGCAGATTTAAATACTCGGAATGCGAAATCTGATGTTGCTGCGAAGCACTTTGGT	744
QY	221	ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer	240
DB	745	GTGTGGGAATATTCTGCCAATAATGCTGATGGCTCCAGCAATTCGCCATGGCTCC	804
QY	241	ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle	260
DB	805	CGTGTGAAGATCCGATGGATACCCCATCTGGTATTAAAGACTCCATTCACACTTGGATC	864
QY	261	AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspPro	280

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QY 367 ProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMet 386
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QY 387 AspIleValHisSerHisAlaSerAsnThrLeuAspGlyLeuAsnMetPheAspCys 406
Db 1296 GATGTTGTTTCCACAGTACCGGCTCAAAATAATACCTTGGACGGTTGATGTTGATGCG 1355
QY 407 ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArg 426
Db 1356 ACGGATACACATTACTTCCAGGCGGTTCCAGGCGCATCAGTGGATGCGGATCCCGT 1415
QY 427 LeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrp 446
Db 1416 GTCTTTAACTATGGAATAAGGAATTAAGGTTTCTACTTCCAAATGCAAGATGGTG 1475
QY 447 LeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyrIle 466
Db 1476 CTAGAGAGATATAAGTTGATGTTTCCGATTCGATGGCGGACCTCCATGATATACC 1535
QY 467 HisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluLutyrPheGlyLeuAlaThr 486
Db 1536 CATCATGGATTACAAGTAACCTTACAGGAAGCTACCATGAATATTTGGCTTTGCCACT 1595
QY 487 AspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhePro 506
Db 1596 GATGTAGATCGCGTCTTACTTGATGCTGATCAATGAUATAATTCATGGGTTTAPCCT 1655
QY 507 AspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProValGln 526
Db 1656 GAAGCGGTAACTACGTAAGATGTAGTGAATGCTACATTTGCCCTTCTCGTCAA 1715
QY 527 GluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGlu 546
Db 1716 GTTGGTGGGTGGTTTTCACATATCGCTTACATATGGCTGTGCCGACAAATGATGAA 1775
QY 547 LeuLeuLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsn 566
Db 1776 CTCTCAAGGAAGAACGATGAAGCTTGGGAGATGGTAAATATGTGCACACATPACAAAC 1835
QY 567 ArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGly 586
Db 1836 AGAAGGTGGCTCGAAAGTGTGTACTATGCTGAAAGTCAAGATCAAGCACTTGTGGA 1895
QY 587 AspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAsp 606
Db 1896 GACAAAGCTATTGCAATCTGGTTGATGGCAAGGATATGATGTTTATGGGAAATGAGTTCGGCATCCT 1955
QY 607 ArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuVal 626
Db 1956 GGACCTTCGACGCCCTAAATATGATCGTGAATAGCACTGCATAAATGATTAGACTATC 2015
QY 627 ThrMetGlyLeuGlyGlyClyGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisPro 646
Db 2016 ACAATGGGTCTAGGAGGAGAGGGTTTATCTTAACTTTATGGGAAATGAGTTCGGCATCCT 2075
QY 647 GluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGly 666
Db 2076 GAATGGATAGACTTTCGAAGAGGCCCAAGTACCTCCAAAGTGGTAAGTTTCATCCAGGA 2135
QY 667 AsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAlaGluTyrLeu 686
Db 2136 AACAAACACAGTACGACAAATGCGGTGCAAGATTTCACCTGGGGTATGCAAAATTCCT 2195
QY 687 ArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGlu 706
Db 2196 AGGTATCATGTATGACAGCTTTCATGAGCAATGAGCACTTTCAGGAAAAAATATGTT 2255
QY 707 PheMetThrSerGluHisGluPheIleSerArgLysAspGluGlyAspArgMetIleVal 726
Db 2256 TTTATGACATCAGACCACGATACGTATCTCGGAAACATGAGGAAGATAAAGTGTGCTG 2315

QY 727 PheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSerTyrSerAsp 746
Db 2316 TTTGAAAAGGGGACTTGTATTTCTGTTCACATTCCTCACTGAGTAGTATTCGAC 2375
QY 747 TyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspPro 766
Db 2376 TACCGGTCGCTGTTTAAAGCCTGGGAAGTACAAAGTGGTCTTAGACTCGGACGCTGA 2435
QY 767 LeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrp 786
Db 2436 CTCTTTGGTGGATTTGGTAGGATCCATCACACTGCAGACGACGCTACTTCTGACTGCCAA 2495
QY 787 TyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValTyr 806
Db 2496 CATGACAACAGGCCCCCAATTCATTCTAGTGTACACTCTCTAGCAGAAACCTGTGTGTCTAT 2555
QY 807 Ala 807
Db 2556 GCT 2558
RESULT 5
US-09-792-127-1
; Sequence 1, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-1
Alignment Scores:
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Score: 2997.00 Matches: 532
Percent Similarity: 88.13% Conservative: 77
Best Local Similarity: 76.99% Mismatches: 82
Query Match: 67.12% Indels: 0
DB: 10 Gaps: 0
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QY 137 ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeu 156
Db 66 CCAACGCTCCGAGACTTTAAGTACCATCTTGATATCGATATAGCCTATACAGGAGAAATA 125
QY 157 ArgGluAlaIleAspLysTyrGlyLeuGluAlaPheSerArgGlyTyrGluLys 176
Db 126 CGTTCAGACATTTGATGAAACACAGGAGCATGATGATTTTCCCGGGTTACGAGAG 185
QY 177 MetGlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGln 196
Db 186 TTIGATTATTCGCGAGCGCTGAAGGTATCACTTACCGAGAAATGGGCTCTCTGGAGCAGAT 245
QY 197 SerAlaAlaLeuIleGlyAspPheAsnAsnTyrAspAlaAsnAlaAspIleMetThrArg 216
Db 246 TCTGAGCATTTAGTTGGCGACTTCAACAAATTTGGATCCAAATGAGACCATATAGCAAA 305

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-254-534-3 (1-1393)

RESULT 7

; CURRENT FILING DATE: 2002-12-03

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Db	542	GCACACAGATGTTGTTACITTCACCTCTGGAGCTCGTGGTTATCATTTGGATGTGGGATTC	601
QY	426	ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp	445
Db	602	CGCCCTCTTAATATGGAACCTGGGAGGTACTTAGTAGTATCTCTCAAAATGCGAGATGG	661
QY	446	TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr	465
Db	662	TGGTGGATGAGTTCAAAATTTGATGCATTTAGATTTGATGCTGACATCAATGATGAT	721
QY	466	IleHisHisGlyLeuSerValClyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla	485
Db	722	ACTCACACAGGATTAATCGTGGGATTCATCGGAACTACGAGGAATACTTTGGACTCGCA	781
QY	486	ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe	505
Db	782	ACIGATGSGATGCTGTGTGTGATCTGATGCTGGTCAACGATCATTCATGGGCTTTTC	841
QY	506	ProaspAlaIleThrIleGlyGluaspValSerGlyMetProThrPheCysIleProVal	525
Db	842	CCAGATGCAATTAACATTTGTTGAAGATCTTAGCGGAATGCGGACATTTTNTATTCGGCT	901
QY	526	GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIle	545
Db	902	CAAGATGGGGTGTGGCTTTTGACTATCGGCTGCATATGGCAATGTGTATAAATGGAT	961
QY	546	GluLeuLeuLysLysArgaspGluaspTrpArgValGlyAspIleValHisThrLeuThr	565
Db	962	GAGTGTCTCAAGAACGGGATCGAGATGGAGCTGGGTGATATGTTCATACACTGACA	1021
QY	566	AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal	585
Db	1022	AATAGAAGATGGTCGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTTAGTC	1081
QY	586	GlyAspLysThrIleAlaPheTrpLeuMetaspLysaspMetTyrAspPheMetAlaLeu	605
Db	1082	GCTGATAAACTATAGCATCTGCTGATGGACGAAGATATGATGATTTATTTGGCTCTG	1141
QY	606	AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeu	625
Db	1142	GATAGACNTCAACATCATTAATAGATCGTGGGATACCATTCACACACATGATAGGCTT	1201
QY	626	ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis	645
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QY	666	GlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAlaGluTyr	685
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RESULT 7

US-09-918-624B-30

; Sequence 30, Application US/09918624B

; Publication No. US20030113720A1

; GENERAL INFORMATION:

APPLICANT: SCHEBYE, XIAO MIN

APPLICANT: SOHASSE, Thierry
: TITLE OF INVENTION: CDNAS EXP

7 TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
: FILE REFERENCE: PA-0033 US

SEE REFERENCE: RA 0033 03
; CURRENT APPLICATION NUMBER: HS/09/918 624B

; CURRENT FILING DATE: 2002-12-03


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QY 790 ArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuVal 809
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QY 810 AspLysGlu 812
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RESULT 11
US-10-329-960-1
; Sequence 1, Application US/10329960
; Publication No. US20030099277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses thereof
; FILE REFERENCE: PB186PL
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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Score:	530.50	Matches:	203
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Best Local Similarity:	25.70%	Mismatches:	282
Query Match:	11.88%	Indels:	179
Db:	9	Gaps:	36

US-10-056-454A-15_COPY_49_882 (1-834) x US-10-329-960-1 (1-1830121)

QY	110	ThrIleIleAspGluSerAspArgIle-----ArgGluArgGlyIleProPro	125
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QY	126	ProGlyLeuGlyGlnLysIleIleTyrGluIleAsp-----	136
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QY	137	ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyr-----	153
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QY	154	-----LysLysLeuArgGluAlaIleAspLysTyrGluGly	165
Db	1436440	GAACACAAATTCGAAGATCCTTATCGTTTTCATCCAAATGATTGACGATTAGAACAA	1436499
QY	166	GlyLeu-----GluAlaPheSerArgGlyTyrGluLysMetGlyPhe-----	179
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QY	180	---ThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAla	198
Db	1436560	GAATGTGATGGTGTGACGGGGTCAATTTCCGCTGTGGACCACTAATGCAAGACAGATT	1436619
QY	199	AlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThr---ArgAsn	217
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QY	218	GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySer-----	233
Db	1436680	AAAAGTGGTGTGGAGCTCTTTTACCAAAACCCAGTTTAGACAGCTCTATAAGTTT	1436739
QY	234	-----ProAlaIleProHisGlySerArgVal	242
Db	1436740	GAATTAATTGATGCCAATCTTCGTTTGAAGCCCGCATTCATTGCTTTCCTTAGTTCG	1436799
QY	243	LysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyr	262
Db	1436800	CAACTTCGCCCTGATACAGCTTCGCAAGTCAGT-----	1436832
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Db 1437091 CCAACCACTGCGCTTTGGTTCACCTGAAGCGCTTCGCGCTTTAGTAAACGCTGCTCAGAA 1437150
QY 380 LeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAsp 399
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Db 1437151 GCAGGATCAACCTGATTTAGATGGTGCCAGGCAATTCACAGTGATACG---CAT 1437207
QY 400 GlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg---Gly 418
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437208 GGTTTAGTCGCAATTCATGCGACA---GCTTTGATCAGCATGAAGACCTCGCGAAGGC 1437264
QY 419 TyrHisTyrMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyr 438
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Db 1437265 TATCATCAAGATTGGAATACCTTGATTTATACTATGGCGGTAATGAGGTCAAAAATTTTC 1437324
QY 439 LeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAsp 458
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437325 TTTATCAGTAATCACTGATTCGCTTGAACGTTTGGCGTAGATGATTCGCGTGAT 1437384
QY 459 GlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyr 478
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437385 GCTGTGCTTCATGATTTACCGTGATATAGCCGTCGCGAGGCG--- 1437429
QY 479 GluGluTyr-----PheGlyLeuAlaThrAspValAspAlaValValTyrLeu 494
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Db 1437430 ---GAGTGGATTCACCAACCAATACGGCGGACGTAAGATTTAGAACCATTTGATTTTAA 1437486
QY 495 MetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAsp 514
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Db 1437487 AACACACCACTGGAAATTCACAGCGAATGCGCGGAGCAATTCATTCGCGAGGAA 1437546
QY 515 ValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyPheAspTyr 534
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437547 TCTACCTCTTTGCGAGCGTAACCCACCAAGCAAGCGCGCTGGGCTTCAATTTTC 1437606
QY 535 ArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAsp 554
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437607 AAATGGAAATATGGGCTGGATCAAGATACACTGGCTTATATG---AAGCTTGACCCCAT 1437663
QY 555 TrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLysCysVal 574
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Db 1437664 TACCCG---CAATATCATCAC-----ACAAAAAGACCTTTGGATGGTGTAT 1437708
QY 575 SerTyrAlaGlu-----SerHisAspGlnAlaLeuValGlyAspLys 588
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QY 589 ThrIleAlaPheTrpLeuMetAspLysAspMetIleAspPheMetAlaLeuAspArgPro 608
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437762 ----- 1437762
QY 609 SerThrSerLeuIleAspArg-----GlyIleAlaLeuHisLysMetIleArgLeu--- 625
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Db 1437763 AAATATTCACITCTTGGCAAGATGCCAGGTGATACGTCGCGGCAAAATTCGCTAACITGGT 1437822
QY 626 -----ValThrMetGlyLeuGlyGlyTyrLeuAsnPheMetGlyAsn 641
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437823 GCATATTACGGTTATATGTGGGCTACCCAGCAAAAAATTTATCTC---TTTATGGGAAT 1437879
QY 642 GluPheGlyHis---ProGluTrp-----IleAspPheProArgAlaGlu 655
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1437880 GAATTTGCTCAAGCGACAGATGGAATTCAGAGAAAGATTTGGACTGGTTCTTGCTTGAT 1437939
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Score:

Percent Similarity: 41.07%
 Best Local Similarity: 24.57%
 Query Match: 11.50%
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US-10-056-454A-15_COPY_49_882 (1-834) x US-09-738-626-1354 (1-2193)

QY	71	ValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeu	90
Db	7	GTGACCCGCGGACACATCAC	60
QY	91	-----ATCCCTGAAGCAGACTGSCCCGCTCGCG	96
Db	61	CACTGCACACATCAGATCCTCATGATTTATGGTTGGCATGAGACCAAGCTGTTGG	120
QY	97	LysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAsp	116
Db	121	GTATATCCGACGCGCAGCTGGCGCGCAGGTAAATTCCTTATCGACGACACCTCC	180
QY	117	ArgIleArgGluArgGlyIleProProProGlyLeuGlyGlnLysIleTyrGluIleAsp	136
Db	181	CACGTC-----ATGACCCCT-----ATCGGCGACGACATTTCGCAATTCAG	222
QY	137	ProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyr-----Ser	151
Db	223	-----TTAGGTACCGGAGCGCGCTGACTATCGCTGGAACTCACCTGGCTGAT	273
QY	152	GlnTyrLysLysLeuArgGluAlaIleAspLysTyr-----Glu	164
Db	274	CAAGAACCGCAGGTCAAG-----GCTGATCCATACTACTCTCCGCCACCGTAGGCGAG	327
QY	165	GlyGlyLeuGluAlaPheSerArgGly-----TyrGluLysMetGlyPhe	179
Db	328	ATGGATATTTACCTCTTCTGACGGGAGCGCATGAGCGTTTGTGGAGATTCTCGTGCC	387
QY	180	Thr-----ArgSerAlaThrGlyIleThrTyrArgGluTrp	191
Db	388	AACATCAAGACCTACCAACTCGCTCGGACACAGTTCGTGGCACCGCATTTACTGTGG	447
QY	192	AlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAla	211
Db	448	GCTCCAAACGCAATTTGGCTGGCAGTGGTCTGCTTCAACGGTGGAAATGCATCCAG	507
QY	212	AspIleMet---ThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnVal	230
Db	508	CATCCGATCGTTCATGGGTGGTTCGGTCTGTGGAGCTGTTCATCCCGCATAGAG	567
QY	231	AspGly-----SerProAla	235
Db	568	GAAGGCGAAGTGACAAATTCGCCGTCCAAACGAGGAGGCCAACGTCGTGATAGGCC	627
QY	236	IleProHisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSer	255
Db	628	GATCCGATGCTGTCTCGCGAGAACTGGCGCGGCAACCGCATCTATTGTGCTTCCTCT	687
QY	256	IleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIle	275
Db	688	GAGTACCAGTGG-----	699
QY	276	HisTyrAspProProGluGluArgTyrIlePheGlnHisProArgProLysLysPro	295
Db	700	-----CAGATTCCGAGTGGCTGGCGGCGGTCCCAAACTGATCTCGCATCCAAAGCC	753
QY	296	LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn	315
Db	754	ATGAGT-----GTCACAGAGGTCACCTCGGTCTTGGCGCTGGGT-----AAG	798
QY	316	SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla	335
Db	799	AACTATGAGGATTTGGCTACTGAGCTGGTTGATACGTCGACGATCTTGCTACACCCAC	858
QY	336	LeuGluIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThr	355

DB	1288435	GATGATTTGG---GGCTTTGCCGCGTTTGTAT---GGCGAAGCCCTCTATGAACACCCCTGAC	128838
QY	415	GlyAlaAraGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGlu	434
DB	1288381	TGGAGCGCGCGACAAAGATGGGGCACCCCTGGTCTTTGACTTTTCGTCGCAACGAA	1288322
QY	435	ValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGly	454
DB	1288321	GTCCGCAACTTCCCTCGTCGTAATGCGTGTACTGGATTGAAGAAATCCACATCGATGGT	1288262
QY	455	PheArgPheAspGlyValThrSerMetMetTyrIleHisGlyLeuSerValGlyPhe	474
DB	1288261	CTGCGCTGCAGCGCGTGGCGTCCATCTGTACTCATGATTACTCCCGGTGAG-----	1288211
QY	475	ThrGlyAsnTyrGlu---GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyr	493
DB	1288210	CACGGCGAATGGGAACCAACATCTACGGTGGTCGCGAGAACCTTCGAGGCAGTGCAGTTT	1288151
QY	494	LeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGlu	513
DB	1288150	CTGCAGAAATGAACGCCAAGGTGCTCGCACTGCACCCTGGTCGCTCACCATCGCTGAG	1288091
QY	514	AspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyPheAsp	533
DB	1288090	GAATCACTTCATCGCGTGGCGTACCGACCAACGTCGAGCGCGCTGGGATCTTCC	1288031
QY	534	TyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArg-----	551
DB	1288030	CTCAAGTGGAACTGGGCTGGATCCAGGCACCTTAGAGTAGTCTTCCAAAACCCCTGTG	1287971
QY	552	AspGluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgTrpSerGlu	571
DB	1287970	CACGCGCAATCCACCAGTAGCTCACTTCTCCTTGGTG--TACCATTCTCTGAG	1287914
QY	572	LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValCysLysThrIleAla	591
DB	1287913	CGTTTGTGA---CTTCGGATCTTCAGATGAAGTCGTCCAGGGAAGGTTCCCTG---	1287860
QY	592	PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThr	611
DB	1287859	---TGG-----GACGTAGTGGCTGGCGAT	1287839
QY	612	LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlu	631
DB	1287838	ACGTGAACAAGCCGCTGGTCTTCGCACCTTCTTGGCTACATGTGGTGCACACCCAGC	1287779
QY	632	GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGly---HisProGluTrpIleAsp	650
DB	1287778	AAGAAG---CTGCTTTTCATGGTCAAGAGTTGTGGFCACGCTGAAGATGG-----	1287731
QY	651	PheProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSer	670
DB	1287730	-----GCTGAAGGCCAGGACTGCCATGGATATGTTCGACGGCTGCCAAGCCAG	1287680
QY	671	TyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGly	690
DB	1287679	TACCAGAACGCCATCCGCACTCTGACC-----CGCTCC	1287647
QY	691	LeuGlnGluPhe-----AspArgProMetGlnTyrLeuGluAspLysTyrGluPheMet	708
DB	1287646	CTCAAGGGTGTACTACAGACTCCCTCGCGTGCACATCTCAGAT-----TTC	1287599
QY	709	ThrSerGluHisGlnPheIleSerArgLysAspGluGly---AspArgMetIleValPhe	727
DB	1287598	ACCGAGAAGGCTTCACATGGAAATAAGGCGCAGCAGCCACCACACAACTTTGGCGTTC	1287539
QY	728	GluLys-----GlyAsnLeuValPheValPheAsnPheHisTrpThrLys	742
DB	1287538	ATCGTTTTCGGCAGCAGCGCTCCACAGATGCTGTGTGATTCAACCTCTCTCGAACCC	1287482
QY	743	SerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAsp	762
DB	1287481	TCCCAGCCTGATACCACTCGTGTTCGACGGGTGCGAATGAAGACTGTTCTCAAC	1287422

QY	763	SerAspAspProLeuphGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThr	782
Db	1287421	ACIGATGATGCTGAATTCCTCGGT---GCAGAAAACGATATCGTACTTCGGTTCACGCA	1287365
QY	783	PheGluGlyTyrTrpAspAspArgProArgSerIleMetValTyrAlaProCysLysThr	802
Db	1287364	CGAGCGACACGCGGATAATTCCCTACTACTCTCTACTGTGATCCAGGAGT	1287305
QY	803	AlaValValTyrAlaLeu	808
Db	1287304	GCTCAGTTCCTACTCACIG	1287287
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US-09-974-300-653			
; Sequence 653, Application US/09974300			
; Patent No. US20020146721A1			
; GENERAL INFORMATION:			
; APPLICANT: Berka, Randy M.			
; APPLICANT: Clausen, Ib Groth			
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene			
; TITLE OF INVENTION: Expression			
; FILE REFERENCE: 10085.500-US			
; CURRENT APPLICATION NUMBER: US/09/974,300			
; CURRENT FILING DATE: 2001-10-05			
; PRIOR APPLICATION NUMBER: 09/680,598			
; PRIOR FILING DATE: 2000-10-06			
; PRIOR APPLICATION NUMBER: 60/279,526			
; PRIOR FILING DATE: 2001-03-27			
; NUMBER OF SEQ ID NOS: 8481			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 653			
; LENGTH: 1877			
; TYPE: DNA			
; ORGANISM: Bacillus licheniformis			
US-09-974-300-653			
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Db	112	GGCTTCGGTCTCTGTGTTGGCCCGCATCGAAGAGGTTCGAATCCCGCACTTT	171
QY	205	AsnAsnTrpAspAlaAsnAlaAspIleMet---ThrArgAsnGluPheGlyValTrpGlu	223
Db	172	AACGGTGTGTCGGGTGTCCTGCACCGAATGGAAAAGCGTCATCAGAAAGGCATATGGAA	231
QY	224	IlePheLeuProAsnAsnValAspGlySer-----ProAlaIleProHisGly	239
Db	232	CTGTTTATCCCGGTATTGGAGAGGGAGCTGTATAATGAATGATACAGCCGCA	291
QY	240	SerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrp	259
Db	292	ATGAAACGAGAAATTGAAGCTGATGCTTATGCTTTTTCGAAAGTCAGCCCGAAACG	351
QY	260	IleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspPro	279
Db	352	GCATCGGTCACTATCAATTGCGCGGA---TACCAATGGGCGACCGGAGTGGCAAAAG	408
QY	280	ProGluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArg	299
Db	409	AAAAAGCAGCAAAAGCCGTGATGAAACCG-----ATTTC	447
QY	300	IleTyrGluSerHisIleGly-----MetSerSerProGluProLysIleAsnSerTyr	317

448	ATCTACGAGCTTCATATCGGTTCTGGTGAAGAAACGCGGATCGAGCTTTTTCACATAC	507
318	ValAsnPheArgAspGluValLeuProArgIleIleLysLysLeuGlyTyrAsnAlaLeuGln	337
508	CGGNACTGACGGAACGGTCACTCCTTACGTCAAGAACACACGATTCACACATATCGAG	567
338	IleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhe	357
568	CTGATCGCGCTGACAGACACCGCTTTTACCGTTCATGGGCTACACAGACAGGGTAC	627
358	PheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAla	377
628	TACATCGCAGCAGCAGATATGGCAACCCGATGACATGATGATTTTCATCGACCGATGC	687
378	HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsn	396
688	CATCAGCATGAGATCGCGCTCATTTATGATGATGGGTTTCCGGCCCATTTTTCGAAAGATGAC	747
397	-----ThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe	412
748	CACGCGTTGATTTTGTGCGGATGCTCTGTATGAA-----TATAAA	792
413	HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn	432
793	CACGACCATGACAGG---GAAATTTGGGAATGGGGACCGCCCAATTTTGACCTCGGAAAA	849
433	TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPhe	452
850	CGAGAAGTTCACAGTTTTTATATCGAATCGGTGATTTGATGGATCGAGATCATCATATA	909
453	AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal	472
910	GATGATTTTCGACTCGATCGCGTTCCGAACTCTCTGATTGCGCAACCGCTCCAGCCT	969
473	GlyPheThrGlyAsnTyrGlnGluTyrPheGlyLeuAlaThrAspValAspAlaValVal	492
970	GAAGCGAAGCGC-----TTTTCGATCGAA	993
493	TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly	512
994	TTTATCAACGCTTAATGACAGAGCTTTTTCGAAAGATCCCGACTTTTGATGATGCA	1053
513	GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyPhe	532
1054	GAGGACTCCACAGACTGGCGCTTCTGACGATCCGACCTATGAAGGGGTCTCGGGTTT	1113
533	AspTyrArgLeuHisMetAlaIleAlaAspLysArgIleGluLeuLeuLysLysArgAsp	552
1114	AATATATAG-----	1122
553	GluAspTrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGluLys	572
1123	-----TGGAAATATGGT-----TGGATGAACGAT	1146
573	CysValSerTyrAlaGlu---SerHisAspGlnAlaLeuValGlyAspLysThrIleAla	591
1147	GTATTAACCTATATGAAGCTTCCCGACAAACAAAGAAACACCTGCATCATCTTGTGTTCA	1206
592	PheTrpLeuMet-----AspLysAsp	598
1207	TTTCTCTTATGATGCTTACTCAGAAATTTACATCTCGCTTCTCCACGATGAAGTG	1266
599	MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla	618
1267	GTCTACCGCAAAAGTCTCTG-----	1287
619	LeuHisLysMet-----IleArg	624
1288	CTTCAATGAATGCGCGCGATTTATGGCAGAAATTCGCCAGATACCGCTGCTGATCAGT	1347
625	LeuValThrMetGlyLeuGlyGlyGluTyrLeuAsnPheMetGlyAsnGluPheGly	644
1348	TATTTTATGATGACCCCGGAAAAAG-----CTCTTTTATGCGCGGTGATGTTGCT	1401
645	His---ProGluTyrIleAspPheProArgAlaGlnHisLeuSerAspGlySerVal	663
1402	CAATTTGATGAATGAAGAACAGACAGCTCGATTGGTTTGGACGAT-----	1452
664	IleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAla	683
1453	-----TTTGACATGCACCGCAACCCGGAATGTTTACAAAGGAGGCTCTA	1497
684	Glu---TyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGlu	702
1498	CACCTCTCAAAAAAGCCGTATCTGTATGAAAATGATCATCGGCACGAGATTCGAG	1557
703	AspLysTyrGluPheMetThrSerGluHisGlnPheIleSer-----ArgLys	718
1558	---TGATTTGACGTTAACAATCGCGAACAGTCGATTGTATCGTTATCCGCTATGGAAAA	1614
719	AspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPhe	738
1615	CAGCCCGGTGAAGCGCTGATTAIC-----GTCGCAATTTTC	1650
739	HisTrpTrpLysSer---TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyr	757
1651	-----ACGCTTCCTCGTCTATCAGCAATATCGGTTCGGCTGCCCTTTTCAACCGAATAT	1704
758	LysValAlaLeuAspSerAspProLeuPheGlyGlyPheGlyArgIleAspHisAsn	777
1705	ATCGAAGTCTTTAACAGCGATGATCAAAATACGAGGCTTCACACCAAAATCACCCCAAAA	1764
778	AlaGluTyrPheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyr	797
1765	---CGCTTTCAGCGCAAGAAAGCGTCTCTGACGCAAAACCATACAGCATCAGCATGACA	1821
798	AlaProCysLysThrAlaValValTyrAlaLeuValAspLys	811
1822	GTCCCTCCCTGGGAGCTCGCGTTTTCAGACAGTCARAAAG	1863
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; Sequence 453, Application US/09925300		
; Patent No. US20020151681A1		
; GENERAL INFORMATION:		
; APPLICANT: Craig Rosen,		
; APPLICANT: Steve Ruben		
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies		
; FILE REFERENCE: PA101		
; CURRENT APPLICATION NUMBER: US/09/925,300		
; PRIOR FILING DATE: 2001-08-10		
; PRIOR APPLICATION NUMBER: PCT/US00/05988		
; PRIOR FILING DATE: 2000-03-08		
; PRIOR APPLICATION NUMBER: 60/124,270		
; PRIOR FILING DATE: 1999-03-12		
; NUMBER OF SEQ ID NOS: 1890		
; SOFTWARE: PatentIn Ver. 2.0		
; SEQ ID NO 453		
; LENGTH: 604		
; TYPE: DNA		
; ORGANISM: Homo sapiens		
; FEATURE:		
; NAME/KEY: misc feature		
; LOCATION: (12)		

OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453

Alignment Scores:

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Query Match:	10.38%	Indels:	8
DB:	10	Gaps:	4

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-925-300-453 (1-604)

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QY	276	HisTyrAspProGluGluArgTyrIlePheGlnHisProArgProLysLysPro	295
DB	114	CACGGGATCCA-----GAACACTCAATAGATTAAAGCATTCAGACCAAGAGCCA	167
QY	296	LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn	315
DB	168	CGGAGTCTAAGAAATTATGATCATGTGGGAATTCCTCCATCAAGGAAAGTAGCT	227
QY	316	SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrRsnAla	335
DB	228	TCITATAAACATTTTACATGCAATGTACTACCAAGAATCAAGGCTTGGATCAACTGC	287
QY	336	LeuGlnIleMetAlaIleGlnHisSerTyrTyrAlaSerPheGlyTyrHisValThr	355
DB	288	ATTGAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTTGGTACCAATCACA	347
QY	356	AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAsp	375
DB	348	AGCTTCTTTGAGCTTCCAGCCGTTATGGAAACCTGAAGAGCTACAGAACTGGTAGAC	407
QY	376	LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn	395
DB	408	ACAGCTCATTYCATGGGTATCATAGTCTCTTAGATGGTACAGCSCATGCTCAAAA	467
QY	396	AsnThr-LeuAspGlyLeuAsnMetPheAsp-----CysThrAspSer---CysTyrph	412
DB	468	AATCCAGCAGATGGGATGGATATGTTGGATGGGGGACAGATCCNGGTAAATTTT	527
QY	412	eHisSerGlyAla-----ArgGlyTyrHis	420
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Job time : 6667 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 02:17:31 ; Search time 2890 seconds
(without alignments)
4673.715 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882

Perfect score: 4465

Sequence: 1 EKSYNSEFRSTVAAGKV.....EEEEEEVAAVEVVVEE 834

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5	
Ygapop 6.0 , Ygapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO.spool/US10056454/runat_01072003_145500_8257/app_query.fasta_1.1031
-DB-EST -QPMT-fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_estl: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2987.5	66.9	2766	11	AY109521	Zea mays
2	2809.5	62.9	2732	11	AY109532	Zea mays
3	2082	45.6	3012	11	AY105679	Zea mays
4	2038	45.6	2738	11	AK009815	Mus muscu
5	1136	25.4	728	14	BU008463	BK008463 QGH7K17.Y
6	1123	25.2	713	14	BQ986883	BQ986883 QGF10L08.Y
7	1121.5	25.1	1524	10	BG366603	rockefell
8	1063	23.8	689	13	BT308555	EST529965
9	1062	23.8	801	10	BE195628	HVSMEH08
10	1060	23.7	1482	17	BH770747	LLMtag49
11	1044	23.4	678	10	AV939010	AV939010
12	1035.5	23.2	898	14	BQ716536	AGENCOURT
13	1027.5	23.0	731	10	BE602527	HVSMEH09
14	989.5	22.2	717	14	BU005876	BU005876 QGG9F08.Y
15	976	21.9	639	10	AW065909	AW065909 687002609
16	973.5	21.8	621	12	BG521671	BG521671 13-3 Stev
17	971	21.7	1088	14	BQ232004	AGENCOURT
18	970	21.7	825	12	BF065047	BF065047 HV_CEP002
19	959	21.5	646	9	AU238577	AU238577
20	956.5	21.4	695	14	BQ240494	BQ240494 TAE05016F
21	951	21.3	573	13	BM526229	BM526229 sal38f02.
22	950	21.3	651	12	BG526727	BG526727 63-11 Ste
23	944.5	21.0	761	13	BM411030	BM411030 EST585357
24	937.5	21.0	918	17	CNS06W72	AL418101 T3 end of
25	934.5	20.9	751	13	BI920158	BI920158 EST540093
26	934	20.9	569	10	AV442128	AV442128 AV442128
27	931	20.9	571	13	BI696880	BI696880 sal25q09.
28	927	20.8	650	10	BE427534	BE427534 PSR7153 I
29	917.5	20.5	734	9	AL043330	AL043330 DKF2p4340
30	916	20.5	1042	13	BM456951	BM456951 AGENCOURT
31	914	20.5	962	17	CNS0607J	AL408509 T7 end of
32	907	20.3	560	14	BM885252	BM885252 sal197a08.
33	897.5	20.1	967	17	BH132946	BH132946 ENTPTC72TF
34	897	20.1	571	13	BI469105	BI469105 sal07e09.
35	895	20.0	589	10	AW596011	AW596011 sal96g03.Y
36	894	20.0	576	10	AW244197	AW244197 687050F06
37	891.5	20.0	693	13	BI091718	BI091718 602859457
38	881	19.7	575	13	BI425610	BI425610 sah69a11.
39	878	19.7	582	13	BM309136	BM309136 sak55b02.
40	872	19.5	801	12	BG741971	BG741971 602633412
41	866	19.4	592	13	BJ268430	BJ268430
42	863	19.3	774	9	AU139463	AU139463
43	861.5	19.3	671	13	BI719233	BI719233 1031042C0
44	860.5	19.3	602	12	BG524041	BG524041 38-25 Ste
45	860	19.3	739	9	AU004044	AU004044

ALIGNMENTS

RESULT 1
AY109521
LOCUS AY109521
DEFINITION Zea mays CL1245_1 mRNA sequence.
ACCESSION AY109521
VERSION AY109521.1 GI:21213273
KEYWORDS HTc.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2766)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whittitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
JOURNAL Overgo Probes
REFERENCE Unpublished (2002)
AUTHORS 2 (bases 1 to 2766)
CoE,E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
Source 1..2766
/organism="Zea mays"
/db_xref="MaizedB:630161"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

BASE COUNT	715 a	546 c	689 g	718 t	98 others
ORIGIN					

Alignment Scores:
Pred. No.: 0 Length: 2766
Score: 2987.50 Matches: 562
Percent Similarity: 79.04% Conservative: 79
Best Local Similarity: 69.30% Mismatches: 147
Query Match: 66.91% Indels: 23
DB: 11 Gaps: 6

US-10-056-454A-15_COPY_49_882 (1-834) x AY109521 (1-2766)

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Dd	56	AGCTGCCTGGTGTCTCCTGGAAAGGTACTGTGCTGGAGCGTGCCAGTCATCGTTGTT	115
Qy	32	SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr	51
Dd	116	TCCTCCGCAGAG-----CCGGTCGTGGCACACTCAACCTGAAGA-----CTACAGATA	163
Qy	52	AspValAspSerSerThrMetGluHisAlaSerGlnIleLysThrGluAsnAspVal	71
Dd	164	CCTGAAGCAGAACTGACTGTGGGAAGAGCATCTCTCCACCACTCAAACA-----	214
Qy	72	GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGln	91
Dd	215	-----ACATACGACGTGGCTGAAGCA-----AGTTCAGGAGTTGAG	250
Qy	92	LeuGlnGluGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIle	111
Dd	251	CTGAGGAGAGCGCTGACCTCTCAGAGATTGGAGTTGGAGGTACTGGTGGAACCAAA	310
Qy	112	IleAsp-----GluSerAspArgIleArgGlu-----ArgGlyIle	123
Dd	311	ATTGATGTTGCAGGCATCAAAAGCCAAGCACCCACTCGTGGAGGAGAAAACCAGGATTATC	370
Qy	124	ProProGlyLeuGlyGlnLysIleTyrgluIleAspProLeuLeuThrAsnTyrrg	143
Dd	371	CCACCACGAGATGGCCACGAATATATGAGATTGCCCAATGTTGGAAGGGTTTCGG	430
Qy	144	GlnHisLeuAspTyrrgTyrrSerGlnTyrrLysLysLeuArgGluAlaIleAspLysTyrr	163
Dd	431	GGTCACCTTGACTACCGATACAGTGAATATAAGAGATTACGTCGGGCTATTGATCAACAT	490
Qy	164	GluGlyLeuGluAlaPheSerargGlyTyrgluLysMetGlyPheThrargSerAla	183
Dd	491	GAAGTGTGTTGGATGCATTTTCACGCGGTTTACGAAAAGCTTGGATTTTACTCGACGGCT	550
Qy	184	ThrGlyIleThrTyrrargGluTrpAlaLeuGlyValaglnSerAlaAlaLeuIleGlyAsp	203

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QY 564 LeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db 1691 TTAACAATAAGAGGTGGCTTGAAGAAGTGTGCACATTATGTGAAAGTCAATGATCAAGCT 1750
QY 584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db 1751 CTGTGTTGGTGAACAAGACAATGCAATCTGTGTTGATGGATAAGGATATGATGATTCATG 1810
QY 604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db 1811 GCTCTGGACAGCCCTTCAACGCTCGCATCGATCGTGGATAGCATACATAAATGAT 1870
QY 624 ArgLeuValThrMetGlyLeuGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
Db 1871 AGGCTGTGTACAAATGGTGTAGAGGTGAAGGCTATCTAAATTTCAATGGGAATGAGTTT 1930
QY 644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db 1931 GGGCATCTTGAATGATAGATTTTCCAAGAGTCTCTCAAAAGTCTTCCAAATGGCTCCGTC 1990
QY 664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla 683
Db 1991 ATTCTGGGATAACAAATAGCTTTGATAAATGCCCGCTAGATTTCACTTTGGAGATGCA 2050
QY 684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyrLeuGluAsp 703
Db 2051 GATTATCTTAGATATCGTGGTATGCAAGAGTTTGACAGGCAATGACACCTTGAGGGA 2110
QY 704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db 2111 AAATATGATTCATGACATCTGATCATCTATGATATGATCATCGGAAGCATGAGGAGATAAG 2170
QY 724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db 2171 GTGATCATCTTTGAGAGAGAGATTTGGTCTTCGTGTTCACTTCCACTGGAGCAATASC 2230
QY 744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db 2231 TATTTTGACTATCGTGGTGTGTTTCAAGCTGGAGTACAGATCGTTTATGATTC 2290
QY 764 AspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
Db 2291 GACGATGCCCTTTTCGGTGGATTTAGTCGGCTTGATGATGATGCTGACTTTCACCTGCT 2350
QY 784 GluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
Db 2351 GACTGGCCGCATGACACAGCCGCTGTTCTTCTTCGGTCTATGACCCCGACGAGAACGCC 2410
QY 804 ValValTyrAlaLeuValAspLysGluGlu 814
Db 2411 GTCGTATATGCACCTGCAGTGCAGAGAGGAA 2443

RESULT 2
AY109532
LOCUS AY109532 2732 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL1742_1 mRNA sequence.
ACCESSION AY109532
VERSION AY109532.1 GI:21213287
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tindley,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
REFERENCE 2 (bases 1 to 2732)
AUTHORS Coe,E.C.

```

```

TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
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Location/Qualifiers
/organism="Zea mays"
/db_xref="MaizeDB:630561"
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/clone="CL1742.1"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 659 a 506 c 679 g 710 t 178 others
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 2732
Score: 2809.50 Matches: 521
Percent Similarity: 79.31% Conservative: 73
Best Local Similarity: 69.56% Mismatches: 134
Query Match: 62.92% Indels: 21
DB: 11 Gaps: 3

US-10-056-454a-15_COPY_49_882 (1-834) x AY109532 (1-2732)
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QY 87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db 329 -----TCGGCTCAATTCAGTCG-----GATGAATGGAGTACAGACAT 370
QY 107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121
Db 371 TCTGAAGAGACAACGTCGGTCTGCTGGTGTGCTGATGCTCAAGCCTTGAACAGAGTTGCA 430
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuPheAsn 141
Db 431 GTGTNNNNNNACCAAGCGATGGACNNNNNNNTATCCAGATTGACCCCATGTTCAGAGC 490
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 491 TATAAGTACCATCTTGATATCGGTACAGCTCTATAGAAGAAATCCGTTTCAGACATTGAT 550
QY 162 LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 551 GAACATGAAGGAGGCTTGAAGCGCTTCTCCGTTAGTATGAGAAGTTGGATTAAATCGC 610
QY 182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db 611 AGCGGGAAGTATCATCATATCGAATGGCTCTCTGGAGCATTTTCTGACGATTGGTG 670
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 671 GTTGACTTCAACACTGGGATCCAAATGCGATGATGACGNNNNNNNTGANNNNNNNN 730
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 731 NNNNNNNNNNNCTGCCTAACAATGCAGATGGTACATCACCTATCTCTCATGATTCGT 790
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaIlePheAsn 261
Db 791 GTAAAGGTGAGAATGGATACTTCCATCAGGCAATAAGGATTCATTCAGCCTGGATCAAG 850
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 851 TACTAGTCAGGCCCCAGGAGAAATACCATATGATGGATTATTATGATCTCTCTGAA 910

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[illegible]

QY 668 GlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAlaGluTyrLeuArg 687
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 Db 1689 AATGAGAGTATACATTATGCCAAGCGAGTTAATTACCGACGATGACCTTCCTCGC 1748
 QY 688 TyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPhe 707
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 QY 708 MetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPhe 727
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 Db 1809 CTTTCAGCTCCACAGCGCTACGTGAGTGAAGAAACATGAAGCCATAGACAATACCTTT 1868
 QY 728 GluLysGlyAsnLeuValPheValPheAsnPheHisThrPheLysSerTyrSerAspTyr 747
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 QY 748 ArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspProLeu 767
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 Db 1929 CGAGTCGGGACACCAACACCGAGGAGTTCAAAATTTGACTAGATTCTGACGCGGAG 1988
 QY 768 PheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTyrTyr 787
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 Db 1989 TATGGAGGTATCAGACACGACGACCAACACCACTACTTTGCTGAGGCTTTGAACAT 2048
 QY 788 AspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValTyrAla 807
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 Db 2049 AATGGGCGCCCTATCTCTCTGTTGATACATCCCAAGCGGAGTGGCTCTCATCTTCAG 2108
 QY 808 LeuValAsp 810
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 Db 2109 AATGTGGAT 2117

RESULT 5

BU008463

LOCUS

DEFINITION QGH7K17.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
 QGH7K17, mRNA sequence.

ACCESSION

BU008463

VERSION

BU008463.1

KEYWORDS

EST.

SOURCE

Lactuca sativa.

ORGANISM

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.

REFERENCE

1 (bases 1 to 728)

AUTHORS

Kozik,A., Micheltore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
 P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
 Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://comphenomics.ucdavis.edu/
 Unpublished (2002)

TITLE

Contact: Alexander Kozik [R.W.Micheltore]

JOURNAL

Department of Vegetable Crops, R.W.Micheltore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [micheltore@vegmail.ucdavis.edu]
 Belongs to contig QG_CA_contig6851, see http://cgpdb.ucdavis.edu/
 for details.

COMMENT

Plate: QGH7 row: K column: 17.

Location/Qualifiers

1. 728

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/cultivar="L.serriola"

/db_xref="taxon:4236"

/clone="QGH7K17"

/lab_host="E.coli"

/note="Vector: pBRCDNASfiab; The library was constructed

FEATURES

Source

from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at <http://cgpdb.ucdavis.edu/>
 TAG_LTB-QG_EFGHJ lettuce serriola
 TAG_TTSUB-leaves dark grow

BASE COUNT 227 a 133 c 149 g 218 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 4.27e-123 Length: 728
 Score: 1136.00 Matches: 205
 Percent Similarity: 92.98% Conservative: 20
 Best Local Similarity: 84.71% Mismatches: 17
 Query Match: 25.44% Indels: 0
 DB: 14 Gaps: 0

US-10-056-454a-15_COPY_49_882 (1-834) x BU008463 (1-728)

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QY 193 LeuGlyAlaGlnSerAlaLeuIleGlyAspPheAsnAsnTyrAspAlaAsnAlaAsp 212

Db 61 CCTGGGCAAGTCTGCTTCACTTACCTGGAGATTTCACAACTGGAATCCAATGCTCAT 120

QY 213 IleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGly 232

Db 121 GTTATGACCGCAATGAAATTTGCTGTGTGGAGATCTTTTGGCAACAACATGTCATCAT 180

QY 233 SerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyVal 252

Db 181 TCTTCACTATTCCTCATGTTCGAGTAAAGATTCGTATGGATACCCATCGGCAT 240

QY 253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272

Db 241 AAAGACATGATCTCTGCTTGGATCAAGTTTTCAGTACAGCACCTGGTGAGATTCCTTAT 300

QY 273 AsnGlyIleHisTyrAspProGluGluArgTyrIlePheGlnHisProArgPro 292

Db 301 AATGGAATATATCTATGATCCCAACAGAGAAAATACGTGTTTCAACATCCAGACCA 360

QY 293 LysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluPro 312

Db 361 AAGAGCGCAATCTCTTAGGATTTATAGGACATGTTCTCCCTCGCATAAAAAATCGGT 480

QY 313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332

Db 421 ATGATCAACACGATGCTAACTTTAGACAGCATGTTCTCCCTCGCATAAAAAATCGGT 480

QY 333 TyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyr 352

Db 481 TACAATGCAGTTCAATCATGCTATTCAAGAGCATTCATATTATGCTAGTTGGGTAC 540

QY 353 HisValThrAsnPheAlaProSerSerArgPheGlyThrProAspAspLeuLysSer 372

Db 541 CATGTGACAAATTTTTCACCAAGTAGTCACTGGAACCTCCAGATGATCTTAATCA 600

QY 373 LeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHis 392

Db 601 ATGATTGATAAAGCACATGAATTAGTCTTGTCTCTCATGGATATTGTCATAGTCAT 660

QY 393 AlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412

Db 661 TCATCAAAACACACATTAGATGATATATATGTTTGAACACATGATGTCATACATCTT 720

QY 413 HisSer 414

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Db      721 CATCTCT 726
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BQ986883      713 bp      mRNA      linear      EST 21-AUG-2002
QGFI0108.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
LOCUS      BQ986883
DEFINITION      QGFI0108, mRNA sequence.
ACCESSION      BQ986883
VERSION      BQ986883.1 GI:22404408
KEYWORDS      EST.
SOURCE      Lactuca sativa.
ORGANISM      Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 713)
Kozik,A., Michelmore, R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmil.ucdavis.edu]
belongs to contig QG_CA_Contig6851, see http://cgdb.ucdavis.edu/
for details.
Plate: QGFI0 row: L column: 08.
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            /lab_host="E.coli"
            /note="Vector: pBRCNDSFIAB; The library was constructed
            from 10 different sources of RNA from a single genotype.
            Separate cDNAs were generated using primers that
            incorporated unique 5' and 3' tags to distinguish each
            source of RNA. cDNAs were then pooled, size-fractionated,
            directionally cloned into a custom medium-copy vector and
            transformations made with four size classes to minimize
            size bias. Details of each source of RNA and library
            construction can be obtained at http://cgdb.ucdavis.edu/
            TAG_LIB=QG_EFGHJ lettuce serriola
            TAG_ISSUE=flowers post-fertilized
            TAG_SEQ=TGCCATCGGG"
BASE COUNT      221 a 132 c 146 g 214 t
ORIGIN
Alignment Scores:
Pred. No.:      1,41e-121      Length:      713
Score:      1123.00      Matches:      203
Percent Similarity:      93.67%      Conservative:      19
Best Local Similarity:      85.65%      Mismatches:      15
Query Match:      25,15%      Indels:      0
DB:      14      Gaps:      0
US-10-056-454a-15_COPY_49_882 (1-834) x BQ986883 (1-713)
QY      178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSer 197
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Db      1 GCTTTCACTCGAGCAACACAGTATCACTTATAGAGATGGCGACCTGGCAAAAGTCT 60
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QY      198 AlaAlaLeuIleGlyAspPheAsnTrpAspAlaAsnAlaAspIleMetThrArgAsn 217
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Db      61 GCTTCACCTATTGGAGATTTCACAACTCGAATCCAAATGCTGATGTTATGACCGGAAT 120
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QY      218 GluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIlePro 237
|||||
Db      121 GAATTTGGTGTCTGGGAGATCTTTTGGCAACAAATGTTGATGATCTTCACCTATTCTCT 180
|||||
QY      238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
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Db      181 CATGGTCTCGAGTAAAGATTCTGATGATACCGCAATCTGCGATTAAAGACTCGATCTCT 240
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QY      258 AlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyr 277
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Db      241 GCTTGGATCAAGTTTTCAGTACAAAGCACCTGGTGAGATCTCTTATAATGGAATATACTAT 300
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QY      278 AspProGluGluGluAlaGlyTyrIlePheGlnHisProArgProLysLysProLysSer 297
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Db      301 GATCCCCCACAAAGAGAAATACGTGTTTCAACATCCAGACCAAGAACGCCGAATCT 360
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QY      298 LeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyr 317
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Db      361 CTTAGGATTTATGAGGCACATGTGGGAATGAGTAGTACGGAACCAATCATCAACACGTAT 420
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QY      318 ValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGln 337
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Db      421 GCTAACCTTTAGAGACGATGTTCTCCCTCGCATATAAAAAAATCGGTTACATGCGAGTTCAA 480
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QY      338 IleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhe 357
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Db      481 ATCATGGCTATTCAAGAGCATTCATATATGCTAGCTTTGGGTACCAATGTCACAAATTTT 540
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QY      358 PheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAla 377
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Db      541 TTTGCACCAAGTAGCTAGTGTGGAACTCCAGATCACTTAATCAATCAATGATTGATAAGCA 600
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QY      378 HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThr 397
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Db      501 CATGAATAGTCTCTGTGTGTTCTCATGGATTTGTCATGATGATGATGATGATGATGATGAT 660
|||||
QY      398 LeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSer 414
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Db      561 TTAGATGATTAATAATATGTTGATGGAACCTGATAGTCAATACATCTTCAATCT 711
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RESULT 7
BE636603      1524 bp      mRNA      linear      EST 03-JAN-2002
LOCUS      rockefeller.0.213 Mastigamoeba balamuthi lambda ZAP II Library
DEFINITION      Mastigamoeba balamuthi cDNA similar to 1,4-alpha-glucan branching
enzyme (BC 2.4.1.1), mRNA sequence.
ACCESSION      BE636603
VERSION      BE636603.1 GI:9919714
KEYWORDS      EST.
SOURCE      Mastigamoeba balamuthi.
ORGANISM      Mastigamoeba balamuthi.
REFERENCE      1 (bases 1 to 1524)
AUTHORS      Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
The analysis of 100 genes supports the grouping of three highly
divergent amoebae: Dictyostellium, Entamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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POLYA=Yes.
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FEATURES
    source

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Pred. No.:      7,99e-121      Length:      1524
Score:          1121.50      Matches:      213
Percent Similarity: 69.77%      Conservative: 64
Best Local Similarity: 53.65%      Mismatches: 98
Query Match:      25.12%      Indels:      22
DB:              10      Gaps:      5

US-10-056-454A-15_COPY_49_882 (1-834) x BE636603 (1-1524)

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Db 8 AAGGGCGGCGAGCTGTGGACAGCGGCTGTTCACCTACCGCAACTGGGAGAGCGTG 67

QY 437 ArgTyrLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArg 456
Db 68 CGGTTCTGCTGAGCAACGTTGGGTGTATCGAGTACGAGTACCGCTTCGACGCTCCGC 127

QY 457 PheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGly 476
Db 128 TTTCAGCGGTGACCTGCTGCTACGTGCACCGGCGGCGGCGGCGGCGGCGGCGGCGG 184

QY 477 AsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeu 496
Db 185 GACTACCGGCACTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244

QY 497 ValAspAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSer 516
Db 245 GCCAACACGCTATCCACGAGATCAACCGCGAGCGGCGGTGTCCATCGCGGAGGAGCGGAGC 304

QY 517 GlyMetProThrPheCysIleProValGlnGlnGlyValGlyPheAspTyrArgLeu 536
Db 305 GGGTTCCGGGGGCTGTGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364

QY 537 HisMetAlaIleAlaAsp-LysArgIleGluLeuLeuLysLys-----ArgaspGluAs 554
Db 365 GCGATGGCTGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424

QY 554 pTTPArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlyLysCysVa 574
Db 425 CTGGGACATGGACCATCTCCACACCCCTCGCCACCGCGGCGGCGGCGGCGGCGGCGGCGG 484

QY 574 lSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLe 594
Db 485 CGGCTACGGCGGATCCCGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544

QY 594 uMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAs 614
Db 545 GATGGACAAGGAGATGTACGACGTGGATGCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 604

QY 614 pArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGluGl 634
Db 605 CGGGGCGATGGCGCTGCACAGATGATCCGGTGTCTGCTACGCTGCGGCGGCGGCGGCGG 664

QY 634 yTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpTrpIleAspProArgAl 654
Db 665 CTACCTGACGCTTTATGGGCAACGAGTTGGTGGCCACCGCGAGTGGATCGACTTCGCGCGC 722

QY 654 aGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCy 674
Db 723 -----CGGGGCAACAAACCGGAGCTACCACTACGC 751

QY 674 sArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPh 694
Db 752 CGGGGCGCATGGTGGTGTGTCAGGACCAACACCTGCGGTACCAACAGATGGCGGCGACTT 811

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QY 694 eAspArgProMetGluTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPh 714
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QY 714 eIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPh 734
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Db 992 CGGAGGTACCGGCTGGCGCTGCTGCTGCGGAGCAGCTGCGTGTGGCGGCGGCGGCGGCT 1051

QY 774 eAspHisAsn-----AlaGluTyrPheThrPheGluGlyTrpTyrAspAspAr 790
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QY 790 gProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyr 806
Db 1107 ---TACTCGCTCATGATCTACGCGCTCGCGCAGCGGCTCGCTCTTT 1151

RESULT 8
LOCUS      B1308555
DEFINITION EST529965 GP0D Medicago truncatula cDNA clone pgPOD-7017 5' end,
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ACCESSION B1308555
VERSION    B1308555.1 GI:14982882
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 689)
AUTHORS   Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
            J. and Fraser,C.M.
            ESTs from developing reproductive tissues of Medicago truncatula
            Unpublished (2001)
            Contact: Michael A. Grusak
            USDA/ARS Children's Nutrition Research Center
            Baylor College of Medicine
            1100 Bates Street, Houston, TX 77030-2600, USA
            Tel: 713-798-7044
            Fax: 713-798-7078
            Email: mgrusakebcm.tmc.edu
            B395410e
            TIGR sequence name: MTOAQ93TX
            More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtg gat CC).
            Location/Qualifiers
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            XhoI; Immature pods, ranging in age from 15 to 30 days
            after pollination, were collected from greenhouse-grown
            plants. At harvest, seeds were removed from pods and
            isolated from walls were collected and immediately frozen
            in liquid nitrogen. Pod walls were pooled for mRNA
            extraction. cDNA was prepared from polyA+ enriched RNA.
            The cDNA was directionally ligated into the Unizap XR
            vector from Stratagene and packaged using Gigapack III

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Db	2	ATT	CATGGGACTTTATCCGGAAGCTGTATCATCTGGTGAAGATGTCAGCGGAATGCCATACA	61
Qy	521	phe	cysileProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaile	540
Db	62	TTT	TGATCCTGTCCAGATGGTGGTCTGGTTTGCATTCGCTTCATATGGCTGA	121
Qy	541	Ala	aspLysArgIleGluLeuLeuLysLysArgaspGluaspThrpargValglyAspile	560
Db	122	GCAGATAAT	TGATTGAACCTCTCAAGCAAAAGTCACGAAATCTTGCAAAATGGCGGAAAT	181
Qy	561	Val	HisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHis	580
Db	182	GTCCACACCCTAACAAATAGAAAGTGGCTTCAGAAAGTGTCACTATTCAGAAAGTCAT	241	
Qy	581	Asp	GlnAlaLeuValGlyAspLysThrIleAlaPheIrpLeuMetAspLysAspMetTyr	600
Db	242	GATCAACACTAGT	TGGTGACAAACACTATTCGCACTCTGGTGTGATGATGAAGATATGAT	301
Qy	601	Asp	PheMetAlaLeuAspArgProSerThrSerLeulleAspArgGlyIleAlaLeuHis	620
Db	302	GATTTTCATGGCTCTGTGATAGACCTTCAACCCCTCGCATGTGATCGCATGACATACAT	361	
Qy	621	Lys	MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly	640
Db	362	AAAATGATCAGCGTTTGACCATGGGTTTAGTGGCGAAGGCTATCTTAATTTCA	421	
Qy	641	Asn	GluPheGlyHisProGluIrpIleAspPheProArgAlaGluGlnHisLeuSerAsp	660
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Db	482	GGCAAAAGTTCTCCTCGCAATTAACAATAGTTATGATAATGCCGCGTAAATTTGATCTT	541	
Qy	681	Gly	AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr	700
Db	542	GGAGATCGAGATTTTCTTAGATATCGTGGAAATGCAGAGTTCGATCAGCGAATGCCCAT	601	
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Qy	740	p-Thr	LysSerTyrSerAspTyr--ArgIleAlaCysLeuLysPro-GlyLysTyr-Lys	758
Db	722	GGAGCAATAACTTTTTCACATCCCGGTGGGGGGTTCCTCAGACCTTGGGAATACCAAG	781	
Qy	759	Val	AlaLeuAspSer	763
Db	782	GTGGCCTTTAAATCT	796	

RESULT 10	
BH770747/c	
LOCUS	
DEFINITION	BH770747 1482 bp DNA linear GSS 01-MAY-2002
	LLMGtag494 MG1363 Random Sequence Tag Library Lactococcus lactis
	subsp. cremoris genomic, DNA sequence.
ACCESSION	BH770747
VERSION	BH770747.1
KEYWORDS	GI:20373704
SOURCE	GSS.
ORGANISM	Lactococcus lactis subsp. cremoris.
	Lactococcus lactis subsp. cremoris
	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
	Lactococcus.
REFERENCE	1 (bases 1 to 1482)
AUTHORS	Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE	Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL	Sci. Aliments, (2002) In press
COMMENT	Contact: Sorokin A
	Genetique Microbienne
	INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is glgB (88%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 1454.
Location/Qualifiers
1. .1482
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prepared by partial AluI digestion or by sonication."
BASE COUNT 455 a 304 c 257 g 465 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.41e-113 Length: 1482
Score: 1060.00 Matches: 220
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Best Local Similarity: 50.34% Mismatches: 125
Query Match: 23.74% Indels: 24
17 Gaps: 9
DB:
US-10-056-454A-15_COPY49_882 (1-834) x BH770747 (1-1482)
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Db 1311 ACTTTCCGCGAATGGCCACCAAAATGCTATAAAAGCTTGCGCTGTGGTGAATTAACAAT 1252
QY 207 TrpAspAlaAsnAlaAAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeu 226
Db 1251 TGGAAACAACACTATGAA--CTAAACAGCGCTATGCGGAGCTTGGGAATTTTCAGTT 1195
QY 227 ProAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMet 246
Db 1194 CCTGGA-----TTATTACCTGGTGTCTAAAGTAAAAATAAAGTTG 1153
QY 247 AspThrProSerGly---vallyAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
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QY 266 LeuProAspGlu---lleProTyrAsnGlyIleHisTyrAspProGluGluGluArg 284
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QY 285 TyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHis 304
Db 1050 TACGAATGGAAAAATAAAGCCCTAAACTAAGCAGACACCTTCATTATTATGAAGACAT 991
QY 305 lleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluVal 324
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Db 870 CGGCTCTATGCTAGTTTTGGTTATCAAGTTTCCAAATTTTTTGGCATCTCTAGTCGCTTT 811
QY 365 GlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 384
Db 810 GGTACGCCAGAAGATTTAATGGAATTGATTGATAAAGCACATGGTTGGGTTCGAAGT 751
QY 385 LeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPhe 404
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ACCESSION BQ716536
VERSION BQ716536.1 GI:21855433
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13605 row: p column: 13
High quality sequence stop: 595.
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/lab_host="DH10B"
/dev_stage="adult, 16 yr"
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Directionally cloned using the following adaptors:
5'-GACTAGTCAGATCGGCGGCGCC(15)-3' and
5'-TCGACACCGGTCGCG-3' and
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."
BASE COUNT 234 a 171 c 225 g 268 t
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Query Match: 14 Gaps: 3
DB:
US-10-056-454a-15_COPY_49_882 (1-834) x BQ716536 (1-898)
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Db 2 CATTCATGGTATCATAGTCTCTAGATGGGTACACGCCATGCTTCAAAAATCA 61
Qy 398 LeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg 417
Db 62 GCAGATGGATGAATATCTTTGATGGGACAGATTCTCTATTTTCATCTGGACCTAGA 121
Qy 418 GlyTyrHisTyrMetTyrAspSerArgLeuPheAsnTyrGlyAsnTyrGluValLeuArg 437
Db 122 GGGACTCATGATCTTTGGGATAGCAGATGTTGCTTACTCCAGTGGGAGATTAGA 181
Qy 438 TyrLeuLeuSerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPhe 457
Db 182 TTCCTTCGTCAACACAAAGATGGTGGTGGGAAGATATCGCTTGTGATGATTTGGTTT 241
Qy 458 AspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsn 477
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Db 242 GATGGTGTACCTCCATGCTTTATCATCACCATGGAGTGGGTCAAGGTTCTTCAGGTGAT 301
Qy 478 TyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuVal 497
Db 302 TACAGTGAATATTCGGACTACAGTAGTAGATGCTTACCTTACCTACCTATGCGCA 361
Qy 498 AsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGly 517
Db 362 AATCATTTGGTTCACACGCTGTGTCCTCCGATTTCTATAACAATAGTAGGATGTATCAGA 421
Qy 518 MetProThrPheCysIleProValGluGluGlyValGlyPheAspTyrArgLeuHis 537
Db 422 ATGCCACTCTGTGCTCTCCAAATTTCCAGGAGGGGTGTTTGTACTATCGACTAGCC 481
Qy 538 MetAlaIleAlaAspLysArgIleGluLeuLeuLysLysLysLysLysLysLysLysLys 556
Db 482 ATGCCAATTCAGATAAGTGCATTACAGTACTTAAAGAGTTTAAAGATGAAGAGTGAAC 541
Qy 557 ValGlyAspIleValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyr 576
Db 542 ATGGCGGATATAGTATACGCTCACAAACAGGGCTACCTTGAAGAGTGCATTTGCTTAT 601
Qy 577 AlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAsp 596
Db 602 GCAGAGACCCATGATCAGGCATTTGGGGATAGTCGCTGGCATTTTGGTTGATGGAT 661
Qy 597 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuLeuAspArgGly 616
Db 662 GCCGAATGTATACAAACATGAGTCTCTGACTCCCTTACTCCAGTTATTGATCGCGGA 721
Qy 617 IleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGluGluGluGluGlu 635
Db 722 ATACAGCTTCAATAATGATTCGACTCATTCAGCATGGGGTGGGGTGGGAGAGGCTAT 781
Qy 636 LeuAsnPheMetGlyAsnGluLysLysLysLysLysLysLysLysLysLysLysLysLys 654
Db 782 CTCATTTTCTGGGGAGAGAAATTTGGGGGATCCCTGAATGGGTAGAGTTTCCCCAGGA 841
Qy 654 aGluGlnHisLeuSerAspGlySerValIlePro 665
Db 842 AAGGAAAAAATGGGAGAGTTCCCTTAATGCC 875
RESULT 13
BE602527 731 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
mRNA sequence.
ACCESSION BE602527
VERSION BE602527.2 GI:13190371
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 731)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9860088.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bq bases = 322
Seq primer: AATTAAACCTCCTACTAAAGGG

```

FEATURES
source

High quality sequence stop: 680.

Location/Qualifiers

1..731

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

/clone="HVSMEH0099J22F"

/lab_host="Hordeum vulgare 5-45 DAP spike EST library

HVCNNA0009 (5 to 45 DAP)"

/tissue_type="5-45 DAP Spike"

/lab_host="SOLR"

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi) in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)"

BASE COUNT 194 a 132 c 186 g 216 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 2.86e-110 Length: 731
Score: 1027.50 Matches: 194
Percent Similarity: 86.78% Conservative: 16
Best Local Similarity: 80.17% Mismatches: 32
Query Match: 23.01% Indels: 2
DB: 10 Gaps: 0

US-10-056-454A-15_COPY_49_882 (1-834) x BE602527 (1-731)

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Db 8 TTTTCATGGCGGCTCACGGGCCATCACTGGATGGGATTCCTGTTGTTCAACTACGGG 67
QY 432 AsnTyrGluValLeuArgTyrLeuLeuSerAsnAlaArgTyrTrpLeuAspAlaPheLys 451
Db 68 AATAAGGAAGTATAGGGTTCTACTTTCATGCCAGCATGGGGCTTGAGGAATATAAG 127
QY 452 PheAspGlyPheArgPheAspGlyValThrSerMetMetTyrTrleHisGlyLeuSer 471
Db 128 TTCATGGGTTCCATTTCGACGGGCCACCTTCATGATGTATACCCCAAGGATTACAA 187
QY 472 ValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspAlaVal 491
Db 188 GTACC-TTTCAGGAGC-TACCATGAATATTTGGCTTTCGCCAGGATGATGATGATGAT 245
QY 492 ValTyrLeuMetLeuValAsnAspLeuLeHisGlyLeuPheProAspAlaLeuThrle 511
Db 246 GTTACTTGATGCTGGTGAATGATCTAATTCACGGCTTATCTCTGAAGCCGTACTATT 305
QY 512 GlyGluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGly 531
Db 306 GGTGAGAGTGTAGTGAATGCTACATTTGCCCTTCCTGTTCAAGTGTGGGGTGGT 365

QY 532 PheAspTyrArgLeuHisMetAlaLeuAlaAspLysArgLleGluLeuLeuLysLysArg 551
Db 366 TTTGACTATCGTTACATATGCGGTGCGGTAATAATGATTCGAATTCCTCAAGGAAGC 425
QY 552 AspGluAspTyrArgValGlyAspLleValHisThrLeuThrAsnArgArgTyrSerGlu 571
Db 426 GATGAGAGTGGAGATGGTAAATATGTGSCACACTAACAAATAGAAGGTGGTGA 485
QY 572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrleAla 591
Db 486 AAGTGTGTTACTTACTTGCTGAAAGTCAATCAAGACACITGTTGGAGACAGACTATGCA 545
QY 592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThr 611
Db 546 TTTCTGGTGTATGACACAAAGATATGATGATTTTCATGGCTCTCAACGACCTTCGACAC 605
QY 612 LeuLeuAspArgGlyLleAlaLeuHisLysMetLleArgLeuValThrMetGlyLeuGly 631
Db 606 AATATGATCGCGGAATAGCAGCTGATAAATGATAGACTTATCACAATGGCTNTAGGA 665
QY 632 GlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTyrPheAspPhe 651
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QY 652 ProArg 653
Db 726 CCAAGA 731

RESULT 14
BU005876
LOCUS
DEFINITION
QGG9F08.yg.abl OG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGG9F08, mRNA sequence.
ACCESSION
BU005876
VERSION
BU005876.1 GI:22440271
KEYWORDS
EST.
SOURCE
Lactuca sativa.
Lactuca sativa.
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

REFERENCE
AUTHORS
1 (bases 1 to 717)
Kozik A., Michelmore, R.W., Knapp S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>

TITLE

JOURNAL
COMMENT
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
Belongs to contig QG_CA.Contig6851, see <http://cgpdb.ucdavis.edu/>
for details.

Plate: QGG9 row: F column: 08.

FEATURES

source

Location/Qualifiers
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/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGG9F08"
/clone_lib="OG_EFGHJ lettuce serriola"
/lab_host="E.coli"

/note="Vector: pBRCDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG LIB=QG_EFGH lettuce serriola
TAG TISSUE=germinating seeds
TAG_SEQ=TCGTGCGG

BASE COUNT 233 a 122 c 155 g 206 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 8 56e-106 Length: 717
Score: 989.50 Matches: 183
Percent Similarity: 82.56% Conservative: 30
Best Local Similarity: 70.93% Mismatches: 26
Query Match: 22.16% Indels: 20
DB: 14 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x BU005876 (1-717)

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Db 2 GAGGAAGTAGATTAGTTCTTCTTATTGATATTGATAA----- 40
QY 102 LysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArg 121
Db 41 -----GAAAGTAGAAGAAATAGAAATTA 64
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db 65 TCGATTCTCTCTCGTGAAGGAGAGAGATATGAAATGATGACCTTTTAAGCAAT 124
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 125 CATCGTGAACATCTTGATATAGATATACATACAAAGAGATACGTAAGCAATGAC 184
QY 162 LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 185 AATATGAAAGTGTGTTGGAGCGTTTTCACGTGTTATGAAATTAGTTTCACATCGA 244
QY 182 SerAlaThrGlyIleThrTyrArgGluTyrPalaLeuGlyAlaGlnSerAlaLeuIle 201
Db 245 AGCAAAACAGGTATCACTTATAGAGATGGCACCTGGGCAAGTCTGCTTCATTTAT 304
QY 202 GlyAspPheAsnAsnThrPalaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 305 GGAGATTCAACAACAGTATGAGATGCTGATGTTATGACCCGGAATGTTGGTGTG 364
QY 222 TrpGluIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 365 TGGGAGATCTTTTGGCAACAATGTTGATGATCTTCACTATTCCTCATGTTCTCGA 424
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db 425 GTAAGATTCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 485 TTTTCAGTACAGCAACCTGTTGAGATGATGATGATGATGATGATGATGATGATGAT 544
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db 545 GAGGAATAATACGTTTCAACATCCAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 604
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 605 GAGGCACATGTTGGGAATGAGTAGTACGGAACCAATGATGATGATGATGATGATGAT 664
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuIleMet 339
Db 665 GACGATGTTCTCCCTCGCATAAAGAA-CTCGGTTACATGATGATGATGATGATGAT 717

RESULT 15

AW065909 639 bp mRNA linear EST 30-MAR-2000
LOCUS 687002609.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
DEFINITION sequence.
ACCESSION AW065909
VERSION AW065909.1 GI:6020981
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 639)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 687002 row: G column: 09.
FEATURES
Location/Qualifiers
1..639
/organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
/tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site: 1: xhoI
; Site: 2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
BASE COUNT 200 a 118 c 151 g 170 t
ORIGIN
Alignment Scores:
Pred. No.: 2.76e-104 Length: 639
Score: 976.00 Matches: 174
Percent Similarity: 91.94% Conservative: 20
Best Local Similarity: 82.46% Mismatches: 17
Query Match: 21.86% Indels: 0
DB: 10 Gaps: 0
US-10-056-454A-15_COPY_49_882 (1-834) x AW065909 (1-639)
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Db 5 TTCTCCCGTAGTTAIGAGAAGTTTGATTTATCCGCGGAGAGGTATCATCATCGA 64
QY 190 GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnTrpAspAla 209
Db 65 GAATGGGCTCCCTGGAGCATTTTCTGCAGCATTTGGTGGTCACTCAACAACCTGGATCCA 124
QY 210 AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn 229
Db 125 AATGAGATCGGTATGAGCAAAATGAGTTGTGTGTTGGAAATTTTTCGCTTACCAT 184
QY 230 ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro 249
Db 185 GCAGATGGTACATCACCTATTCTCATGATCTCGTGTAAAGGTGAGATGATGATCTCA 244

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QY 250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
Db 245 TCAGGGATAAAGGATTCAATTCAGCCTGGATCAAGTACTCAGTCAGGCCCCAGAGAA 304
QY 270 IleProTyrAsnGlyIleHisTyrAspProGluGluArgTyrIlePheGlnHis 289
Db 305 ATACCATATGATGGGATTATATATCACTCTGGAAGAGTAAAGTATGTGTCAGGCAT 364
QY 290 ProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSer 309
Db 365 GCGCAACCTTAACACCAAAATCAATGCGGATATATGAACACACATGTCGGAATGAGTASC 424
QY 310 ProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLys 329
Db 425 CCGGAACCGAAGATAAACAACATATGTAACCTTTAGGGATGAAGTCCCTCCCAAGATAAAA 484
QY 330 LysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSer 349
Db 485 AAACCTGGATACAATGCGTGCAGTCAATAATGSCAATCCAAAGAGCACTCATATTATGGAAGC 544
QY 350 PheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGlyThrProAspAsp 369
Db 545 TTTGGATACCATGTAACTAATTTTTCGCCCAAGTAGTCGTTTGGTACCCCAAGAGAT 604
QY 370 LeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db 605 TTGAAGTCTTTGATTGATGAGACACATGAGCTT 637
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Search completed: July 6, 2003, 05:35:58
Job time : 2970 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:12:47 ; Search time 8049.92 Seconds
(without alignments)
11409.857 Million cell updates/sec

Title: US-10-056-454a-18_COPY_45_3200

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3154.2	99.9	3231	6	A58168	A58168 Sequence 18
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4	2847.4	90.2	3033	6	A58164	A58164 Sequence 14
5	2846.4	90.2	2992	8	STU011890	STU011890 Solanum t
6	2838	89.9	3003	6	A58162	A58162 Sequence 12
7	2733.2	86.6	2955	8	STU011885	STU011885 Solanum t
8	2707.6	85.8	2975	6	A58163	A58163 Sequence 13
9	2485.8	78.8	2563	6	AX256072	AX256072 Sequence
10	2474.4	78.4	2529	6	A58167	A58167 Sequence 17
11	2446.6	77.5	2523	8	STU011889	STU011889 Solanum t
12	2445	77.5	2578	6	A58169	A58169 Sequence 19
13	2436.6	77.2	2493	8	STISBE11	STISBE11 Solanum t
14	2431	77.0	2576	6	A58166	A58166 Sequence 16
15	1717.6	54.4	3123	8	AB071286	AB071286 Ipomoea b
16	1511.8	47.9	2517	8	AB042937	AB042937 Ipomoea b
17	1479.4	46.9	1481	8	STU011891	STU011891 Solanum t
18	1442.8	45.7	3090	6	A92164	A92164 Sequence 30
19	1429.8	45.3	3360	8	AB029548	AB029548 Phaseolus
20	1390.2	44.0	3549	8	PSBEIGEN	PSBEIGEN Phaseolus
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22	1372.2	43.5	1393	6	AR123356	AR123356 Sequence
23	1323	41.9	2542	8	ATU22428	ATU22428 Arabidopsis
24	1296	41.1	2577	6	AX412751	AX412751 Sequence
25	1296	41.1	2577	6	AX412752	AX412752 Sequence
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27	1275.6	40.4	3015	6	E14723	E14723 Rice mRNA f
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30	1272	40.3	2554	8	AF064560	AF064560 Hordeum v
31	1260.4	39.9	2918	6	RICBCE3	RICBCE3 Gene of sta
32	1260.4	39.9	2918	6	E08183	E08183 Gene of sta
33	1257.6	39.8	2726	8	AF338432	AF338432 Triticum
34	1257.6	39.8	2970	8	AF286319	AF286319 Triticum
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36	1255.8	39.8	2795	8	ZM065948	ZM065948 Triticum ae
37	1254.4	39.7	2853	8	TAU66376	TAU66376 Zea mays st
38	1200.4	38.0	2725	6	AR106495	AR106495 Sequence
39	1200.4	38.0	2725	8	M2EGLUCTRN	M2EGLUCTRN Corn starch
40	1171.4	37.1	2780	8	AF064561	AF064561 Hordeum v
41	796.8	25.2	833	8	STU011887	STU011887 Solanum t
42	788	25.0	844	8	STU011886	STU011886 Solanum t
43	663.8	21.0	770	6	AX256073	AX256073 Sequence
44	555	20.8	2732	8	AB029549	AB029549 Phaseolus
45	647.8	20.5	2843	8	MESBERNA	MESBERNA M.esculenta

ALIGNMENTS

RESULT 1
A58168
LOCUS A58168 3231 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 18 from Patent WO9634968.
ACCESSION A58168
VERSION A58168.1 GI:3713893
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 3231)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 18 07-NOV-1996;

Db	2025	GA	TGAGG	AT	GGAG	TGGG	TGAT	TGTT	CT	CAT	CACT	GA	CAAA	TAGA	GAAT	GGT	CGGA	2084
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Db	2085	AAG	TGTT	TT	CAT	ACGT	GAAG	TCAT	GAT	CA	AGCT	CT	TAG	TCGG	TGAT	AAAC	TATAGCA	2144
QY	2101	TT	CTGG	CT	GA	TGG	CAAG	ATAT	GTAT	GA	TTTT	TG	CTTT	TGG	TATAG	CGCT	CAACATCA	2160
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QY	2161	TT	AT	PAG	AT	CGT	GGAT	TAG	CAT	TCC	ACA	AG	TAT	GAT	TAG	CGT	TGAT	2220
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QY	2281	CT	PAG	GG	CT	GA	AA	CA	CT	CT	CT	CT	GA	TG	CT	CA	AT	2340
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QY	2581	CT	GA	GC	CT	GG	AA	AT	TAC	AG	GT	TG	CT	TT	GG	AC	T	2640
Db	2625	CT	GA	GC	CT	GG	AA	AT	TAC	AG	GT	TG	CT	TT	GG	AC	T	2684
QY	2641	GG	GAG	AT	TG	AT	TC	AT	TG	CC	GA	AT	TT	CA	CT	TT	GA	2700
Db	2685	GG	GAG	AT	TG	AT	TC	AT	TG	CC	GA	AT	TT	CA	CT	TT	GA	2744
QY	2701	CG	TT	CA	AT	TAT	GT	TAT	GC	AC	CT	TAG	CA	CAG	AG	TGG	T	2760
Db	2745	CG	TT	CA	AT	TAT	GT	TAT	GC	AC	CT	TAG	CA	CAG	AG	TGG	T	2804
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Db	2805	GA	GA	GA	GA	GA	GA	AT	TAG	CA	GT	PAG	TAG	GA	GA	GA	AT	2864
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QY	3001	TT	AT	TC	GA	AT	TC	TGG	AC	GG	CT	TAC	G	AG	TT	TG	CT	3060
Db	3045	TT	AT	TC	GA	AT	TC	TGG	AC	GG	CT	TAC	G	AG	TT	TG	CT	3104
QY	3061	CAT	CT	TT	T	AN	AT	GT	AC	AG	CC	CAC	T	AGA	AT	CA	AT	3120

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QY 3121 CATAAATGGGAATAGTGCTGAICTAATGAIGTTTTT 3156
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RESULT 2

ARI23355-
LOCUS ARI23355 3074 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169226.
ACCESSION ARI23355
VERSION ARI23355.1 GI:14108321
KEYWORDS jca jcaaccg3,ref
SOURCE Unknown.
ORGANISM Unknwn.
Unclassified.

REFERENCE Ek B., Khosnoodi J., Larsson C.-T., Larsson H. and Rask L. du te
AUTHORS Starch branching enzyme II of potato ✓
TITLE Location/Qualifiers
JOURNAL Patent: US 6169226-A 1 02-JAN-2001;
FEATURES 1. 3074
source /organism= "unknown"

BASE COUNT 902 a 558 c 712 g 896 t 6 others

Query Match 93.6%; Score 2955.2; DB 6; Length 3074;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3019; Conservative 2; Mismatches 41; Indels 14; Gaps 3;

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QY 63 AACTCAGCAATTTGACACTGAGTTAGTTCACACTCCTATCACTCATCAGAATCTATTTTT 122
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RESULT 3
LOCUS STU011888
DEFINITION Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE A-4.
ACCESSION AJ011888
VERSION AJ011888.1 GI:4584508
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2982)
Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2982)
Jobling,S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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QY	1005	GCCAAATATGTCGATGGTCTCTCTGCAATTCCTCATGSGTCCAGAGTGAAGATACCAT	1064	QY	2085	TGATAAAACATATGACTTCTGCTGATGCGCAAGGATATGATGATTTTATGGCTTTGGA	2144
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Solanum tuberosum
Solanum tuberosum
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1 (bases 1 to 2992)
Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M., Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2992)
Jobling,S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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REFERENCE 1 (bases 1 to 2578)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
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QY 1518 TTTAGATGACTGAACATGTTTACGGGACAGATGTTTACTTCTACTCTGGAGCTCG 1577
Db 1256 TTTAGATGACTGAACATGTTTACGGGACAGATGTTTACTTCTACTCTGGAGCTCG 1315
QY 1578 TGGTTATCAATGAGTGGGATTCGCGCTCTTTAACTATGGAACCTGGAGGTACTTAG 1637
Db 1316 TGGTTATCAATGAGTGGGATTCGCGCTCTTTAACTATGGAACCTGGAGGTACTTAG 1375
QY 1638 GTATCTTCTCAAAATGCGAGATGTTGGTGGATGATGTCACAAATTTGATTTAGATT 1697
Db 1376 GTATCTTCTCAAAATGCGAGATGTTGGTGGATGATGTCACAAATTTGATTTAGATT 1435
QY 1698 TGATGTTGACATCAATGATGATATCTCACACCGATTTACGTTGGGATTCACCTGGGA 1757
Db 1436 TGATGTTGACATCAATGATGATATCTCACACCGATTTACGTTGGGATTCACCTGGGA 1495

QY	328	GAAGAGCTCTTACGATCCGAATCCGACCTTCTACAGTTCAGCATCGGGGAAGTC	387		1081	AGCAGCGTTTGGAACTCCGACGACCTTAAAGTCTTTGATGTAAGCTCATGACCTA	1140
Db	1	GAAGAGCTCTTACGATCCGAATCCGACCTTCTACAGTTCAGCATCGGGGAAGTC	60		1468	GAATTCCTGTTCTCATGGACATGTTACAGCCATGCATCAATAATACATTTAGATGGA	1527
QY	388	CTTGTTACCTGGAAATCCAGAGTATAGTCTCTCATCTCAACAGACCAATTTAGTTCACCT	447		1141	GAATTCCTGTTCTCATGGACATGTTACAGCCATGCATCAATAATACATTTAGATGGA	1200
Db	61	CTTGTTACCTGGAAATCCAGAGTATAGTCTCTCATCTCAACAGACCAATTTAGTTCACCT	120		1528	CTGAACATGTTTGGCGGCACAGATAGTGTTCACCTCTGAGAGCTGCTGGTGTATCAT	1587
QY	448	GAGACAGCTCCAGAAATCCCGACGATCAACTGATGTGATGTCACAAATGGAACAC	507		1201	CTGAACATGTTTGGCGGCACAGATAGTGTTCACCTCTGAGAGCTGCTGGTGTATCAT	1260
Db	121	GAGACATCTCCAGAAATCCCGACGATCAACTGATGTGATGTCACAAATGGAACAC	180		1588	TGGAATGGGATCCCGCTCTTTAACTATGGAACCTGGGAGTACTAGTATCTCTC	1647
QY	508	GCTAGCCAGATTTAAACCTGAGAGTATGAGTGTGAGCGCTCAAGTATCTTACAGGAAT	567		1261	TGGATGGGATCCCGCTCTTTAACTATGGAACCTGGGAGTACTAGTATCTCTC	1320
Db	181	GCTAGCCAGATTTAAACCTGAGAGTATGAGTGTGAGCGCTCAAGTATCTTACAGGAAT	240		1648	TCAATGGGAGATGGTGGTGGATGAGTCAAAATTTGTTGATTTAGATTTGATGGTGTG	1707
QY	568	GTGGAAGATGGATTTGCTTCATCACTACAACCTACAAGAGTGTGTAACCTGAGGAG	627		1321	TCAATGGGAGATGGTGGTGGATGAGTCAAAATTTGTTGATTTAGATTTGATGGTGTG	1380
Db	241	GTGGAAGATGGATTTGCTTCATCACTACAACCTACAAGAGTGTGTAACCTGAGGAG	300		1708	ACATCAATGATTTACTCACCGGATTTACGGTGGGATTCACCTGGGAACTACAGGAA	1767
QY	628	TCTAAACATTAATCTCTGAGAGACAAATTAATGATGAATCTGATAGGATCAGAG	687		1381	ACATCAATGATTTACTCACCGGATTTACGGTGGGATTCACCTGGGAACTACAGGAA	1440
Db	301	TCTAAACATTAATCTCTGAGAGACAAATTAATGATGAATCTGATAGGATCAGAG	360		1768	TACTTGGACTCGCAACTGATGTGATGCTCGGTGATCTGATGCTGCGCAACGATCTT	1827
QY	688	AGGGCATCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTTTGACA	747		1441	TACTTGGACTCGCAACTGATGTGATGCTCGGTGATCTGATGCTGCGCAACGATCTT	1500
Db	361	AGGGCATCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTTTGACA	420		1828	ATCATGGCTTTTCCAGATGCAATTACCAATGCTGAGATGTTAGCGGAATCCGACA	1887
QY	748	AACATGCTCAACACCTTGATTTACAGTATTCACAGTACAAGAAATGAGGAGCAAT	807		1501	ATTCAGGCTTTTCCAGATGCAATTACCAATGCTGAGATGTTAGCGGAATCCGACA	1560
Db	421	AACATGCTCAACACCTTGATTTACAGTATTCACAGTACAAGAAATGAGGAGCAAT	480		1888	TTTTGATTTCCGTTTCAAGATGGGGTGTGGCTTGACTATCGCTGCATATGGCAAT	1947
QY	808	GACAGATGAGGTTGGTGGAGCTTTTCTCGTGTATGAAATGAGTTCACCT	867		1561	TTTTGATTTCCGTTTCAAGATGGGGTGTGGCTTGACTATCGCTGCATATGGCAAT	1620
Db	481	GACAGATGAGGTTGGTGGAGCTTTTCTCGTGTATGAAATGAGTTCACCT	540		1948	GCTGATAATGATTTGATGTTGCTCAAGAAACGGGATGAGATTTGAGAGTGGTGTAT	2007
QY	868	CGTAGTGTACAGTATCACCTTACCGTGGTGGGCTCCTGGTGGCCAGTCACTGCTC	927		1621	GCTGATAATGATTTGATGTTGCTCAAGAAACGGGATGAGATTTGAGAGTGGTGTAT	1680
Db	541	CGTAGTGTACAGTATCACCTTACCGTGGTGGGCTCCTGGTGGCCAGTCACTGCTC	600		2008	GTTCATACACTCACAAATAGAAGTGGTCCGAAAAAGTGTGTTTACCTACCTGAAAGT	2067
QY	928	ATTGAGATTTCAACAAATGGGACGCAAAATGCTGACATTTATGACTCGGAATTTGGT	987		1681	GTTCATACACTCACAAATAGAAGTGGTCCGAAAAAGTGTGTTTACCTACCTGAAAGT	1740
Db	601	ATTGAGATTTCAACAAATGGGACGCAAAATGCTGACATTTATGACTCGGAATTTGGT	660		2068	GATCAAGCTCTAGTGGTGTATTAACATATAGCAATTTGCTGCTGATGACAGGATAT	2127
QY	988	GTCGGGAGATTTTCTGCCAAATATGTTGATGTTCTCTGCAATTCCTCATGGTCC	1047		1741	GATCAAGCTCTAGTGGTGTATTAACATATAGCAATTTGCTGCTGATGACAGGATAT	1800
Db	661	GTCGGGAGATTTTCTGCCAAATATGTTGATGTTCTCTGCAATTCCTCATGGTCC	720		2128	GATTTTATGGCTTTGGATAGACCGCTCAACATCATTTAATAGATCGTGGGATAGC	2187
QY	1048	AGAGTGAAGATACGATGACACTTTCATCAGTGTAAAGATTCCTGCTGGATC	1107		1801	GATTTTATGGCTTTGGATAGACCGCTCAACATCATTTAATAGATCGTGGGATAGC	1860
Db	721	AGAGTGAAGATACGATGACACTTTCATCAGTGTAAAGATTCCTGCTGGATC	780		2188	AAGATGATTTAGGCTTTAATAGGATTTAGGAGGACAGGGTACCTAATTTTCATGGGA	2247
QY	1108	AACTACTCTTTACAGCTTCTGATGAATTCATATATAGGAATATATATCATCCACC	1167		1861	AAGATGATTTAGGCTTTAATAGGATTTAGGAGGACAGGGTACCTAATTTTCATGGGA	1920
Db	781	AACTACTCTTTACAGCTTCTGATGAATTCATATATAGGAATATATATCATCCACC	840		2248	AATGAATTCGGCCACCTGAGTGGATTTGATTTCCCTGAGGCTCAACAAACCTCTGAT	2307
QY	1168	GAGAGGAGATGATGTTCTCCAAACACCCCGCCAAAGAAACCAAGTGGTGAATA	1227		1921	AATGAATTCGGCCACCTGAGTGGATTTGATTTCCCTGAGGCTCAACAAACCTCTGAT	1980
Db	841	GAGAGGAGATGATGTTCTCCAAACACCCCGCCAAAGAAACCAAGTGGTGAATA	900		2308	GGCTCAGTAATTCGGGAAACCAATTCAGTATGATTAATAGATGAGAGATTTGACCTG	2367
QY	1228	TATGAATCTCATATTTGGAATGATAGTCCGAGCCCTAAAATTAACATACAGGAATTT	1287		1981	GGCTCAGTAATTCGGGAAACCAATTCAGTATGATTAATAGATGAGAGATTTGACCTG	2040
Db	901	TATGAATCTCATATTTGGAATGATAGTCCGAGCCCTAAAATTAACATACAGGAATTT	960		2368	GGAGATGCAGAAATTTAGATACCGTGGTTCGCAAGAAATTTGACCGGCTATGAGTAT	2427
QY	1288	AGAGATGAAGTCTTCTCGCATAAAAACCTTGGTACAAATCGGTGCAAAATTTGGCT	1347		2041	GGAGATGCAGAAATTTAGATACCGTGGTTCGCAAGAAATTTGACCGGCTATGAGTAT	2100
Db	961	AGAGATGAAGTCTTCTCGCATAAAAACCTTGGTACAAATCGGTGCAAAATTTGGCT	1020		2428	CTTCAAGATAAATAGTATGACTTCAGAACACCACTTCATATCAGAAAGATGAA	2487
QY	1348	ATTCAAGACATCTTATTTATGCTAGTTTGGTTATCATGCTCAAAATTTTTCACCA	1407		2101	CTTCAAGATAAATAGTATGACTTCAGAACACCACTTCATATCAGAAAGATGAA	2160
Db	1021	ATTCAAGACATCTTATTTATGCTAGTTTGGTTATCATGCTCAAAATTTTTCACCA	1080		2488	GGAGATGAGTATGATTTGATTTGAAAAAGAAACCTAGTTTTGTCTTAATTTTCACCTG	2547
QY	1408	AGCAGCCGTTTGGAAACGCCGACGACCTTAAAGTCTTTGATGATAAGCTCATGACCTA	1467				

[illegible]

QY		261	TGATCGAGGAATCTAATAATTTCCTGTATTCTTGTAAGAAGCAGTCC---TCTTTACGGAA	317
Db		189	TGATCGCGCAATACCNAATCCCCTCTCTCTCTGTGAAAAGAAATTCGTTTTCTTCATGGA	248
QY		318	GATCTTGGCHGAAGAATCTTCTTTACGATTCCGAATCCGACCTTCCTACAGTTGCAGCATC	377
Db		249	GATCTTTTGGCAGAAATACTTCCTTATGAATCCGAACCTCTCTCTTTTAGAGTTGCAGCATC	308
QY		378	GGGGAAGTCTTGTATACCTGGAATCCAGAGTGATAGTCTCTCATCTCACAGACAATAAT	437
Db		309	AGNAGAAGTCTTTGGCTTGGTGGCGAGGGCAGGGAICATCGTTTCCAATCATCAGTT	368
QY		438	TGAGTTCACTGAGACAGCTCCGAAAAATFCCCCAGCATCAACATGATGTGGATAGTTCAAC	497
Db		369	AGAGGTTGCTGAGGCCATTATCAGACATACCCAAAGTATCGGTGACGTGGATTAATGTGAA	428
QY		498	AATGGAACAGCTAGCCAGATTAAAACITGAGAACGATGACGTTGAGCCCTCAAGTGATCI	557
Db		429	GATGGAAGAGAACAGCAACAGTGAAGCAATGTGGATTTCGTCAAAGTAGCAAGTGAATC	488
QY		558	JTACGAGAAGTGTGAAGAGTTCGATTTGCTTCATCCTACAACTPACAAGTGGTGTAA	617
Db		489	TAAAGAACGTTTCAAGCAGGATACACAGCTCTTCTACTTCAAATTTGAAGAATGTGTA	548
QY		618	ACTGGAGGAGTCTAAAACATTAATTAACITCTGAGAGACAATATTGATGAATCTGATAG	677
Db		549	TCTGCAAGTTTCACAAAAACACAGACACTTTGATGA---CATCAGTGCCTGAATCTGAAT	605
QY		678	GATCASAGAGGGGCGATCCCTCCACCTGGACTTTGGTCAGAGATTTATGAATAGACCC	737
Db		606	GGTGAAGAAGAGGGCCATTCCTCCACCTGGACTTTGGTCAGAGGATCATGAGATAGACCC	665
QY		738	CCTTTTGAACAACTATCGTCAACACCTTGATTCACAGTATTCACAGTACAGAAATAGAG	797
Db		666	TCCTCTGGAANAATTTCTGACACATCTTGATATAGGTTTTCCGACATATAGSAAATCCG	725
QY		798	GGAGCAATTCACAGTAAGSGGTGGTTTGGAAAGCTTTTCTCGTGGTATGAAAAAT	857
Db		726	GGAAGCAATTAACCAAGTATGAGGTGGCTTGGAAAGTATCTCTCGTGGCTATGAGAAAT	785
QY		858	GGGTTTCACTCGTAGTCTACAGTNATCACTTACCCTGAGTGGGCTCTCTGGTCCCACTC	917
Db		786	AGGTTTCACTCGGAGTGTACAGTATCACCATTCGGGAGTGGGCTCTCGAGCCACGTG	845
QY		918	AGCTGCTCTCATTTGGAGATTTTCAAACATTTGGAGCGAAATGCTGACATTTATGACTCGAA	977
Db		846	GGCAACACTCATTTGGAGATTTCAACAATTTGSANATCCAAATGCTGATTTATGACTCGAA	905
QY		978	TGANTTTGGTCTGGGAGATTTTCTGCAAAATTAATGTGAGTGGTCTCTCTGCAATTC	1037
Db		906	TGANTTTGGTGTGGGAGATCTTTTGGCAAAACATGAGATGGCTCACCTCGCAATTC	965
QY		1038	TCATGGGTCCAGAGTGAAGATACGATGGACACTTCATCAGGTGTTAAGGATTPCCATTC	1097
Db		966	ACATGGCTCTAGAGTGAAGATAGTATGAGACACTCTCTTCAGGCAATTAAGACTCTATTC	1025
QY		1098	TGCTTGGATCAACTACTCTTTACAGCTTCTGATGAAATTCOAATTAATGGAATATATTA	1157
Db		1026	CGCTTGGATCAATTTCTCTGACAAAGCTCTGTTGCAATTTCTTTATGATGGAATATATA	1085
QY		1158	TGATCCACCGAAGAGGAGGTATGTTCTTCCAAACACCAGGCCAAAGAAACCAAGTTC	1217
Db		1086	TGATCTTCCAGAAGAGGAGGTACAAAATTCACATCCACGGCCAAAAGACCAAGTTC	1145
QY		1218	GCTGAGAATATATGAATCTCATATTCGAATGGAATAGTCTCGGAGCCATAAATTAACATCA	1277
Db		1146	ACTGAGAAATATGAATGTCAATTTGAATGAGTAGTCTCGGAGCCATAAATAAATACATA	1205
QY		1278	CGTGAATTTTAGAGATGAAGTTCTTCTCGCATAAAAACCTTGGTACAAATGCGGTGCA	1337
Db		1206	TGCAGAGTTTAGAGATGATGTACTTCCTCGATTAAGAAGCTTGGCTACATGCTCTCCA	1265

QY	1338	AAATTATGGCTATTCAAGAGCATCTTTATTATGCTAGTTTGGTATCATGTCACAAATTT	1397
Db	1266	GATAATGGCCATTCAGAGCAATCTTAATATGCTAGTTTGGCTATCATGTTACGAATTT	1325
QY	1398	TTTTGCAACAAGAGCCGTTTTGGAAAGCCGACGACCTTAAGTCTTTGATTGATAAAGC	1457
Db	1326	CTTTGCACCAAGACAGTCGTTTTGGGACTCCAGATGATCTTAATCTTTGATTGATAGGC	1385
QY	1458	TCATCAGCTAGCAATTGTTGTTCTCATGACAICTGTTACAGCCATGCAATCAATAATAC	1517
Db	1386	CCATGAACCTTGGACGGTTGTTCTTAATGGAATATTGTGCACAGTCATPGCGTCAATAATAC	1445
QY	1518	TTTAGATGGACTGAACATGTTTGCAGGCACAGATAGTTCTACTTTCACTCTTGGAGCTCG	1577
Db	1446	TTTGATGGACTGAACATGTTTGATGCTACAGATAGTTGTTTATTTCCACTCTTGGAAACCG	1505
QY	1578	TGGTTATCATTTGGATGGGATPCCGGCTCTTTAACTATGAAACTGGGAGGTACTTAA	1637
Db	1506	GGGTATCATTTGGATGGGATTCCTCTCTTCAACTATGAAACTGGGAAGTACTGAG	1565
QY	1638	GTATCTTCTTCAAAATGCGAGATGGTGGTGGATGAGTGCAAAATTTGRTGGATTTAGATT	1697
Db	1566	GTATCTGGCTCAAAACGCAAGATGGTGGTGGATGAGTACAAGTTTGTATGGCTTCAGATT	1625
QY	1698	TGATGGGTGACATCAATGATGTATFATCAACACGAGTATTCGGTGGGATTCACHTGGNA	1757
Db	1626	TGATGGGTGACTTCAATGATGTATFATCAATCATGGTGTGATGTAGGAATTCACHTGGNA	1685
QY	1758	CTACAGGAATACHTTTGGACHTCGCAACTGATGTGTGATCTGCGCTGTATCTGATGCTGSC	1817
Db	1686	CTACAGTGAATATTTTGGGTATGCAACCGATGTTGATGCTGTGGTGTATCTGATGCTCGT	1745
QY	1818	CAACGATCTTATTCATGGGCTTTTCCAGATGCAATACCAATGCTGTGAAGATGTTAGCGG	1877
Db	1746	CAATGATCTCATTCATGCTCTCTTCCCTGAAGCCATAACCAATGGTGAAGATGTTAGTGG	1805
QY	1878	AAATGCCACATTTTGTATTCCTGTTCAAGATGGGGTGTGTGGCTTTGACTATCGGCTGCA	1937
Db	1806	CATGCCAACATTTTGTATTCCTGTCAGAGATGGAGCGTAGTGTTTGACTATCGGCTTCA	1865
QY	1938	TATGGCAATTCGTGATAAAGTATGAGTTCTCTCAAGAACCGGATGAGGATTTGGAGAGT	1997
Db	1866	TATGGCAATTCCTGATAAATGGAATGAGATTCTCAAGAGAGAGATGAGGATTTGGCAAT	1925
QY	1998	GGGTGATATTGTTTCATACACTGACAAATAGAAGATGTCGGAAGAGTGTGTTTCATACGC	2057
Db	1926	GGGTGAATTTGTTTCACACATTTACTTAACAGAAGATGCTCGGAANAATGTGTTCTTATGC	1985
QY	2058	TGAACCTCATGATCAAGCTCTAGTCGGTGATATAAACHATAGCAATTCGTGGCTGATGGCAA	2117
Db	1986	TGAACCTCAGGACCAAGCTCTTGTGGTGATAAAACTATAAGCGTCTGTGTTGATGGCAA	2045
QY	2118	GGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGAT	2177
Db	2046	GGACATGTATGACTTCATGGCTCTGATAGACCAACCGCCAGTAAATAGACCGTGGGAT	2105
QY	2178	AGCATTCACAGATGATTAGGCTTTAATCATATGGGATTAGGAGGAGAAGGGTACCTAAA	2237
Db	2106	AGCATTCATAAAATGATCAGACTTATAACTATGGGATTAGGAGGAGAGGATATCTAAA	2165
QY	2238	TTTCATGGGAATGATTCGGCCACCTCAGTGGATTTGATTTCCCTAGGGCTGAACAACA	2297
Db	2166	TTTCATGGGAACGAATTTGGTCACCCAGATGGATTTGATTTCCCTAGAGGTGAACAACG	2225
QY	2298	CTCTCTGATGGCTCAGTAATTTCCCGGAACCAATTCAGTTATGATAAATGACAGCGAG	2357
Db	2226	CTTCTCTGATGTTTCAGTTCCTCTCCCTGGAAACAATTTTCAGTATGATAAATGCGTGTAG	2285
QY	2358	ATTTCACCTGGGAGATGCAGAAATTTTAAGATACCGTGGTTCGAAGAATTTTCACCGGCG	2417
Db	2286	ATTTGATCTGGGTGATGCAGATTTATCTAAGATATCGGGCATTCGAAGAATTTTGACCAACG	2345
QY	2418	TAAGCAGTATCTGAAGATAAATAGGTTTAAGCTTCAAGAACACCGATTCTATATCAGG	2477

Mon Jul 7 12:40:58 2003

		TATGATCACCTTGAGAGAAATPACGGCTTCATCGGCCAAACACCAGTACATATACAG	2346	Dd
		AAAGGTGAAGGAGATAGGATGATTGTATTTGAAAAAGAAACCTVAGTTTTTGTCTTTAA	2478	Qy
		CCAGCAGCAAGGAGATAGGGTGATCATTTTGAAGGGGTGCCTGGTGTGTCTTCAA	2406	Dd
		TTTTCACGCGAACAACCTAITCAGACTATCGCATAGCTGGCTGAAGCCTGGAAAATA	2538	Qy
		TTTCACCTGGACAAATGTTATTCCAGATTACCGTGTAGCTGCTTAAGCCAGAGAAATA	2466	Dd
		CAAGGTGTCCTGGACTCAGATGATPCCACTTTTGGTGGCTTCGGGAGAATTGATCAATA	2598	Qy
		TAAGGTAGCCCTGGACTCCGACAGTCCGCTGTTTGGAGGCTTTGGCAGAGTTCAACCCGA	2526	Dd
		TGCCGAATGTTTACCTTTGAAGGATGGTATGATGATCGTCTCGTTCAAATTATGGTGTA	2658	Qy
		TGCAGAAATTTTCATATCGAAGGGTATCACAGATGTCCTCGTTCCTTCATUGGTGTA	2586	Dd
		TGCACCTAGTAGAACAGCAGTGGTCTATGCACCTAGTAGACAAGAGAGAGAGAGA	2718	Qy
		GCCACCCAGTAGAATCGCAGTGGTGTACGCTCTAGCGAAGGAGGAGGACGAACAAAAC	2646	Dd
		AGTAGCAGTAGTAG	2778	Qy
		AGTTGAGGAATGAG	2706	Dd

Search completed: July 5, 2003, 17:59:02
Job time : 8073.92 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 12:28:17 ; Search time 657.636 Seconds

(without alignments)
10807.357 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200

Perfect score: 3156

Sequence: 1 AAAAACCTCCCTCCACTAGT.....TGCATGCTAATGATGTTT 3156

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3154.2	99.9	3231	17	AAT42632
2	2958.4	93.7	3074	18	AAT69587
3	2847.4	90.2	3033	17	AAT42630
4	2838	89.9	3003	17	AAT42634
5	2706	85.7	2975	17	AAT42635
6	2485.8	78.8	2563	23	ABK50301
7	2474	78.4	2531	17	AAT17267
8	2471.2	78.3	2529	17	AAT42637
9	2445	77.5	2578	17	AAT42631

Class A starch bra					
Potato starch bran					
Class A starch bra					
Class A starch bra					
Class A starch bra					
Potato cDNA encodi					
Class A starch bra					
Class A starch bra					
Class A starch bra					

10	2427.8	76.9	2576	17	AAT42636
11	1442.8	45.7	3090	19	AAV38720
12	1377.8	43.7	2913	19	AAV38719
13	1296	41.1	2715	21	AAC45939
14	1275.6	40.4	3015	19	AAV05639
15	1260.4	39.9	2919	15	AAQ73750
16	1257.6	39.8	2726	22	AAH78337
17	1203.6	38.1	2640	19	AAV70961
18	1200.4	38.0	2665	18	AAV69729
19	1200.4	38.0	2725	19	AAV29757
20	1185.6	37.6	3039	24	ABK15494
21	1182.4	37.5	2968	22	AAH78342
22	1059.8	33.6	2307	21	AAZ99938
23	1049.8	33.3	2087	18	AAV69737
24	1048.2	33.2	2165	18	AAV69736
25	963.2	30.5	1919	19	AAV38722
26	730	23.1	1452	21	AAK36957
27	663.8	21.0	770	23	ABK50302
28	642.8	20.4	4563	22	AAF30910
29	637.4	20.2	3128	16	AAV00774
30	632.4	20.0	2487	18	AAV69747
31	632.4	20.0	2565	18	AAV69752
32	632.4	20.0	2763	19	AAV29758
33	632.4	20.0	2771	13	AAQ24257
34	632.4	20.0	2772	18	AAV69740
35	623.2	19.7	2909	13	AAQ27778
36	618.8	19.6	2687	20	AAK34646
37	611.8	19.4	2733	15	AAQ54674
38	611.8	19.4	2733	15	AAQ62135
39	598.2	19.0	3075	24	AAK54880
40	596.6	18.9	2899	22	AAH02926
41	596.6	18.9	2955	24	ABN95650
42	593	18.8	2713	19	AAV70962
43	585.2	18.5	728	23	ABK50303
44	546	17.3	1809	18	AAV69753
45	546	17.3	1865	18	AAV69748

ALIGNMENTS

RESULT 1
AAT42632
ID AAT42632 standard; DNA; 3231 BP.
XX
AC AAT42632;
XX
XX 25-FEB-1997 (first entry)
DT
XX Class A starch branching enzyme (psbe2con.seq).
DE
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
XX Solanum tuberosum.
OS
XX
XX
FH Key Location/Qualifiers
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FT FT /*tag= c

WO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Db 1845 GTGATATGATGCTGGCCACGATCTTATTCATGGGCTTTTCCAGATGCAATTAACCAAT 1904
 QY 1861 GGTGAAGATGTTAGCGGAATCCGACATTTGTTATTCGGTTCAGAGATGGGGTGTGGC 1920
 Db 1905 GGTGAAGATGTTAGCGGAATCCGACATTTGTTATTCGGTTCAGAGATGGGGTGTGGC 1964
 QY 1921 TTTGACTATCGCTGCATATGCGCAATTCGCTGATAAATGATGATGCTCAAGAAACGG 1980
 Db 1965 TTTGACTATCGCTGCATATGCGCAATTCGCTGATAAATGATGATGCTCAAGAAACGG 2024
 QY 1981 GATGAGGATTTGGAGATGGGTGATATGTTTCATACACACGCAATAGAGATGTCGAA 2040
 Db 2025 GATGAGATTTGGAGATGGGTGATATGTTTCATACACACGCAATAGAGATGTCGAA 2084
 QY 2041 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACAATAGCA 2100
 Db 2085 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACAATAGCA 2144
 QY 2101 TTTCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGATAGACCGTCAACATCA 2160
 Db 2145 TTTCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGATAGACCGTCAACATCA 2204
 QY 2161 TTAATAGATGCTGGATAGCATTCACAAAGATGATTTAGGCTTTAACTATGGGATAGGA 2220
 Db 2205 TTAATAGATGCTGGATAGCATTCACAAAGATGATTTAGGCTTTAACTATGGGATAGGA 2264
 QY 2221 GGGAGGGTACCTTAATTTTCATGGAAATGAATTCGGCCACCCCTGAGTGATGATTC 2280
 Db 2265 GGGAGGGTACCTTAATTTTCATGGAAATGAATTCGGCCACCCCTGAGTGATGATTC 2324
 QY 2281 CCTAGGGCTCAACAACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTAT 2340
 Db 2325 CCTAGGGCTCAACAACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTAT 2384
 QY 2341 GATAAATGACAGCGAGATTTGACCTGGGAGATGCGCAATATTAAGATACCGTGGTTG 2400
 Db 2385 GATAAATGACAGCGAGATTTGACCTGGGAGATGCGCAATATTAAGATACCGTGGTTG 2444
 QY 2401 CAAGAATTTGACCGGCTATGCGATATCTTGAAGATAAATATGATGATGATGATGATGAT 2460
 Db 2445 CAAGAATTTGACCGGCTATGCGATATCTTGAAGATAAATATGATGATGATGATGATGAT 2504
 QY 2461 CACCACTTCATACAGAAAGATGAGGATAGGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2505 CACCACTTCATACAGAAAGATGAGGATAGGATGATGATGATGATGATGATGATGATGATGAT 2564
 QY 2521 CTAGTTTTTGTCTTTAATTTTCACTGGCAAAAGCTATTCAGACTATCGCATAGGCTGG 2580
 Db 2565 CTAGTTTTTGTCTTTAATTTTCACTGGCAAAAGCTATTCAGACTATCGCATAGGCTGG 2624
 QY 2581 CTGAAGCCCTGGAAATACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTTC 2640
 Db 2625 CTGAAGCCCTGGAAATACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTTC 2684
 QY 2641 GGGAGATTTGATCAATATCCCAATGTTTCACCTTTGAAGGATGATGATGATGATGATGATGAT 2700
 Db 2685 GGGAGATTTGATCAATATCCCAATGTTTCACCTTTGAAGGATGATGATGATGATGATGATGAT 2744
 QY 2701 GGTTCAAATATGTTGATGACCTAGTAGAAGCAGAGTGGTCTATGCCACTAGTAGACAA 2760
 Db 2745 GGTTCAAATATGTTGATGACCTAGTAGAAGCAGAGTGGTCTATGCCACTAGTAGACAA 2804
 QY 2761 GAAGAAGAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2820
 Db 2805 GAAGAAGAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2864
 QY 2821 AACTTGTGATCGCTTGAAGATTTGAAGCTTACATAGAGCTTCTTGAGCTATCGGCA 2880
 Db 2865 AACTTGTGATCGCTTGAAGATTTGAAGCTTACATAGAGCTTCTTGAGCTATCGGCA 2924
 QY 2881 TATTGCACTAGCTTCTGGCGGAATTTTCATGTCGCAAAAGGTTTGCAATCTTCTCCACTATT 2940
 Db 2925 TATTGCACTAGCTTCTGGCGGAATTTTCATGTCGCAAAAGGTTTGCAATCTTCTCCACTATT 2984

QY 2941 AGTAGTGCAACCATATACGAGATGAAGTGTGCAACAAACATATGTAATTCGATGA 3000
 Db 2985 AGTAGTGCAACCATATACGAGATGAAGTGTGCAACAAACATATGTAATTCGATGA 3044
 QY 3001 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTGGTTAGTGTGATGATGATGATGAT 3060
 Db 3045 TTTATGTCGAATGCTGGGACGGGCTTCAGCAGGTTTGGTTAGTGTGATGATGATGATGAT 3104
 QY 3061 CATCTCTTANATGATACAGCCACACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3120
 Db 3105 CATCTCTTANATGATACAGCCACACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3164
 QY 3121 CATAAATGGAATAGTGTGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGAT 3156
 Db 3165 CATAAATGGAATAGTGTGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGAT 3200

RESULT 2

AAT69587
 ID AAT69587 standard; cDNA; 3074 BP.
 XX
 AC AAT69587;
 XX
 DT 26-AUG-1997 (first entry)
 XX
 DE Potato starch branching enzyme II gene (beII).
 XX
 KW starch branching enzyme II; beII gene; potato; transgenic plant;
 KW amylopectin; amylose; starch; ss.
 XX
 OS Solanum tuberosum.

Key Location/Qualifiers

CDS 189..2825

FT sig_peptide 189..332

FT mat_peptide 333..2822

FT /*tag= c

XX WO9720040-A1.

XX 05-JUN-1997.

XX 28-NOV-1996; 96WO-SE01558.

XX 19-APR-1996; 96SE-0001506.

XX 29-NOV-1995; 95SE-0004272.

XX (EKBB/) EK B.

XX (KHOS/) KHOSNOODI J.

XX (LARS/) LARSSON C.

XX (LARS/) LARSSON H.

XX (RASK/) RASK L.

XX (AMYL-) AMYLOGENE HB.

XX Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;

XX WPI; 1997-310596/28.

XX P-PSDB; AAM19113.

XX Isolated potato starch branching enzyme II - useful for altering

XX degree of amylopectin branching and amylopectin/amylose ratio in

XX potato starch

XX Claim 4; Page 12-15; 24pp; English.

XX A cDNA clone (AAT69587) codes for potato starch branching enzyme II

XX (BEII) (AAM19113). It was isolated from potato tuber cDNA by PCR

XX amplification using primers (AAT69588-89) based on tryptic peptides

XX of isolated BEII; the 5' and 3' ends of the sequence were detd. by

XX RACE. A vector comprising the whole or a functional active part of

Db 1979 GAAACGGGATGAGGATGGGATGATATCTTCATACACTGACAAATAGAGATG 2038
QY 2034 GTCGGAAGAGTGTGTTTCATACGCTCAAGCTCATGATCAAGCTAGTCGGTCAATAAC 2093
Db 2039 GTCGGAAGAGTGTGTTTCATACGCTCAAGCTCATGATCAAGCTAGTCGGTCAATAAC 2098
QY 2094 TATAGCATTCGGCTGATGGCAAGATATGATGATTTATGGCTTGATAGACCGTC 2153
Db 2099 TATAGCATTCGGCTGATGGCAAGATATGATGATTTATGGCTTGATAGACCGTC 2158
QY 2154 AACATCATTAATAGATCTGGATAGCATTCACAGATGATAGCTTGTAACTATGGG 2213
Db 2159 AACATCATTAATAGATCTGGATAGCATTCACAGATGATAGCTTGTAACTATGGG 2218
QY 2214 ATTAGGAGGAAAGGTACCTAAATTTTCATGGGAATGAATTCGGCCACCTGAGTGAT 2273
Db 2219 ATTAGGAGGAAAGGTACCTAAATTTTCATGGGAATGAATTCGGCCACCTGAGTGAT 2278
QY 2274 TGATTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAAATTCGGGAACCAAT 2333
Db 2279 TGATTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAAATTCGGGAACCAAT 2338
QY 2334 CAGTTATGATAAATGCACAGCGAGATTTGACCTGGGAGATGCAGAAATTTAAAGTACCG 2393
Db 2339 CAGTTATGATAAATGCACAGCGAGATTTGACCTGGGAGATGCAGAAATTTAAAGTACCG 2398
QY 2394 TGGGTTGGAAGAAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATGAGTTATGAC 2453
Db 2399 TGGGTTGGAAGAAATTTGACCGGGCTATGCAGTATCTTGAAGATAAATGAGTTATGAC 2458
QY 2454 TTCAGAACCCAGTTTCATATACCAAGAGATGAAGGATAGGATGATTTGATGAAA 2513
Db 2459 TTCAGAACCCAGTTTCATATACCAAGAGATGAAGGATAGGATGATTTGATGAAA 2518
QY 2514 AGGAAACCTAGTTTTCCTTTTAAATTTTCACTGACAAAGATGATTCAGACTATCGAT 2573
Db 2519 AGGAAACCTAGTTTTCCTTTTAAATTTTCACTGACAAAGATGATTCAGACTATCGAT 2578
QY 2574 AGGCTGCTGAGCCTGGAAATACAAAGTTTGCCTTGGACTCAGATGATCCACTTTTGG 2633
Db 2579 AGGCTGCTGAGCCTGGAAATACAAAGTTTGCCTTGGACTCAGATGATCCACTTTTGG 2638
QY 2634 TGCTTCGGGAGATTCATATATGCCGAATTTTCACTTGAAGGATGGTATGATGA 2693
Db 2639 TGCTTCGGGAGATTCATATATGCCGAATTTTCACTTGAAGGATGGTATGATGA 2698
QY 2694 TCCTCTCGTTCAATTAATGATGATGACCTAGTAGACAGCAGTGTCTATGCACTAGT 2753
Db 2699 TCCTCTCGTTCAATTAATGATGATGACCTAGTAGACAGCAGTGTCTATGCACTAGT 2758
QY 2754 AGACA---AGAGAAGAGAAGAGATGAGTAGTAGAGAAGATGATAGTAGAAGA 2810
Db 2759 AGACAAGAGAAGAGAAGAGATGAGTAGTAGAGAAGATGATAGTAGAAGA 2818
QY 2811 AGAATGAACGAATTCGTGATCGGTTGAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
Db 2819 AGAATGAACGAATTCGTGATCGGTTGAAGATTTGAAGCTACATAGAGCTTCTTGACG 2878
QY 2871 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTGACAAAGCTTTCATTTCT 2930
Db 2879 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTGACAAAGCTTTCATTTCT 2938
QY 2931 TTCCACTATAGTAGCAAGATATACGAGAGATGAAGTGTGCAACAAACATATGTAA 2990
Db 2939 TTCCACTATAGTAGCAAGATATACGAGAGATGAAGTGTGCAACAAACATATGTAA 2998
QY 2991 AATCGATGAATTTATCTCAATGCTGGGACGGCTTCAGCAGGTTTGTAGTAGGTTTC 3050
Db 2999 AATCGATGAATTTATCTCAATGCTGGGACGGCTTCAGCAGGTTTGTAGTAGGTTTC 3058
QY 3051 TGTAAATGTCATCTC 3066
Db 3059 TGTAAATGTCATCTC 3074

RESULT 3

AAT42630

ID AAT42630 standard; DNA; 3033 BP.

XX AAT42630;

AC AAT42630;

XX 25-FEB-1997 (first entry)

XX Class A starch branching enzyme (19con.seq).

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.

XX Solanum tuberosum.

XX Key Location/Qualifiers
FH CDS 145..2793

FT sig_peptide /*tag= a

FT 145..288

FT mat_peptide /*tag= b

FT 289..2790

XX /*tag= c

PN W09634968-A2.

XX 07-NOV-1996.

XX 03-MAY-1996; 96WO-GB01075.

XX 10-APR-1996; 96GB-0007409.

XX 05-MAY-1995; 95GB-0009229.

XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

XX Sidebottom CM, Westcott RJ;

XX WPI; 1996-506170/50.

XX P-PSDB; AAW06399.

XX New potato plant starch having high amylose content - also class A
starch branching enzyme and corresp. DNA to alter the viscosity of
starch; for use in food, biodegradable products, adhesives, etc.

XX Claim 28-30; Page 42-46; 142pp; English.

XX Class A starch branching enzyme (SBE) has been obtained from
potatoes. In class A SBE mols., a flexible N-terminal domain,
is found, which is not found in class B mols.

XX Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

QY Query Match

Db Best Local Similarity 90.2%; Score 2847.4; DB 17; Length 3033;

QY Matches 2919; Conservative 2; Mismatches 48; Indels 24; Gaps 2;

QY 53 TGGGGCCTTGAACCTCAGCAATTTGACACTCAGTTAGTACCTCCTTACTCATCATCAT 112
Db 5 TGGGGCCTTGAACCTCAGCAATTTGACACTCAGTTAGTACCTCCTTACTCATCATCAT 64QY 113 CTTCTATTTTCTTTCTTTAATTCACCAAGGATGAATTAAGAT-----TAGATT 163
Db 65 CTTCTATTTTCTTTCTTTAATTCACCAAGGATGAATTAAGATGAATTTGTAAGAAC 124QY 164 TGNAGCAGAGAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTCTTACTGTTTC 223
Db 125 CTAAGAGAGAGAAGAAAGATGGTGTATACACTCTCTGGAGTTCGTTTCTTACTGTTTC 184QY 224 CATCAGTGTACAAATCTAATGATGATTCAGCAGTAAATGTTGATCGGAGGATGCTAATGTTT 283
Db 185 CATCAGTGTACAAATCTAATGATGATTCAGCAGTAAATGTTGATCGGAGGATGCTAATGTTT 244

QY	1364	ATTATGCTAGTTTGGTTATCATGTCCAAATTTTTCACCAACAGACCGCTTTTGGAA	1423
Db	1325	ATTACGCTAGTTTGGTTATCATGTCCAAATTTTTCACCAACAGACCGCTTTTGGAA	1384
QY	1424	CGCCCCACGACCTTAACTGTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTGTTCTCA	1483
Db	1385	CGCCCCACGACCTTAACTGTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTGTTCTCA	1444
QY	1484	TGGACATTTGTTACAGCCATCATCAATTAATTTAGTAGTGAACATGTTGACG	1543
Db	1445	TGGACATTTGTTACAGCCATCATCAATTAATTTAGTAGTGAACATGTTGACG	1504
QY	1544	GCACAGATAGTTTACTTTTCACTCTGGAGCTCGTGGTTATCATGAGCTGGGATTC	1603
Db	1505	GCACAGATAGTTTACTTTTCACTCTGGAGCTCGTGGTTATCATGAGCTGGGATTC	1564
QY	1604	GCCTCTTAACTATGGAACCTGGGAGTACTTAGGTATCTCTCTCAAAATCGGAGATGGT	1663
Db	1565	GCCTCTTAACTATGGAACCTGGGAGTACTTAGGTATCTCTCTCAAAATCGGAGATGGT	1624
QY	1664	GGTTGGATGAGTGCATAATTTGRTGGATTTAGATTGATGGTGTGACATCAATGATATA	1723
Db	1625	GGTTGGATGAGTGCATAATTTGRTGGATTTAGATTGATGGTGTGACATCAATGATATA	1684
QY	1724	CTCACCACGGATATTCGGTGGGATTCACCTGGGAACTACGAGGAATCTTTGAGCTCGCAA	1783
Db	1685	CTCACCACGGATATTCGGTGGGATTCACCTGGGAACTACGAGGAATCTTTGAGCTCGCAA	1744
QY	1784	CTGATGTGATGCTGCGGTGTATCTGATGCTGGCAACGATCTTTATTCATGGGCTTTTCC	1843
Db	1745	CTGATGTGATGCTGCGGTGTATCTGATGCTGGCAACGATCTTTATTCATGGGCTTTTCC	1804
QY	1844	CAGATGCAATTTACCAATTTGGTGAAGATGTTAGCGGAATGCCGACATTTTATTCCTGTC	1903
Db	1805	CAGATGCAATTTACCAATTTGGTGAAGATGTTAGCGGAATGCCGACATTTTATTCCTGTC	1864
QY	1904	AAGATGGGCTGTTGGCTTTGACTATCGGCTGCATATGGCAATTCCTGATTAATGATG	1963
Db	1865	AAGATGGGCTGTTGGCTTTGACTATCGGCTGCATATGGCAATTCCTGATTAATGATG	1924
QY	1964	AGTTGCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATTTGTTACATACAGCAAA	2023
Db	1925	AGTTGCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATTTGTTACATACAGCAAA	1984
QY	2024	ATAGAAGTGTGCGAAAGTGTGTTTCATACGCTGAAGTCAATCAAGCTCAGTCG	2083
Db	1985	ATAGAAGTGTGCGAAAGTGTGTTTCATACGCTGAAGTCAATCAAGCTCAGTCG	2044
QY	2084	GTGATAAATATAGCATTTCTGGCTGATGGCAAGGATATGATTTATGCTTTGCTTTGG	2143
Db	2045	GTGATAAATATAGCATTTCTGGCTGATGGCAAGGATATGATTTATGCTTTGCTTTGG	2104
QY	2144	ATAGACCTCAACATCATTAATAGATCGTGGGATGAGCATTCGACAGATGATAGGCTG	2203
Db	2105	ATAGACCTCAACATCATTAATAGATCGTGGGATGAGCATTCGACAGATGATAGGCTG	2164
QY	2204	TAACTATGGGATGAGAGAGAGGTACCTTAAATTTTCATGGGAATGAATTCGGCCACC	2263
Db	2165	TAACTATGGGATGAGAGAGAGGTACCTTAAATTTTCATGGGAATGAATTCGGCCACC	2224
QY	2264	CTGAGTGGATTTGATTTCCCTAGGCTGGAACACCTCTCTCATGCTCAGTAAATTC	2323
Db	2225	CTGAGTGGATTTGATTTCCCTAGGCTGGAACACCTCTCTCATGCTCAGTAAATTC	2284
QY	2324	GAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGGGAGATGAGATAT	2383
Db	2285	GAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGGGAGATGAGATAT	2344
QY	2384	TAAATACCGTGGGTTGGAAGATTTGACCGGGCTATGACATCTGAGATGAGATAT	2443
Db	2345	TAAATACCGTGGGTTGGAAGATTTGACCGGGCTATGACATCTGAGATGAGATAT	2404
QY	2444	AGTTTATGACTTCAGAACACCGATTCATATCAGAAAGGATGAAGGATGAGATGAT	2503

QY	944	ATTGGGACGAAATCCTGACATATATGACTCGGAATGAATTTGGTCTGGGAGATTTTC	1003	QY	2023	AATAGAAGATGTCGGAAAAGTGTGTTTCATACGCTGAAGTCAATCATCAAGCTCTAGTC	2082
Db	903	ATTGGGACGAAATGCTGACTTTATGACTCGGAATGAATTTGGTCTGGGAGATTTTC	962	Db	1983	AATAGAAGATGTCGGAAAAGTGTGTTTCATACGCTGAAGTCAATCATCAAGCTCTAGTC	2042
QY	1004	TCCCAAAATATGTGATGGTCTCTCTGCAATCCCTCATGGGTCCAGAGTGAAGATACGCA	1063	QY	2083	CGTGATAAACHATAGCATTCCTGGCTGATGGACAAGGATATGATGATTTATGCGTTTG	2142
Db	963	TGCCAAATATGTGATGGTCTCTGCAATCCCTCATGGGTCCAGAGTGAAGATACGCA	1022	Db	2043	GGTGATAAACHATAGCATTCCTGGCTGATGGACAAGGATATGATGATTTATGCGTTTG	2102
QY	1064	TGSCACACTTCATCAGTGTTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGC	1123	QY	2143	GATAGACCCCTCAACATCATTAATAGATCGTGGGATAGCATTTGCACAAGATGATAGCTT	2202
Db	1023	TGSCACACTTCATCAGTGTTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGC	1082	Db	2103	GATAGACCCCTCAACATCATTAATAGATCGTGGGATAGCATTTGCACAAGATGATAGCTT	2162
QY	1124	TTTCCTGATGAATATTCATATATGAATATATGATCCACCCGGAAGAGGAGGTATG	1183	QY	2203	GTAACATATGGGATAGGAGAGAGGAGGTACCTTAATTTTCATGGAATGAATTCGGCCAC	2262
Db	1083	TTTCCTGATGAATATTCATATATGAATATATGATCCACCCGGAAGAGGAGGTATG	1142	Db	2163	GTAACATATGGGATAGGAGAGAGGAGGTACCTTAATTTTCATGGAATGAATTCGGCCAC	2222
QY	1184	TCCTCCACACCCACGCGCAAGAAACCAACCAAGTCGCTGAGATATATGATCTCATATTG	1243	QY	2263	CTGAGTGGATTCATTTCCCTAGGGTGAACACACCTCTCTGATGGCTCAGTAATTTCC	2322
Db	1143	TCCTCCACACCCACGCGCAAGAAACCAACCAAGTCGCTGAGATATATGATCTCATATTG	1202	Db	2223	CTGAGTGGATTCATTTCCCTAGGGTGAACACACCTCTCTGATGGCTCAGTAATTTCC	2282
QY	1244	GAATGATAGTCCGGAGCCCTAAATTAACATACATGATGATTTTAGAGTGAAGTCTTC	1303	QY	2323	GGAACCAATTCAGTTATGATAATGACGACGGAGATTTGACCTGGGAGATGCGAATAT	2382
Db	1203	GAATGATAGTCCGGAGCCCTAAATTAACATACATGATGATTTTAGAGTGAAGTCTTC	1262	Db	2283	AGAACCAATTCAGTTATGATAATGACGACGGAGATTTGACCTGGGAGATGCGAATAT	2342
QY	1304	CITCGAT-AAAAACCTTGGGTACATGCGGTGCAAAATATGCTATTCAAGAGCATTC	1362	QY	2383	TTAAGTACCGTGGGTGCAAGATTTGACCGGGCTATGCAATCTTTGAAGATAAATAT	2442
Db	1263	CITCGATAAAAAAGCTTGGGTACATGCGGTGCAAAATATGCTATTCAAGAGCATTC	1322	Db	2343	TTAAGTACCGTGGGTGCAAGATTTGACCGGGCTATGCAATCTTTGAAGATAAATAT	2402
QY	1363	TATTAATGCTAGTTTGGTATCATGTCACAAATTTTTTTCACCAAGCAGCGTTTGGG	1422	QY	2443	GAGTTTATGACTTCAGAACACCCAGTTTCATATCAGAAAGGATGAAGAGATAGGATGAT	2502
Db	1323	TATTAATGCTAGTTTGGTATCATGTCACAAATTTTTTTCACCAAGCAGCGTTTGGG	1382	Db	2403	GAGTTTATGACTTCAGAACACCCAGTTTCATATCAGAAAGGATGAAGAGATAGGATGAT	2462
QY	1423	ACGCGGACGACCTTAAGTCTTTGATGATGAAGTCAATGAGCTAGGATGTTGTTCTC	1482	QY	2503	GTAATTTGAAAAGGAAACCTAGTTTGTCTTTAATTTTCTACTGGACAAGAGCTATTCA	2562
Db	1383	ACGCGGACGACCTTAAGTCTTTGATGATGAAGTCAATGAGCTAGGATGTTGTTCTC	1442	Db	2463	GTAATTTGAAAAGGAAACCTAGTTTGTCTTTAATTTTCTACTGGACAAGAGCTATTCA	2522
QY	1483	ATGGACATTTCTCACAGCCATGATCAAAATTAATTTTAGATGAGCTGAACATTTTGAC	1542	QY	2563	GACTATCGCATAGCTGGCTGAACCTGGAAATACAAAGTGTGCTTGGACTCAGATGAT	2622
Db	1443	ATGGACATTTCTCACAGCCATGATCAAAATTAATTTTAGATGAGCTGAACATTTTGAC	1502	Db	2523	GACTATCGCATAGCTGGCTGAACCTGGAAATACAAAGTGTGCTTGGACTCAGATGAT	2582
QY	1543	GGCACAGATAGTTGTTACTTTCATCTGGAGCTCGTGTTATCAATGGATGGGATTC	1602	QY	2623	CCACTTTTGTGGCTTCGGGAGAAATGATCATATGCCGAATGTTTCCCTTTGAAGGA	2682
Db	1503	GGCACAGATAGTTGTTACTTTCATCTGGAGCTCGTGTTATCAATGGATGGGATTC	1562	Db	2583	CCACTTTTGTGGCTTCGGGAGAAATGATCATATGCCGAATATTCACCTTTGAAGGA	2642
QY	1603	CGGCTCTTTAATGGAATCTGGGAGTACTTAGTATCTTCTCAAAATGCCAGATGG	1662	QY	2683	TGGTATGATGATCGCTCTCGTTCAATTTATGTTGATGACCTAGTAGAACACGAGTGTG	2702
Db	1563	CGGCTCTTTAATGGAATCTGGGAGTACTTAGTATCTTCTCAAAATGCCAGATGG	1622	Db	2643	TGGTATGATGATCGCTCTCGTTCAATTTATGTTGATGACCTAGTAGAACACGAGTGTG	2702
QY	1663	TGGTGTGATGATGCAAAATTTGRTGATTTAGATTTGATGTTGATCAATGATGAT	1722	QY	2743	TATGCACTAGTAGACA---AAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAAGTA	2799
Db	1623	TGGTGTGATGATGCAAAATTTGRTGATTTAGATTTGATGTTGATCAATGATGAT	1682	Db	2703	TATGCACTAGTAGACA---AAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAAGTA	2762
QY	1723	ACTCACACGATTTATCGGTGGATTCACCTGGGAATACAGGAGAAATTTTGGACTCGCA	1782	QY	2800	GTAGTAGAAGAAGAAATGAACGAACCTTGTGATCGCTTGAAGATTTGAACGCTCATAGA	2859
Db	1683	ACTCACACGATTTATCGGTGGATTCACCTGGGAATACAGGAGAAATTTTGGACTCGCA	1742	Db	2763	GTAGTAGAAGAAGAAATGAACGAACCTTGTGATCGCTTGAAGATTTGAACGCTCATAGA	2822
QY	1783	ACTGATGRTGATGCGGTGATGCTGATGCTGCCACGATCTTATTCATGGGCTTTTC	1842	QY	2860	GCTTCTTGACGTATCTGGCAATATTTGATCATCTTGGCGGAATTTCTATGTCACAAAAGG	2919
Db	1743	ACTGATGRTGATGCGGTGATGCTGATGCTGCCACGATCTTATTCATGGGCTTTTC	1802	Db	2823	GCTTCTTGACGTATCTGGCAATATTTGATCATCTTGGCGGAATTTCTATGTCACAAAAGG	2882
QY	1843	CCAGATGCAATTAACATTTGTTGAAGATTTAGCGGAATGCCGACATTTTGTATCCCGTT	1902	QY	2920	TTTGCATTTCTTCCACTATTAGTAGTGCACGATATACCGAGATGAAGTGTCTGAAC-	2978
Db	1803	CCAGATGCAATTAACATTTGTTGAAGATTTAGCGGAATGCCGACATTTTGTATCCCGTT	1862	Db	2883	TTTGCATTTCTTCCACTATTAGTAGTGCACGATATACCGAGATGAAGTGTCTGAAC	2942
QY	1903	CAAGATGGGGTGTGTTGCTTGTACTATCGGTGATATGCGAATTTGCTGATGAATGAT	1962	QY	2979	AAACATATGTAATAATCGATGAATTTATGTCGAATGCTGGGACG 3021	
Db	1863	CAAGATGGGGTGTGTTGCTTGTACTATCGGTGATATGCGAATTTGCTGATAAATGAT	1922	Db	2943	AAACATATGTAATAATCGATGAATTTATGTCGAATGCTGGGACG 2986	
QY	1963	GAGTGTCTCAAGAACCGGATGAGGATTTGGAGTGGGTGATTTGTTCAACACTGACA	2022				
Db	1923	GAGTGTCTCAAGAACCGGATGAGGATTTGGAGTGGGTGATTTGTTCAACACTGACA	1982				

RESULT 5
AAT42635
ID AAT42635 standard; DNA; 2975 BP.
XX

QY	1605	CCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCTCAAAATGGAGATGSG	1664	2685	GTATGATGATCGCTCCCTGCTCAATTTATGGTGTATGACCTAGTAGAAGACAGCTGGTCTA	2744
Db	1564	CCTCTTTAACTATGGAACCTGGAGGTACTTAGGTATCTTCTCTCAAAATGGAGATGSG	1623	2644	GTATGATGATCGCTCCCTGCTCAATTTATGGTGTATGACCTAGTAGAAGACAGCTGGTCTA	2703
QY	1665	GTGATGAGTCAAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATATAC	1724	2745	TGCACCTAGTAGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2804
Db	1624	GTGATGAGTCAAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATATAC	1683	2704	TGCACCTAGTAGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2745
QY	1725	TCACCAACGATTTATCGGTGGGATTCACCTGGGAACCTACGAGGAATACCTTTGGACTCCAC	1784	2805	AGAAGAAGAAATGAACGAACCTTTGTGATCGGCTTCAAAAGATTTGAACGCTACATAGAGCTTC	2864
Db	1684	TCACCAACGATTTATCGGTGGGATTCACCTGGGAACCTACGAGGAATACCTTTGGACTCCAC	1743	2746	CATTGAAGAATGAACGAACCTTTGTGATCGGCTTCAAAAGATTTGAACGCTACATAGAGCTTC	2803
QY	1785	TGATGTGATGCTGCGGTGATCTGATGCTGCGCAACGATCTTATTCATGGCTTTTCC	1844	2865	TTGACCTAATCTGCAATATTCGATCATCTTCTGGGGAATTTCAATGTGACAA-AAGGTTTG	2923
Db	1744	TGATGTGATGCTGCGGTGATCTGATGCTGCGCAACGATCTTATTCATGGCTTTTCC	1803	2804	---CCACATAGAGCTCTTGCATCATCTTCTGGGGAATTTCAATGTGACAA-AAGGTTTG	2860
QY	1845	AGATGCAATTTACCAATGCTGAAGATCTTAGCGGAATGCGGACATTTTGHATTCGCCGTCA	1904	2924	CAATCTCTTCCACTATTAGTAGTGAACGATATACGAGAGATGAAGTGTGTAACAAACA	2983
Db	1804	AGATGCAATTTACCAATGCTGAAGATCTTAGCGGAATGCGGACATTTTGHATTCGCCGTCA	1863	2861	CAGTCTCTTCCACTATTAGTAGTGAACGATATACGAGAGATGAAGTGTGTAACAAACA	2920
QY	1905	AGATGGGGGTGTGGGTGTGACATCGGTGATATGGCAATTTGCTGATAAATGGATTTGA	1964	2984	TATGTAATAATCGATGAATTTATGTCGAATCTCTGGGACG 3021	
Db	1864	AGATGGGGGTGTGGGTGTGACATCGGTGATATGGCAATTTGCTGATAAATGGATTTGA	1923	2921	TATGTAATAATCGATGAATTTATGTCGAATCTCTGGGACG 2958	
QY	1965	GTTCCTCAAGAACGGGATGAGGATTTGGAGGTGGGTGATATTTGTTTCATACACTGACAAA	2024	RESULT 6		
Db	1924	GTTCCTCAAGAACGGGATGAGGATTTGGAGGTGGGTGATATTTGTTTCATACACTGACAAA	1983	ABK50301	standard; cDNA; 2563 BP.	
QY	2025	TAGAAGATGCTGGGAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG	2084	XX	ABK50301;	
Db	1984	TAGAAGATGCTGGGAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG	2043	XX	15-JUL-2002 (first entry)	
QY	2085	TGATAAATATAGCATCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGA 2144		DE	Potato cDNA encoding starch branching enzyme, SBE II.	
Db	2044	TGATAAATATAGCATCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGA 2103		XX	Potato; starch branching enzyme; SBE II; glucan branching enzyme;	
QY	2145	TAGACCTCCACATCAATATAGATCGTGGATAGCATGTCACAAAGATGATAGGCTTGT 2204		KW	GBE; ss; gene; plant; transgenic; antisense; food industry;	
Db	2104	TAGACCTCCACATCAATATAGATCGTGGATAGCATGTCACAAAGATGATAGGCTTGT 2163		KW	paper industry; chemical industry.	
QY	2205	AACATGCGGATTTAGGAGGAGAAGGTACCTAAATTTTCATGGGAATGAATTCGCCACCC 2264		OS	Solanum tuberosum.	
Db	2164	ANCTATGGATTTAGGAGGAGAAGGTACCTAAATTTTCATGGGAATGAATTCGCCACCC 2223		PH	Key Location/Qualifiers	
QY	2265	TGATGATGATTTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAATTCGCCG 2324		FT	CD5	
Db	2224	TGATGATGATTTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAATTCGCCG 2283		FT	/*tag= a	
QY	2325	AAACCAATTCAGTTATGATAATGCAGACGGAGATTTGACCTGGGAGATGCAGATATTT 2384		FT	/product= "SBE II"	
Db	2284	AAACCAATTCAGTTATGATAATGCAGACGGAGATTTGACCTGGGAGATGCAGATATTT 2343		FT	/partial	
QY	2385	AAGATACCGTGGTGTGCAAGATTTGACCGGGTATGACGATCTTTGAAGATAATATGA 2444		FT	/note= "No start codon shown"	
Db	2344	AAGATACCGTGGTGTGCAAGATTTGACCGGGTATGACGATCTTTGAAGATAATATGA 2403		PN	GB2360521-A.	
QY	2445	GTATATGATTCAGAACACCTGATATCATACGAAGGATGAAGGATAGGATGATTTGT 2504		XX	26-SEP-2001.	
Db	2404	GTATATGATTCAGAACACCTGATATCATACGAAGGATGAAGGATAGGATGATTTGT 2463		XX	20-MAR-2000; 2000GB-0006733.	
QY	2505	ATTGAAAAAGAAACCTAGTTTGTCTTTAAATTTTCACTGGACAAAAAGCTATTCAGA 2564		XX	20-MAR-2000; 2000GB-0006733.	
Db	2464	ATTGAAAAAGAAACCTAGTTTGTCTTTAAATTTTCACTGGACAAAAAGCTATTCAGA 2523		PA	(DANI-) DANISCO AS.	
QY	2565	CTATCGATAGCTGGCTGGAACCTGGGAAATACAGGTTGCTTGGACTCAGATGATCC 2624		PI	Poulsen P, Sorensen IS;	
Db	2524	CTATCGATAGCTGGCTGGAACCTGGGAAATACAGGTTGCTTGGACTCAGATGATCC 2583		DR	WPI: 2001-650142/75.	
QY	2625	ACTTTTGGTGGCTTCGGGAGAAATTCATCATATGCGGAATGTTTCACTTTGAAGGATG 2684		XX	P-PSDB; AAU80169.	
Db	2584	ACTTTTGGTGGCTTCGGGAGAAATTCATCATATGCGGAATGTTTCACTTTGAAGGATG 2643		XX	New transformed plants with reduced endogenous starch branching enzyme	
				PT	and heterologous glucan branching enzyme activities, useful for	
				PT	producing starch with improved properties, which is in the food, paper	
				PT	and chemical industries	
				XX	Example 1; page 31-35; 61pp; English.	
				PS	The invention relates to a transformed organism, preferably a transformed	
				XX	plant, having a reduced endogenous starch branching enzyme (SBE)	
				CC	activity, and having a heterologous glucan branching enzyme (GBE)	

activity. The reduced SBE activity is effected via expression of a nucleotide sequence that is antisense to at least part of a SBE exon. Also included are a method of producing starch with altered characteristics comprising (a) providing a plant having reduced endogenous SBE activity, and having heterologous SBE activity (b) propagating the plant of (a) and optionally GSE activity from the plant; starch obtainable from the transformed plant; and a nucleic acid construct system capable of directing the expression of all or part of one or more antisense SBE exons and optionally one or more heterologous GSE. The transformed plants are useful for producing starch with modified and improved properties, which is an important raw material and used in the food, paper and chemical industries. The present sequence encodes Potato SBE II, used to make transgenic plants of the invention.

Query Match	78.8%;	Score 2485.8;	DB 23;	Length 2563;
Best Local Similarity	98.4%;	Pred. No. 0;		
Matches 2508;	Conservative 2;	Mismatches 39;	Indels 0;	Gaps 0;
1	TCAGCAGTAATGGGTATCGGAGGAATGCTAATGTTCTGTATTTCTGTAATTTCTGAAAAAGCACACTCTC	307		
308	TTTCACGGAAGATCTTGCTCGAAGAGTCTCTTACGATTCGGAATCCGACCTTCTACAG	367		
61	TTTCACGGAAGATCTTGCTCGAAGAGTCTCTTACAAATTCGGAATCCGACCTTCTACAG	120		
368	TTGCAGCATCGGGGAAAGTCTTGCTGCTGGAATCCAGAGTATAGCTCTCATCTCAAC	427		
121	TTGCAGCATCGGGGAAAGTCTTGCTGCTGGAACCCAGAGTATAGCTCTCATCTCAAC	180		
428	CAGACCAATTTGAGTTTCACTGAGACAGCTCCAGAAAAATCCCGACATCAACTGATGG	487		
181	CAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAAAATCCCGACATCAACTGATGG	240		
488	ATAGTTCAACAATGGAACAGCTAGCCAGATTTAAACTGAGACGATGAGCTTGAGCCGT	547		
241	ATAGTTCAACAATGGAACAGCTAGCCAGATTTAAACTGAGACGATGAGCTTGAGCCGT	300		
548	CAAGTGAATTTACAGGAAAGTGTGAAGAGTTGGATTTTGCTTCATCACTACAACACTACAAG	607		
301	CAAGTGAATTTACAGGAAAGTGTGAAGAGTTGGATTTTGCTTCATCACTACAACACTACAAG	360		
608	AAGGTGTAACCTGGAGGAGTCTAAACATTTAAATCTTCTGAAGACACAATTTATGATG	667		
361	AAGGTGTAACCTGGAGGAGTCTAAACATTTAAATCTTCTGAAGACACAATTTATGATG	420		
668	AATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGTGTGAGAGATTTATG	727		
421	AATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGTGTGAGAGATTTATG	480		
728	AAATAGACCCCTTTTGACAAACTATCTGTCACACACCTTGATTTACAGGATTTACAGATCA	787		
481	AAATAGACCCCTTTTGACAAACTATCTGTCACACACCTTGATTTACAGGATTTACAGATCA	540		
788	AGAAATGAGGGAGGCAATGACAAGTATGAGGGTGGTTTGAAGCTTTTTCTCGTGGTT	847		
541	AGAAATGAGGGAGGCAATGACAAGTATGAGGGTGGTTTGAAGCTTTTTCTCGTGGTT	600		
848	ATGAAAAATGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTGAAGTGGCTCCG	907		
601	ATGAAAAATGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTGAAGTGGCTCCG	660		
908	GTGCCCAGTCAGTGTCTCATTTGGAGATTTCAACAATTTGGACCGCAATCTGCATTA	967		
661	GTGCCCAGTCAGTGTCTCATTTGGAGATTTCAACAATTTGGACCGCAATCTGCATTA	720		
968	TGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAAATTAATGTGGATGTTCTC	1027		
721	TGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAAATTAATGTGGATGTTCTC	780		

Db 661 TGGAGATTTCACAAATTGGGACGCAAAATGCTGACATATATGACTCGGAATGAATTTGGTGT 720
QY 990 CTGGGAGATTTTCTGCCAAATAATCTGGATGGTCTCTCTGCAATTCCTCATGGGCCAG 1049
Db 721 CTGGGAGATTTTCTGCCAAATAATGCTGGATGGTCTCTCTGCAATTCCTCATGGGCCAG 780
QY 1050 AGTGAAGATACGATGGACACTTCATCAGGTGTTAAGGATTCATTCCTGCTGGATCAA 1109
Db 781 AGTGAAGATACGATGGACACTTCATCAGGTGTTAAGGATTCATTCCTGCTGGATCAA 840
QY 1110 CTACCTCTTACAGCTTCCTGATGAATTCCTCATATATGAAATATATATGATCCACCGA 1169
Db 841 CTACCTCTTACAGCTTCCTGATGAATTCCTCATATATGAAATATATATGATCCACCGA 900
QY 1170 AGAGAGAGGTATGCTTCCACACCCAGCGGCAAAAGAACCAAGTCTCAGAAATA 1229
Db 901 AGAGAGAGGTATGCTTCCACACCCAGCGGCAAAAGAACCAAGTCTCAGAAATA 960
QY 1230 TCAATCTCATATTTGGAATGAGTAGTCCGGAGGCTAAATTAATCTCATAGCTGAATTTAG 1289
Db 961 TGAATCTCATATTTGGAATGAGTAGTCCGGAGGCTAAATTAATCTCATAGCTGAATTTAG 1020
QY 1290 AGATGAAGTCTCTCTCCATCAAAAACCTTGGGTACAAATCGGTCGCAATATGCGCTAT 1349
Db 1021 AGATGAAGTCTCTCTCCATCAAAAACCTTGGGTACAAATCGGTCGCAATATGCGCTAT 1080
QY 1350 TCAGAGCAATCTTATATGCTAGTCTTTGGTTATCATGTCACAAATTTTTTGCACCAAG 1409
Db 1081 TCAAGAGCAATCTTATATGCTAGTCTTTGGTTATCACTGTCACAAATTTTTTGCACCAAG 1140
QY 1410 CAGCGGTTTGGACGCCGACGACCTTAAGTCTTTGATGATAAAGCTCATGAGCTAGG 1469
Db 1141 CAGCGGTTTGGACGCCGACGACCTTAAGTCTTTGATGATAAAGCTCATGAGCTAGG 1200
QY 1470 AATTGTTGTTCTCATGACATGTTTCAGCGCATGTCATCAATTAATCTTTAGATGGACT 1529
Db 1201 AATTGTTGTTCTCATGACATGTTTCAGCGCATGTCATCAATTAATCTTTAGATGGACT 1260
QY 1530 GAACATGTTTGACGGCACAGATGTTTACTTCACTCTGGAGCTCGTGTATCAPTG 1589
Db 1261 GAACATGTTTGACGGCACAGATGTTTACTTCACTCTGGAGCTCGTGTATCAPTG 1320
QY 1590 GATGCGGATTCGCCCTCTTAACTATGAACTGGAGTACTTAAAGTATCTCTCTC 1649
Db 1321 GATGCGGATTCGCCCTCTTAACTATGAACTGGAGTACTTAAAGTATCTCTCTC 1380
QY 1650 AAATCGAGATGCTGGTGGATGATGTCAAATTTGRTGGATTTAGATTTGATGCTGAC 1709
Db 1381 AAATCGAGATGCTGGTGGATGATGTCAAATTTGRTGGATTTAGATTTGATGCTGAC 1440
QY 1710 ATCAATGATGTAFACTCACCAAGGATATCGGIGGATTCAGTGGGAATACGAGGAATA 1769
Db 1441 ATCAATGATGTAFACTCACCAAGGATATCGGIGGATTCAGTGGGAATACGAGGAATA 1500
QY 1770 CTGTTGACTCGCACTGATGATGCTGCGGTGATCTGATGCTGGCCCAAGCATCTAT 1829
Db 1501 CTGTTGACTCGCACTGATGATGCTGCGGTGATCTGATGCTGGCCCAAGCATCTAT 1560
QY 1830 TCAATGCGCTTTCCAGATGCAATTAACATTTGTTGAAGATTTAGCGGAATGCGGACAT 1889
Db 1561 TCACGGCTTTCCAGATGCAATTAACATTTGTTGAAGATTTAGCGGAATGCGGACAT 1620
QY 1890 TTGATTCGGTTCAAGATGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTCG 1949
Db 1621 TTGATTCGGTTCAAGATGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTCG 1680
QY 1950 TGATAAATGATGAGTGTCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATGT 2009
Db 1681 TGATAAATGATGAGTGTCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATGT 1740
QY 2010 TCATACACTGACAAATAGAGATGCTCGGAAGATGCTGTTTCATAGCTGAAAGTCA 2069
Db 1741 TCATACACTGACAAATAGAGATGCTCGGAAGATGCTGTTTCATAGCTGAAAGTCA 1800

QY 2070 TCAAGCTCTAGTCGGTGAATAAACTATAGCAATTCCTGCTGATGACGAAGATATGTATGA 2129
Db 1801 TCAAGCTCTAGTCGGTGAATAAACTATAGCAATTCCTGCTGATGACGAAGATATGTATGA 1860
QY 2130 TTTTATGGCTTTGGATAGACCCGTCACATCAATTAATAGATCTGGGATAGCATGACAA 2189
Db 1861 TTTTATGGCTCTGGATAGACCCGTCACATCAATTAATAGATCTGGGATAGCATGACAA 1920
QY 2190 GATGATTAGCTTTGAATAGGATAGGAGAGAGGATGATGATGATGATGATGATGATG 2249
Db 1921 GATGATTAGCTTTGAATAGGATAGGAGAGAGGATGATGATGATGATGATGATGATG 1980
QY 2250 TGAATTCGGCCACCCCTGAGTGGATGATGATGATGATGATGATGATGATGATGATG 2309
Db 1981 TGAATTCGGCCACCCCTGAGTGGATGATGATGATGATGATGATGATGATGATGATG 2040
QY 2310 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAATGCAGACGAGATTTGACCTGG 2369
Db 2041 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAATGCAGACGAGATTTGACCTGG 2100
QY 2370 AGATCAGATAATTTAAGATACCGTGGGTTGCAAGAAATTTGACCGGCTATGCACTAT 2429
Db 2101 AGATCAGATAATTTAAGATACCGTGGGTTGCAAGAAATTTGACCGGCTATGCACTAT 2160
QY 2430 TGAAGATAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2489
Db 2161 TGAAGATAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
QY 2490 AGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2549
Db 2221 AGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
QY 2550 AAAAGCTATTACAGACTATCGCATAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2609
Db 2281 AAAAGCTATTACAGACTATCGCATAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2340
QY 2610 GGACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2669
Db 2341 GGACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
QY 2670 CACCTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2729
Db 2401 CACCTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
QY 2730 AACAGAGTGTCTATGCACTAGTAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2789
Db 2461 AACAGAGTGTCTATGCACTAGTAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2790 AGAAGAAGT 2798
Db 2521 AGAAGAAGT 2529
RESULT 8
AAT42637
ID AAT42637 standard; DNA; 2529 BP.
XX AC AAT42637;
XX AC
XX AC
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (persbe2con.seq) cloned in QE32.
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX

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PF 03-MAY-1996; 96WO-CB01075.
XX
XX 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
XX (NAUT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 51-53; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
XX Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
XX
XX Query Match 78.3%; Score 2471.2; DB 17; Length 2529;
XX Best Local Similarity 98.1%; Pred. No. 0;
XX Matches 2482; Conservative 12; Mismatches 35; Indels 0; Gaps 0;
XX
XX 270 GAATGCTATGTTCTGATATCTTGAAGAAGCACTCTCTTCACGGAGATCTTGGCTGA 329
XX 1 GGATGCTAATGTTCTGATATCTTGAAGAAGCACTCTCTTCACGGAGATCTTGGCTGA 60
XX
XX 330 AATGCTCTCTACGATTCGGAATCCGACCTCTACAGTTTGCAGCATCGGGGAAAGTCC 389
XX
XX 61 AATGCTCTCTCAATTCGGAATCCGACCTCTACAGTTTGCAGCATCGGGGAAAGTCC 120
XX
XX 390 TGTACCTTGAATCCAGAGTGATAGCTCTCTCATCTCAACAGACAAATTTGAGTTCATGA 449
XX
XX 121 TGTGCTTGAATCCAGAGTGATAGCTCTCTCATCTCAACAGACAAATTTGAGTTCATGA 180
XX
XX 450 GACAGCTCCAGAAATTCGCCAGCATCACTGATGTAGATGTATCAACATGGAACAGC 509
XX 181 GACATCTCCAGAAATTCGCCAGCATCACTGATGTAGATGTATCAACATGGAACAGC 240
XX
XX 510 TAGCCAGATTAATACTCAGAACGATGACGTTGACCGCTCAAGTGATCTTACAGGAAGTGT 569
XX 241 TAGCCAGATTAATACTCAGAACGATGACGTTGACCGCTCAAGTGATCTTACAGGAAGTGT 300
XX
XX 570 TGAAGAGTGGATTTGCTTCACTCACTACAACTACAACTACAACTACAACTACAACTAC 629
XX 301 TGAAGAGTGGATTTGCTTCACTCACTACAACTACAACTACAACTACAACTACAACTAC 360
XX
XX 630 TAAACATTAATACTCTGAAGAGCAATTTATGATGAATCTGATAGGATCAGAGAGAG 689
XX 361 TAAACATTAATACTCTGAAGAGCAATTTATGATGAATCTGATAGGATCAGAGAGAG 420
XX
XX 690 GGGATCCCTCCACTGACCTTGGTCAGAGATTTATGAATAGACCCCTTTTACAAA 749
XX 421 GGGATCCCTCCACTGACCTTGGTCAGAGATTTATGAATAGACCCCTTTTACAAA 480
XX
XX 750 CTATCGTCAACACCTTGATTAACAGGTATTCAGATACAGAAATGAGGGAGGCAATTTGA 809
XX 481 CTATCGTCAACACCTTGATTAACAGGTATTCAGATACAGAAATGAGGGAGGCAATTTGA 540
XX
XX 810 CAAGTACAGGCTGTTGGAGCTTTTCTCGTGGTTATGAAAATGGGTTTCACTCG 869
XX 541 CAAGTACAGGCTGTTGGAGCTTTTCTCGTGGTTATGAAAATGGGTTTCACTCG 600
XX
XX 870 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTCTGGTCCCGAGTCAGTCTCTCAT 929
XX 601 TAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTCTGGTCCCGAGTCAGTCTCTCAT 660
XX
XX 930 TGGAGATTTCAACATTTGGGAGCGAAATGCTGACATTAAGTCTCGGAATGATTTGGTGT 989
XX
661 TGGAGATTTCAACATTTGGGAGCGAAATGCTGACATTAAGTCTCGGAATGATTTGGTGT 720
990 CTGGGAGATTTTCTGCCCCAAATATGTGGATGTTCTCTCTGCAATTTCCCATATGGTCCAG 1049
721 CTGGGAGATTTTCTGCCCCAAATATGTGGATGTTCTCTCTGCAATTTCCCATATGGTCCAG 780
1050 AGTGAAGATACGATGAGACACTTCATCAGGTGTTAGGATTCATTCCTCTGTTGGANCAA 1109
781 AGTGAAGATACGATGAGACACTTCATCAGGTGTTAGGATTCATTCCTCTGTTGGANCAA 840
1110 CTACTCTTTACAGCTTCTCTGATGAATTCATATTAATGAATATTAATGATCCACCGGA 1169
841 CTACTCTTTACAGCTTCTCTGATGAATTCATATTAATGAATATTAATGATCCACCGGA 900
1170 AGAGGAGAGGTATGTTTCCCAACACCCACCGCCCAAGAAACCAAGTTCGTGAGATATA 1229
901 AGAGGAGAGGTATGTTTCCCAACACCCACCGCCCAAGAAACCAAGTTCGTGAGATATA 960
1230 TGAATCTCATATTTGGAATGAGTAGTCCGGAGCCCTTAAATTAACATCACTACGTGAATTTAG 1289
961 TGAATCTCATATTTGGAATGAGTAGTCCGGAGCCCTTAAATTAACATCACTACGTGAATTTAG 1020
1290 AGATGAAGTTCCTCTCGCATATAAAACCTTGGGTACAAATCGCGTGCATAATTAATGCGTAT 1349
1021 AGATGAAGTTCCTCTCGCATATAAAACCTTGGGTACAAATCGCGTGCATAATTAATGCGTAT 1080
1350 TCAAGAGCAATCTTATATGCTAGTTTGGTATCATGTCTACAAATTTTTCGACCAAG 1409
1081 TCAAGAGCAATCTTATATGCTAGTTTGGTATCATGTCTACAAATTTTTCGACCAAG 1140
1410 CAGCCGTTTGGAAAGCCGACGACCTTAACTTTCATGATTAAGTCTAGTACGATGAGT 1469
1141 CAGCCGTTTGGAAAGCCGACGACCTTAACTTTCATGATTAAGTCTAGTACGATGAGT 1200
1470 AATGTTGTTCTCATGAGCATTTTTCACAGCATCATCAATTAATTAATTAATTAATTAAT 1529
1201 AATGTTGTTCTCATGAGCATTTTTCACAGCATCATCAATTAATTAATTAATTAATTAAT 1260
1530 GAACATGTTTTCAGCCGACAGATAGTTTTCATCTCTGAGAGTCTGTTGTTATCATTTG 1589
1261 GAACATGTTTTCAGCCGACAGATAGTTTTCATCTCTGAGAGTCTGTTGTTATCATTTG 1320
1590 GATGTTGGATTCGCGCTCTTTTAACTATGAAACTGGGAGTACTTAGTATCTCTCTCTC 1649
1321 GATGTTGGATTCGCGCTCTTTTAACTATGAAACTGGGAGTACTTAGTATCTCTCTCTC 1380
1650 AATGTCGAGATGGTGGTGGATGAGTGCATAATTTGTTGAGATTTAGATTTGATGTTGATG 1709
1381 AATGTCGAGATGGTGGTGGATGAGTGCATAATTTGTTGAGATTTAGATTTGATGTTGATG 1440
1710 ATCAATGATGATATCTACCCAGGATTTATCGTGGGATCTACTGGGAATCTAGGAAATA 1769
1441 ATCAATGATGATATCTACCCAGGATTTATCGTGGGATCTACTGGGAATCTAGGAAATA 1500
1770 CTTTGGATCTGCAACTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1829
1501 CTTTGGATCTGCAACTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1830 TCAUGGGCTTTTCCAGATGCAATTTACCATTTGGTGAAGATTTAGCGGAATGCCGACAT 1889
1561 TCACGGGCTTTTCCAGATGCAATTTACCATTTGGTGAAGATTTAGCGGAATGCCGACAT 1620
1890 TTGTAATCCCGTTCAAGATGGGGTGTGGCTTTGACATCTCGGCTGCATATGGCAATTTGC 1949
1621 TTGTAATCCCGTTCAAGATGGGGTGTGGCTTTGACATCTCGGCTGCATATGGCAATTTGC 1680
1950 TCATAAATGGATGAGTTCCTCAAGAAAGGATGAGGATTTGAGAGTGGTGGATTTGCT 2009
1681 TGATAAATGGATGAGTTCCTCAAGAAAGGATGAGGATTTGAGAGTGGTGGATTTGCT 1740
2010 TCATACATCTGCAAAATAGAAGATGGTTCGGAAGTGTGTTTTCATACGCTGGAAGTCA 2069
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Db 1741 TCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATMCGCTGAAAGTCATGA 1800
QY 2070 TCAAGCTCTAGTCGGTGATATAAACTATAGCATCTGCTGATGACACAGGATATGATGA 2129
Db 1801 TCAAGCTCTAGTCGGTGATATAAACTATAGCATCTGCTGATGACACAGGATATGATGA 1860
QY 2130 TTTATGGCTTTGGATAGACCGCTCAACATCAATTAATAGATCGTGGGATAGCATTCGCACAA 2189
Db 1861 TTTATGGCTTTGGATAGACCGCTCAACATCAATTAATAGATCGTGGGATAGCATTCGCACAA 1920
QY 2190 GATGATAGGCTTTGATACCTATGGGATAGGAGAGAGGCTACCTAAATTTTCATGGGAAA 2249
Db 1921 GATGATAGGCTTTGATACCTATGGGATAGGAGAGAGGCTACCTAAATTTTCATGGGAAA 1980
QY 2250 TGAATTCGGCCACCTGAGTGGATTCATTTCCCTAGGCTGAGACACACCTCTCTGATGG 2309
Db 1981 TGAATTCGGCCACCTGAGTGGATTCATTTCCCTAGGCTGAGACACACCTCTCTGATGG 2040
QY 2310 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGACAGACGGAGATTTCACCTGGG 2369
Db 2041 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGACAGACGGAGATTTCACCTGGG 2100
QY 2370 AGATCAGATATTTAAGATACCGTGGTTCGAGAAATTTGACCGGGCTATGACGATCT 2429
Db 2101 AGATCAGATATTTAAGATACCGTGGTTCGAGAAATTTGACCGGGCTATGACGATCT 2160
QY 2430 TGAAGATAAATATGATTTATGACTTCAGAACACACAGTTTCATATCAGCAAGGATGAAG 2489
Db 2161 TGAAGATAAATATGATTTATGACTTCAGAACACACAGTTTCATATCAGCAAGGATGAAG 2220
QY 2490 AGATAGGATGATGATTTGAAAGAGAAACCTAGTTTGTCTTTAAATTTTCACGAGAC 2549
Db 2221 AGATAGGATGATGATTTGAAAGAGAAACCTAGTTTGTCTTTAAATTTTCACGAGAC 2280
QY 2550 AAAAGCTATTCAGACTATCGCATAGGCTGGCTGAGCCCTGGAAGATCAATGCGGAATGTT 2609
Db 2281 AAAAGCTATTCAGACTATCGCATAGGCTGGCTGAGCCCTGGAAGATCAATGCGGAATGTT 2340
QY 2610 GGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATGCGGAATGTT 2669
Db 2341 GGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATGCGGAATGTT 2400
QY 2670 CACCTTTGAGGATGGTATGATGATCGCTTCCTTCAATATGCTGATGACACCTAGTAG 2729
Db 2401 CACCTTTGAGGATGGTATGATGATCGCTTCCTTCAATATGCTGATGACACCTAGTAG 2460
QY 2730 AACAGCAGTGGTCTATGACTAGTAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2789
Db 2461 AACAGCAGTGGTCTATGACTAGTAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2790 AGAAGAGT 2798
Db 2521 NGAAGAAAT 2529

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RESULT 9

AA42631

ID AA42631 standard; DNA; 2578 BP.

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FT sig_peptide 24...56
FT mat_peptide /*tag= b
FT 57...2564
FT /*tag= c
XX WO9634968-A2.
XX 07-NOV-1996.
XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
XX 05-MAY-1995; 95GB-0009229.
XX (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
XX Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
XX P-PSDB; AAW06400.
XX New potato plant starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX Claim 32; Page 55-56; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;

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Query Match 77.5%; Score 2445; DB 17; Length 2578;
Best Local Similarity 98.4%; Pred. NO. 0;
Matches 2482; Conservative 2; Mismatches 27; Indels 12; Gaps 1;

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QY 318 GATCTTGGCTGAAAAGTCTTCTTACGATTCGGAATCCGACCTTCTACAGTTTCAGCATC 377
Db 56 GATCTTGGCTGAAAAGTCTTCTTACGATTCGGAATTCGACCTTCTACAGTTTCAGCATC 115
QY 378 GGGGAAAGTCTTGTACCTGGAAATCCAGAGTATAGTCTCCTCATCTCAACAGACCAAT 437
Db 116 GGGGAAAGTCTTGTACCTGGAAATTCGACCTTCTACAGTTTCGACCTTCTACAGTTTC 175
QY 438 TGAGTTTCACTGAGACAGCTCCAGAAATTCGACCTTCTACAGTTTCGACCTTCTACAG 497
Db 176 TGAGTTTCACTGAGACATCTCCAGAAATTCGACCTTCTACAGTTTCGACCTTCTACAG 235
QY 498 AATGGAACACGCTAGCCAGATTAAACTGAGAACGATGAGCTTGGCTGAGAAATTCGACCT 557
Db 236 AATGGAACACGCTAGCCAGATTAAACTGAGAACGATGAGCTTGGCTGAGAAATTCGACCT 295
QY 558 TACAGGAACTGTTGAAGAGTTCGATTTTCTTCACTACACTACAACTACAAAGAGTGTAA 617
Db 296 TACAGGAACTGTTGAAGAGTTCGATTTTCTTCACTACACTACAACTACAAAGAGTGTAA 355
QY 618 ACTGGAGGAGTCTAAAACATTAATACCTTCTCAAGAGCAATTAATGATGATCTGATAG 677
Db 356 ACTGGAGGAGTCTAAAACATTAATACCTTCTCAAGAGCAATTAATGATGATCTGATAG 415
QY 678 GATCAGAGAGGGGATCTCCCTCCACCTGGACTTGGCTGAGAAATTCGACCTTCTACAGTCC 737
Db 416 GATCAGAGAGGGGATCTCCCTCCACCTGGACTTGGCTGAGAAATTCGACCTTCTACAGTCC 475
QY 738 CCTTTTGACAACTATCTCAACCTTGAATTCAGAGTATTCACAGTACAAAGAAATGAG 797
Db 476 CCTTTTGACAACTATCTCAACCTTGAATTCAGAGTATTCACAGTACAAAGAAATGAG 535
QY 798 GGAGCAATTCACAGTATGAGGTTGGTTCGAGAGCTTTTCTCTGTTGTTTGAAGAAAT 857
Db 536 GGAGCAATTCACAGTATGAGGTTGGTTCGAGAGCTTTTCTCTGTTGTTTGAAGAAAT 595

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Class A starch branching enzyme (psbe2con.seq - clone psJ90).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

amylose; viscosity; potato; ss.

Solanum tuberosum.

Key Location/Qualifiers

FT CDS 24...2567

FT /*tag= a


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QY 858 GGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTGAGTGGGTCCTGGTGCCAGTTC 917
Db 1676 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTTGGAGAGT 1735
QY 918 AGCTGCTCTCAATTTGGAGATTTTCAACAATTTGGACGCAAAATGCTGACATTTATGACACGGAA 977
Db 656 AGCTGCCCTCAATTTGGAGATTTTCAACAATTTGGACGCAAAATGCTGACATTTATGACACGGAA 715
QY 978 TGAATTTGGTGTCTGGGAGATTTTCTGCCAAATTAATGGGATGGTTCCTTGCATTC 1037
Db 716 TGAATTTGGTGTCTGGGAGATTTTCTGCCAAATTAATGGGATGGTTCCTTGCATTC 775
QY 1038 TCATGGGTCCAGAGTGAACATACGCATGGACATTCATCAGCGTGTAAAGGATTCATTC 1097
Db 776 TCATGGGTCCAGAGTGAACATACGCATGGACATTCATCAGCGTGTAAAGGATTCATTC 835
QY 1098 TGCCTGGATCACTACTCTTTACAGCTTCCTGATGAATTCATATTAATGGATATATTA 1157
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QY 1218 GCTGAGATATATGAATCTCATATTTGGAATGAGTAGTCCGGAGCCTTAAATTAACATCA 1277
Db 956 GCTGAGATATATGAATCTCATATTTGGAATGAGTAGTCCGGAGCCTTAAATTAACATCA 1015
QY 1278 CBTGAATTTAGAGATGAAGTCTTCTCCTCGCATAAACCTTTGGGTACAAATCGGTGCA 1337
Db 1016 CBTGAATTTAGAGATGAAGTCTTCTCCTCGCATAAACCTTTGGGTACAAATCGGTGCA 1075
QY 1338 AATTATGGCTATTCAGAGCATTTCTATTATGCTAGTTTGGTATCATGCTCAACAATTT 1397
Db 1076 AATTATGGCTATTCAGAGCATTTCTATTATGCTAGTTTGGTATCATGCTCAACAATTT 1135
QY 1398 TTTTGCACCAAGCAGCCGTTTGGACGCGCCGACGACCTTAACTCTTTGATTGATAAAGC 1457
Db 1136 TTTTGCACCAAGCAGCCGTTTGGACGCGCCGACGACCTTAACTCTTTGATTGATAAAGC 1195
QY 1458 TCATGAGTAGGAATTTGTTCTCTCATGACATTTGTCACAGCCATGATCAATATATAC 1517
Db 1196 TCATGAGTAGGAATTTGTTCTCTCATGACATTTGTCACAGCCATGATCAATATATAC 1255
QY 1518 TTTAGATGGACTGAACATGTTTGACGCGCACAGATAGTTGTTACTTTTCACTCTGGAGCTCG 1577
Db 1256 TTTAGATGGACTGAACATGTTTGACGCGCACAGATAGTTGTTACTTTTCACTCTGGAGCTCG 1315
QY 1578 TGCTTATCATTTGATGGGATTCGCCCTTTTAACTATGGAACCTGGGAGGTACTTAG 1637
Db 1316 TGCTTATCATTTGATGGGATTCGCCCTTTTAACTATGGAACCTGGGAGGTACTTAG 1375
QY 1638 GTATCTCTCTAAATTCGAGATGGTGTGGATGAGTGCAAATTTGRTGGATTTAGATT 1697
Db 1376 GTATCTCTCTAAATTCGAGATGGTGTGGATGAGTGCAAATTTGRTGGATTTAGATT 1435
QY 1698 TGATGTTGTCACATCAATGATGTATCTCACACCGGATTTATCGGTGGGATTCACCTGGGAA 1757
Db 1436 TGATGTTGTCACATCAATGATGTATCTCACACCGGATTTATCGGTGGGATTCACCTGGGAA 1495
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QY 1878 AATGCCGACATTTTGTATTCCTCGTTCAAGATGGGGGTGTTGGCTTTTGACATACGGCTGCA 1937
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1938 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTTGGAGAGT 1997
Db 1676 TATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTTGGAGAGT 1735
QY 918 GGGTGATATTTTCATACACTGACAAATAGAGATGCTCGGAAACGTGTGTTTCATACGC 2057
Db 1736 GGGTGATATTTTCATACACTGACAAATAGAGATGCTCGGAAACGTGTGTTTCATACGC 1795
QY 2058 TGAAGTCTATGATCAAGCTCTAGTCGGTGATATAAATATAGCAATTCGCTGATGACAA 2117
Db 1796 TGAAGTCTATGATCAAGCTCTAGTCGGTGATATAAATATAGCAATTCGCTGATGACAA 1855
QY 2118 GGATATGATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGAT 2177
Db 1856 GGATATGATGATTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGAT 1915
QY 2178 AGCATTGCAAGATGATAGGCTTGTAACTATGGGATAGGAGGAGAGGGTACCTAAA 2237
Db 1916 AGCATTGCAAGATGATAGGCTTGTAACTATGGGATAGGAGGAGAGGGTACCTAAA 1975
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QY 2478 AAGGATGAAGGAGATAGGATGATGTTTGAAGAGGAAACCTAGTTTGTCTTTAA 2537
Db 2216 AAGGATGAAGGAGATAGGATGATGTTTGAAGAGGAAACCTAGTTTGTCTTTAA 2275
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QY 2658 TGCCGAATGTTTCACTTTTGAAGGATGATGATGCTGCTGCTTCAATTTATGTTGTA 2717
Db 2396 TGCCGAATGTTTCACTTTTGAAGGATGATGATGCTGCTGCTTCAATTTATGTTGTA 2455
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Db 2576 GTG 2578

RESULT 10
AAT42636
ID AAT42636 standard; DNA; 2576 BP.
XX AAT42636;
XX AC
XX DT 03-MAR-1997 (first entry)
XX

QY	537	CGTTGAGCGGTCAAGTGATCTTACAGGAAGTGTGAAGAGTTGGATTTTGCTTCATCACT	596	Db	1477	TGGAAGCTGGAGGTGCTAAGATTTCTTCTTCAATGCAAGATGGTGGTGGAGAGTA	1536
Db	490	AAAAAGTCG-----	499	QY	1577	CAAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGTATATACTCACCACGGAAT	1736
QY	597	ACAACTACAGAAAGGTGGTAACCTGGAGGAGTCTAAACAAATTAATATACHTTCTGAAGAGAC	656	Db	1537	CAGTTTGATGGTGTAGATTTGATGGGTGACHTTCCATGATGATACACTCCCCATGGGTT	1596
Db	500	-----GTTCCATTTGCATGAGAC	516	QY	1737	ATCGGTGGGATTCACCTGGGAACCTACGAGGAATACHTTGGACTCGCAACTGATSTGATGC	1796
QY	657	AATTTATTGATGATCTGATAGGATCAGAGAGAGGGCAUCCCTCCACCTGGACTTGGTCA	716	Db	1597	GCAGGTAGCTTTTACTGGCAACTACAATGATGACTTCTGGATATGCAACTGATGATGC	1656
Db	517	AATTACATTTGAAAAAGTGAATCTAAACCAAGGTCCTATCTCCACCTGGCAGTGGCA	576	QY	1797	TGCGGTGATCTGATGCTGCCACACGATCTTATTCATCGGCTTTTCCCAAGATGCAATAC	1856
QY	717	GAAGATTTATGAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGTATACAGGTA	776	Db	1657	TGTGATTTATTTGATGCTTGTGAATGATATGATTCACGGTCTTTTCCCTGAGGCTGTAC	1716
Db	577	GAGAAATATGACATAGATCCAAAGCTTGGCAGGTTTCCGTCACGATCTTGACATCCGATA	636	QY	1857	CATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTCCCTCAAGATGGGGTGT	1916
QY	777	TTACAGTACAGAAATGAGGAGGCAATGTACAAGTATGAGGGTGGTTTGAAGCTTT	836	Db	1717	CATTGGTGAAGATGTTAGCGGAAGCCAAATTTTGCATTTCCAGTGGAAAGATGGTGGTGT	1776
Db	637	TTACAGTACAGAAAGGCTCGGTGAGCAATTGACAAGTATGAAGGTGGTTTGGATGCAAT	696	QY	1917	TGCTTTGATCTCGGCTGCATATGGAATTTGCTGTGATPAATGGAATGAGTTGCTCAAGAA	1976
QY	837	TTCTCGTGTATGAAAAATGGTTTCACTCGTAGTGTACAGGTATCACTTTACCGTGA	896	Db	1777	TGATTTGATTTACCGTCTCCACATGGCCATTTGCCGATATAATGGATTCAGATTCCTAAGAA	1836
Db	697	CTCTCGTGAATGAAAGTTTGGTTTCTTACGCACTGAACAGGAATTAATATATAGGA	756	QY	1977	ACGGATGAGGATTTGGAGAGTGGGTGATATTTTATACACTGACAAATGAGAGATGGTC	2036
QY	897	GTGGGCTCTGTTGCCAGTCAGCTCTCTCATTTGGAGATTTCAACAATTTGGGACGAAA	956	Db	1837	GAGATGAGGACTGGAAATGGGTGACATTTGTGCATACACTCACCACAGAGAGGTGTT	1896
Db	757	ATGGGCACCTGGAGCTACCTGGGCTGCACCTTATTTGGAGATTTCAACAATTTGGAATCCTAA	816	QY	2037	GGAAATGTTGTTTCACTACGCTGAAAGTCAATGATCAAGCTCTAGTCGGTGATATAAACTAT	2096
QY	957	TGCTGACATATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATAGT	1016	Db	1897	GGAAATGTTGTTTCTATCTGAAAGTCAATGACCAAGCTCTTTGGTGCACAAACTAT	1956
Db	817	TCAGATGATGACTCGGAATGAGTTTGGTGTCTGGGAGATTTTCTGCGCAAAATAGC	876	QY	2097	AGCAATTTGCTGCTGATGCAAGGATATGATGATTTTATGGCTTTGGATAGCGCTCAAC	2156
QY	1017	GGATGTTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATGACGATGACATTCATC	1076	Db	1957	TGCAATTTGCTGCTGATGCAAGGACATGTACGACTTCATGGCTCGTGACAGACATCTAC	2016
Db	877	AGATGTTTCAACCACTTCCTCATGGTCTTCTGAGTAAAGATACGATGGATCTCCATC	936	QY	2157	ATCAATTAATAGATCGTGGGATAGCATTTGCAAGATGATGATTTTATGGCTTTGGATAGCGGAT	2216
QY	1077	AGTGTATAGGATTCATTCCTGCTTGGATCAACTACTCTTTACAGCTCTCTGATGAAAT	1136	Db	2017	TCTCTTTATAGATCGTGGATAGCATTTGCAAAATGATCAGGCTTATTTACCATGGCTT	2076
Db	937	TGGCATCAAGATTCATTCCTGCTTGGATCAAGTTCTCAGTTCAGGCACCTGGTGAAT	996	QY	2217	AGGAGAGAGGTTACCTAAATTTTCATGGAAATGAATTTGGCCACCTCGAGTGAATGA	2276
QY	1137	TCATATATGAAATATATATGATCCACCCAGAGGAGAGATGATGCTTCCAAACACC	1196	Db	2077	AGCGGAGAGGATTTTGAATTTTATGGGAAATGAATTTGGACATCTCTGAGTGAATGA	2136
Db	997	CCATACATGCAATATGATATGATCCACCAAGAGGAGAGATGATGCTTCCAAACATCC	1056	QY	2277	TTTCCCTAGGCTTGAACACACCTCTCTGATGCTCAGTAATTTCCCGGAAACCAATTCAG	2336
QY	1197	ACGGCCAAAGAACCAAGTCTGAGATATATGATCTCATTTTGAATGGAATGAGTAGTCC	1256	Db	2137	TTTCCAGAGGAGTTCGACATCTGCCAATGTTAAAGTAAATTTCCAGGGAACCAACACAG	2196
Db	1057	TCAGCCAAAGACCAAAATCACTAGGATTTATGAACTCACTGTTGGATGGATAGTAT	1116	QY	2337	TTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAAGATATTTTAAGATACCGTGG	2396
QY	1257	GGAGCCTAAATTAACATCACTGATGAATTTTGAAGATGAAGTCTTCTCCGCAATAAAAA	1316	Db	2197	TTATGATAAATGCGCTCGTAGATTTGATCTAGGATGATGCAAGTATCTTAAGATATCAIGG	2256
Db	1117	GGAGCCAAATTAACACATATGCCAATTTAGAGATGATATGCTTCTCCGCAATCAAAA	1176	QY	2397	GTTGCAAGATTTGACCGGCTATGCAATCTTTGAAGATATAATATGATTTATGACTTC	2456
QY	1317	CCTTGGGTACATCGGTGCAAAATATGCTATTTCAAGAGATCTTATTTAGCTAGTTT	1376	Db	2257	AATGCAAGATTTTGATCAGGCAATGCAACATCTTTGAAGAAGCCTATGTTTCACTGACTTC	2316
Db	1177	GCTTGGCTACAAGGTGTTCAGATATGCTATTTCAAGAGCATTTCTATTTAGCTAGTTT	1236	QY	2457	AGAACACCACTTCAATACAGGAAGATGAGGAGATGAGATGATTTGATTTGAAAAAGG	2516
QY	1377	TGGTTATCATGTCACAAATTTTTCACCAAGCAGCCGCTTTTGGAAACCCCGACCACT	1436	Db	2317	TGAGCACCAGTATATATACGGAAGATGAAGGAGATCGGATCAITTTCTTTGAGAGGG	2376
Db	1237	TGSGTACCATGTCAACAACTTTTTCACCTAGCAGCCGATTTGAACTCTCTGATGATTT	1296	QY	2517	AAACCTTAGTTTGTCTTTAAATTTTTCACCTGGACAAAAGCTATTTACAGACTATCGCATAG	2576
QY	1437	TAAGCTTTGATGATAAGCTCATGAGCTAGGAATTTGTTTCTCATGGACATGTTTCA	1496	Db	2377	AAACCTTGTTTGTATTCACTTTTCATTTGAGTAAACAGCTATTCAGATTTACCGAGTTGG	2436
Db	1297	GAACTCTTTAATAGATAAAGCTCATGATAGGCTGCTGTTTCTCATGGATATGTTCA	1356	QY	2577	CTGGCTGAAGCCTTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCTCTTTTGGTGG	2636
QY	1497	CAGCCATGATCAAAATATACHTTTAGATGGAATGAACATGTTTGAAGGACAGATAGTGT	1556	Db	2437	CTGCTTCAAGTACAGGAAGTACAAGATTTGTTTGGACTCGGATGATGGCTTTTTCGAGG	2496
Db	1357	TAGCCATGCGTCAAAATATACCTTGAATGGGCTGAACATGTTTGAATGATGATGCA	1416	QY	2637	CTTTCGGGAAATGATCATTAATGCCGAATGTTTACCTTTGAAAGGATGATGATGATCG	2696
QY	1557	TTACTTTCACCTGAGGCTCGGTTTATCATTTGATGAGGATTTCCCGCTCTTTAACTA	1616	Db	2497	CTTCAACAGGCTTAGTTCATGATGCCGAGCCTTCACTTTTGAAGGCTGATGATAACCG	2556
Db	1417	CTACTTCCACTCCGATCAGGGGTCATCATTTGGTTGGGACTCTCGGCTTTTCAACTA	1476	QY	2697	TCTCTCTCAATATGCTGTATGCACTAGTACAGCAGCAGTGGTCTATGCTACTAGTAGA	2756
QY	1617	TGAAACTGGGAGTACTTAGGTATCTTCTCTCAAAATGCGAGATGGTGTGGATCAGTG	1676				

PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	08-OCT-1999;	99US-0157865.
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PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
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PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159638.
PR	20-JUL-1999;	99US-0144884.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0144814.	PR	21-OCT-1999;	99US-0160741.
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PR	21-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160768.
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PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0148684.			
PR	16-AUG-1999;	99US-0149368.			
PR	17-AUG-1999;	99US-0149175.			
PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
<div> <div>Query Match</div> <div>41.1%; Score 1296; DB 21; Length 2715;</div> <div>Best Local Similarity 76.2%; Pred. No. 0;</div> <div>Matches 1593; Conservative 1; Mismatches 456; Indels 0; Gaps 0;</div> </div>					
QY	686	AGAGGGGCGATCCCTCCACCTTGGTCAGAGATTTATGAATAGACCCCTTTTGA	745		
Db	443	AGAGGAAGATCCACCTCCCTGGAGATGGGAGAGATATATGACATTTGCTTATGTTGA	502		
QY	746	CAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAGAAATAGGGAGGCAA	805		
Db	503	ACAGTCATGATATCATCTTGATTACCGATATGGGAGTACAGAAATCGGTGAAGAA	562		
QY	806	TTGACAAAGTATGAGGGTGGTTGGAAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCA	865		
Db	563	TTGACAAAGATGAAGGTGGTTGGAGGCAATTTCTCGTGGTTATGAAATATTTGGCTTCA	622		
QY	866	CTCGTAGTGTACAGGTATCATCTTACCGTGAGTGGGCTCTCGTGGTCCAGTCAGCTGTC	925		
Db	623	CTCGAAGCGGCACTGGTATCATCTTACCGGGAATGGGAGCTTAAGGCGCATCAC	682		
QY	926	TCATTGGAGATTTCAACAATTTGGACGCAATGCTGACATTTACCTCGGAATGAATTTG	985		
Db	683	TGATCGGAGATTTTAAACUGGAATCGGAAATCTGATGTTATGGCTCGGACGACTTG	742		

XX 13-JAN-1998.
 PD 24-JUN-1996; 96JP-0162983.
 PF 24-JUN-1996; 96JP-0162983.
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MIK) MITSUI TOATSU CHEN INC.
 PA WPI; 1998-133625/13.
 DR P-PSDB; AAW411763.
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield
 PT high quality starch
 PS Claim 4; Pages 5-8; 13pp; Japanese.
 XX The present sequence encodes the rice type IV starch branching
 CC enzyme, which has the ability to synthesise amylopectin. The
 CC quality of starch is improved by the use of the protein.
 XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;
 SQ
 Query Match 40.4%; Score 1275.6; DB 19; Length 3015;
 Best Local Similarity 75.3%; Pred. No. 0;
 Matches 1587; Conservative 1; Mismatches 520; Indels 0; Gaps 0;
 QY 663 TGATGATCTGATAGATCAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCAGAGAT 722
 DB 554 TGAACCAACTGTGGAGGATAAACCCACGAGTTATCCACCACCCAGGAGATGGGAGAGAT 613
 QY 723 TTATGAATAGACCCCTTTTGACAAACTATGCTCAACACCTTGATACAGGATTTCACA 782
 DB 614 ATACCAAAATGACCAATGCTGGAAGGATTCGGAAACCATCTGACTACCGATACAGTGA 673
 QY 783 GTACAGAAATGAGGGAGGCAATTCACAAAGTATGAGGTGGTTTGGAACTTTTCTCG 842
 DB 674 ATACAGAGAAATGCGTGCAGTATTGACCAACATGAAGTGGCTTGGATGCAATTTCTCG 733
 QY 843 TGGTTATGAAATAGGTTTCTACTGTAGTGTACAGTATCAGTATCAGTATCAGTATGAGTGGC 902
 DB 734 TGGTTACGAAAGCTTGGATTCACCGCAGCGCTGAAGGATTAACCTACCGAGATGGGC 793
 QY 903 TCCTGTGCCCAGTACGCTGCTCAATGGAGATTTCAACAATTTGGAGCACAATGCTGA 962
 DB 794 ACTGGAGCACAGTCTGCAGCATTTAGTGTGATTCACAAATTTGGAACCCAAATGCAGA 853
 QY 963 CATTATGCTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATGAATGTGGATGG 1022
 DB 854 TACTATGACAGAAATGAGTATGGTGTGGGAGATTTCCCTGCCTAACCAATGCTGATGG 913
 QY 1023 TTCTCTCGAAATTCCTCATGGGTCAGAGTGAAGATACGATGAGTATCAGTATTCATCAGTGT 1082
 DB 914 ATCCCTGCTATTCCTCATGGCTCAGCTGTAAGATTCGGATGATACACCATCTGCGGT 973
 QY 1083 TRAGATTCATTCCTGCTTGGATCACTACTTTTACAGCTTCCTGATGAATTCGATA 1142
 DB 974 AAGAGATTCAATTCCTGCTGGATTAAGTTGCTGTGCGAGGCTCCAGGTGAAATACGGTA 1033
 QY 1143 TRATGAATATATATGATVCCACCCGAGAGAGAGATGATGCTTCCACACCCACCGGCC 1202
 DB 1034 CAACGATATATATGATVCCACCTGAAGAAGAAATATGATATTCACATCCTCAACC 1093
 QY 1203 AAGAAGAACCAAGTCTGAGATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
 DB 1094 TAACAGCAAAATTCCTGCGGATATATGATVCCACATATGATGATGAGTAGCCGGAACC 1153
 QY 1263 TAAATTAATCACTGATGAATTTTATGATGAAGTTCCTTCGCAATAAAAACCTTGG 1322
 DB 1154 GAAGATAAACACATATGCTAAATTTTAGGATGAGGTGCTACCAAGAATTAAGAAAGCTTGG 1213
 QY 1323 GTACATGGGTCGAATATGCTATTACAGAGCATCTTATATGCTAGTTTGGTTA 1382

DB 1214 GTACAATGCTGTACAGATAATGGCAATCCAGGAGCACTCTTATTACCAAGCTTTGGSTA 1273
 QY 1383 TCATGTACAAAATTTTTTCCACCAACAGCCGCTTTTGGAAACCCGACACCTTAAGTC 1442
 DB 1274 TCAITGTTACTAACTCTTTGGCCCAAGTAGCCGTTTGGAAACCCGACAGACTGAATC 1333
 QY 1443 TTTGATTTGATAAAGCTCATGAGTAGSAAATGTTGTTCTCATGACATTTTTCACAGCCA 1502
 DB 1334 TCTGATTTGATAAAGCTCACGAGCTTGGTTTGGCTTACTTATGATGATTTGTTACAGTCA 1393
 QY 1503 TGCATCAATAATATCTTTAGATGACACAGACATGTTTGGAGGACACAGATAGTTTACTT 1562
 DB 1394 TGCATCAACAATATCCCTGGATGTTTGAATGTTTGGTGGTACTGATACACATTAAT 1453
 QY 1563 TCACTCTGGAGCTGCTGGTTTATCATTTGATGAGTGTGGGATTCCTGCTTTTAACTATGAAA 1622
 DB 1454 CCATGTGGACCAACGGGCTCATCAGGATGGGATTCCTGCTTCAACTATGGGAG 1513
 QY 1623 CTGGAGGTACTTTAGGTATCTTCTCAAAATGCGAGATGTTGTTGATGAGTGCATAAT 1682
 DB 1514 TTGGGAAGTTTTAAGATATTTACTGTCGAATGCAAGGTGGTGGCTTGAAGAATACAGTT 1573
 QY 1683 TGTGATTTAGATTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
 DB 1574 TGAITGGTTTCGATTTGATGGGTGACCTCCATCATGATGATGATGATGATGATGATGATGAT 1633
 QY 1743 GGCATTCACCTGGGAATACAGGAATACTTTTGACTGCGAACTGATGATGATGATGATGATGAT 1802
 DB 1634 GGCATTTACHGGCAACTATGCGGAATATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1693
 QY 1803 GTATCTGATCTGGCCCAACGATCTTATTCATGGCTTTTCCCAAGAACATTAACCAATGG 1862
 DB 1694 TTACTTGATCTGCTGTAACGATCTAATTCATGGCTTTATCTTGAGCTGTAGCCATTTG 1753
 QY 1863 TGAAGATTTAGCGGAATGCCGACATTTTGTATTCCTGTTTCCAGATGGGGTGTGGCTT 1922
 DB 1754 TGAAGATGTGACGGGATGCCACATTTTGTATTCCTGTTTCCAGATGGGTGTGGTGT 1813
 QY 1923 TGACTATGCTGCTGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
 DB 1814 TGACTATGCTGCTGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1873
 QY 1983 TGAGGATTTGAGAGTGGGTGATATTTGTTATACACTGACAAATAGAGATGTTGCGGAAA 2042
 DB 1874 CGAATATGGAATGGGTGATATTCCTGACACCTTAAACGAATAGAGTGGTGCAGAGAA 1933
 QY 2043 GTGTGTTTCATGCTGAAAGTCAATGATCAAGCTCTAGTCTGCTGATGATGATGATGATGATGAT 2102
 DB 1934 GTGTGTTTACTATGACAGAAAGTCAATGACCAAGCACTAGTGGTGGTACAGACATATGATGAT 1993
 QY 2103 CTGGCTGATGACCAAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
 DB 1994 CTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2053
 QY 2163 AATAGATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
 DB 2054 CATGATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2113
 QY 2223 AGAAGGTACTTAAATTTTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 2282
 DB 2114 CGAAGGTATCTTAAATTTTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 2173
 QY 2283 TAGGGCTGAACACACCTCTCTGATGCTCAGTAATTTCCGGAACCAATTCAGTATGA 2342
 DB 2174 AAGAGGCCCGCAAGTCTTCCAAATGCTGCTTCCAGAGAAACCAATACAGTTTGA 2233
 QY 2343 TAAATGACAGGAGATTTGACCTGGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 2402
 DB 2234 TAAATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2293
 QY 2403 AGAATTTGACCGGCTATGAGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2462

Db 2294 AGAGTTTGATCAGGCCATGCGATCTTGAGGAAAAATATGGATTCAIGACATCTGAGCA 2353
 QY 2463 CCAGTTTCATATCAGAAAGATCAAGAGATAGGATGATGATTTGAAAGAAACCT 2522
 Db 2354 CCAGTATATATCGCGAAACACAGAGAGATAGGATGATCTTCCGAGAGAGATTT 2413
 QY 2523 AGTTTTTGCTTTAAATTTTCACTCGACAAAAAGCTATTCAGACTATCGCATAGGCTGGCT 2582
 Db 2414 GGTATTCGTCTCAACTTCCACTGGAGTATAGCTATTTTGATATCGCGTCGGTGT 2473
 QY 2583 GAAGCCTGGAATAATACAGGTTGCCCTTGAGCTCAGATGATCCACTTTTGGTGGCTCGG 2642
 Db 2474 AAAGCCTGGAAGTACAAGATTTGTTGACTCAGACGATGGCTCTTTGGTGGATTGAG 2533
 QY 2643 GAGAAATTGATCAATGCGGAATGTTTACCTTTTGAGGATGATGATGATGCTGCTCG 2702
 Db 2534 TCGCTTGATCATGATGCTGAGTACTGCTGACTGGCCGATGACAAACAGACCAIG 2593
 QY 2703 TTCAATTATGTTGATGACCTAGTAGAAGACAGTGGTCTATGCACTAGTAGACAAAGA 2762
 Db 2594 TTCAATTCGGTGTACACCCCAAGCAGACCGCGTGTGTATGCACTTACAGAGGACTA 2653
 QY 2763 AGAAGAG 2770
 Db 2654 ATGATCAG 2661

RESULT 15

AAQ3750
 ID AAQ3750 standard; cDNA to mRNA; 2919 BP.

AC AAQ3750;

DT 05-JUL-1995 (first entry)

XX Rice starch branching enzyme.

XX Starch branching enzyme; rice; starch content; ds.

XX Oryza sativa.

XX Key Location/Qualifiers

FT 5'UTR 1..127

FT /*tag= a

FT transit_peptide 128..322

FT /*tag= b

FT mat_peptide 323..2606

FT /*tag= c

FT /product= branching_enzyme

FT 2603..2919

FT /*tag= d

XX JP06261767-A.

XX 20-SEP-1994.

XX 22-OCT-1993; 93JP-0265171.

XX 29-OCT-1992; 92JP-0291719.

XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

XX WPI; 1994-337418/42.

XX P-PSDB; AAR60811.

XX New gene of branching enzyme of rice starch - useful for increasing starch yield of rice grains

XX Claim 1; Page 9-12; 13pp; Japanese.

XX The rice starch branching enzyme is encoded by the cDNA sequence AAQ3750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants.

XX Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;
 SQ Query Match 39.9%; Score 1260.4; DB 15; Length 2919;
 Best Local Similarity 74.6%; Pred. No. 0;
 Matches 1582; Conservative 1; Mismatches 537; Indels 0; Gaps 0;
 QY 659 TTATGTATGATCTGATPAGATCAGAGAGAGGGGCATCCCTCCACCPGGACTTGGTCAGA 718
 Db 504 TTGAAGAATATAGTGTCTGAGCAGAAACACAGAGTTGTCCCAACACAGAGATGGGCAA 563
 QY 719 AGATTATGAATAGACCCCTTTTGACAAACTATCTCAACACTTGTACAGGTAT 778
 Db 564 AAATATCCAGATGGACTCTATGCTTAATGGCTAATAGTACCATTCCTTGAATATCGATA 623
 QY 779 CACAGTACAAGAAATGAGGGAGCAATTCACAAAGTATGAGGGTGGTGGTGGAGCTTTT 838
 Db 624 GCATATAGGAGACTCGCTTCAGACATTCATCAGTATGAGGAGGACTGGAACATTTT 683
 QY 839 CTGCTGGTTATGAAAAATGGTTTCACTGCTAGTGTCTACAGTATCACTTACCGTGT 898
 Db 684 CTCGCGTTATGAGAGTTTGGATTTAATCACAGTGTCTGAAGGTGTCACTTATCGAAT 743
 QY 899 GGGCTCCTGTGCCCCAGTCACTGCTCTCATTTGGAGATTTCAACAATTTGGACCAATG 958
 Db 744 GGGCTCCCGGGGCACATTCGACAGCATTAGTGTGACTTCAACAATTTGAATCCAAATG 803
 QY 959 CTCACATTTACTCGGCAATGAAATTTGGTGTCTGGAGATTTTCTGCCAAATAATG 1018
 Db 804 CAGACCGCATGAGCAAAAATGAGTTGGTGTCTGGAGATTTTCTGCCAAATAATG 863
 QY 1019 ATGTTTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACCGATGCACTTCAATC 1078
 Db 864 ATGGCTCATCTCTTATCCACATGGCTCAGCTTAAAGTGTGAAATGAACTCCATCTG 923
 QY 1079 GTGTTAAGGATTCCTCTCTGGATCACTTCTTACAGTTCCTTCGATGAAATTC 1138
 Db 924 GTATAAGGATTTCTATCTCTGGATCACTTCTGTCAGGAGGCGGAGGAAATCC 983
 QY 1139 CATATAATGGAATATATTAATGATCCACCGAGAGAGAGGTATGTTCTTCAACACCCAC 1198
 Db 984 CATACATGGAATATATATATGATCTCTGAGAGAGAGATACATATTCACGATCCTC 1043
 QY 1199 GGCCAAAGAAACCAAGTCTGAGATATATGAACTCAATGTAATGTAATGTAATGTCGG 1258
 Db 1044 AACCTAAAGACCAAAAGTCAATTCGGATATACGAACTCATGTGGAATGAGTAGCAGG 1103
 QY 1259 AGCTTAAATTAATCATAGTCAATTTTATGATGAAATTCCTTCGATGAAATTC 1318
 Db 1104 AGCCAAAGATCAACAGCTATGCAAACTTTAGGATGAGGTCTTCCAGAAATCAAAAGC 1163
 QY 1319 TTGGTACATGCGGTGCAAAATATGCTATTCAGAGCATTTCTTATGCTAGTTTG 1378
 Db 1164 TTGGATACATGCAATTAATGCAATTTCAAGAGCATGATATATGGAAGCTTG 1223
 QY 1379 GTATCATGTCACAAATTTTTCACCAAGAGCGCTTTTGAACGCCCGAGACCTTA 1438
 Db 1224 GTTACCATGTCCAAATTTCTTTGACCAAGTATGCTTTGCGGACCCCAAGAGATTAA 1283
 QY 1439 AGTCTTTGATTAAGCTTCATGAGCTAGGAATTTGTTCTTCATGAGCATTTGTTTCA 1498
 Db 1284 AGTCATGATTAAGCTCAAGCTTGGTTTGTGCTGCTAGGATGTTGTTTCA 1343
 QY 1499 GCCATGCATCAAAATATCTTTAGTGGACTGAACATGTTTACGCGACAGATAGTTGT 1558
 Db 1344 GCCATGCGTCAAAATATACCTAGATGGTTTGAACGTTTGTGATGTACAGATACCAAT 1403
 QY 1559 ACTTTCACCTGAGCTGCTGTTATCATGATGATGAGTGGGATTCGCCCTCTTTAATG 1618
 Db 1404 ACTTTCATAGTGGTTTCAAGCGGCATCATGGAATGGAATTCGCCCTTTTCAACTATG 1463
 QY 1619 GAACTGGGAGGTACTTAGTATCTTCTCAATGCGATGCTGTTGGATGAGTGCA 1678

Db 1464 GGAATGGGAAGTTCCTAAGATTCTACTATCCAAATGCAAGATGGTGGCTCGAGGAGTATA 1523

QY 1679 AATTTGRTGGATTAGATTGGTGGTGCACATCAATGATGTATCTACTCACCACGGATTAT 1738

Db 1524 AGTTTGAUGGTTTCAGATTGACGGTGAACCTCAATGATGTACACTCATCATGTGATAC 1583

QY 1739 CGGTGGGATTCACCTGGGAACCTACGAGGAATACTTTGGACTCGCAACTGATGRTGATCGT 1798

Db 1584 AAGTAGCAATTTACGGGGAACCTACAGTGAATACTTTGGATTGCGCACTGATGTCGACG 1643

QY 1799 CCGTGTATCTGATGCTGGCCACAGATCTTATTCATGGGCTTTTCCAGATGCAATTAACA 1858

Db 1644 TAGTTACTGTGATGCTGTAATGATTTAAATTCATGGACTTTATCCTGAGGCCATAACCA 1703

QY 1859 TTTGGCTCAAGATGTTAGCGAATCCGACATTTTGTATCCCGTTCAAGATGGGGGTGTTG 1918

Db 1704 TCGGTGAAGATGTCAGTGGAAATGCCATATTTGCCCTTCCTGTTCAAGATGGTGGGTTG 1763

QY 1919 GCTTTGACTATCGGCTGCATATGGCAATTCCTGATAAATGGATTTGGATTCCTCAAGAAAC 1978

Db 1764 GTTTTGATTTATCGCCTTCATATGGCTGTTCCCTGACAAATGGATTGAACCTCCTCAAGCAA 1823

QY 1979 GGGATCAGGATTTGGAGATGGGTGATATTTGTTTCATACACTGACAAATAGCAATGCTCGG 2038

Db 1824 GTGATGAATCTTGGAGATGGGTGATATTTGTGCACACACTGACTAACAGAAGGTGTCAG 1883

QY 2039 AAAAGTGTCTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAG 2098

Db 1884 AGAAGTGTCTTACTTATGCTGAAGATCATGATCAAGCACTAGTGGTGACAAAACPATTTG 1943

QY 2099 CATCTGGCTGATGGACAAAGGATATGTATGATTTTATGCTTTGATAGCTAGACCCGTCAACAT 2158

Db 1944 CATCTGGTGTGACAAAGGATATGTATGATTTTATGGCTCTGGACAGACCCGGCAACAC 2003

QY 2159 CATTAAATAGATCGTGGATAGCATTCACAAAGATGATTAGGCTTTGTAACATATGGGATTAG 2218

Db 2004 CTAGCAATTCATCGTGAATAGCATTCGATAAATGATATAGACTTATCACAATGGGGTTAG 2063

QY 2219 GAGGAGAGGGTACCTTAATTTTCATGGGAAATGAATTCGCCACCCTGAGTGGATTGATT 2278

Db 2064 GAGGAGAGGCTATCTTAATTTATGGGAAATGAGTTCGGACATCCTGAATGGATTGATT 2123

QY 2279 TCCCTAGGCTGAACAAACACCTCTCTGATGGCTCAGTAATTCGCCGAAACCAATTCAGTT 2338

Db 2124 TTCCAAGAGCTCCCAAGTACTTCCAATGGTAAATTCATCCAGGGGAATAACAACAGTT 2183

QY 2339 ATGATAAATGCAGACGAGATTTGACCTGSGAGATGCAGAAATTTAAGATACCGTGGGT 2398

Db 2184 ATGATAAATGCGGTCGAAGATTGACCTGGGTGATGCGGACTATCTTAGGTATCGTGGCA 2243

QY 2399 TGCAAGAATTTGACCGGGCTATGCACTATCTTGAGATAAATGATGATTTTATCACTTCAG 2458

Db 2244 TGCTAGAGTTTCACCGCGGGATGAGTCTCTCGAGGAAAATATGGGTTCAATGACATCAG 2303

QY 2459 AACACAGTTTCATACCAAAAGGATGAAGAGATAGGATGATTGTTTGAAGAAAGGAA 2518

Db 2304 ACCACAGTACATATCTCGAAAGCAGTGAAGAGATGAAGATGATTATATTTGAGAGGGAG 2363

QY 2519 ACCTAGTTTTCGTTTAAATTTTCACTGACAAAAGCTTTCAGACTATCGCATAGGCT 2578

Db 2364 ATCTGGTATTTGTTTCACTTCCATTTGGAGTAAACAGCTATTTTGACTACCGGTGTTGTT 2423

QY 2579 GGCCTGAAGCCTGAAATACAAAGTTTGCCTTGGCTGAGCTCAGATCCACTTTTGTGGCT 2638

Db 2424 GTTTAAAGCCAGGAAATATAAGTGGTCTTGGCTCAGATGCTGGACTCTTTGGTGGAT 2483

QY 2639 TCGGGAGATTTGATCATATATCGGAATGTTTACCTTTGAAGATGCTGATGATCGTTC 2698

Db 2484 TTGGCAGGATTCATCACACTGGACAGCACTTTCCTGCCGATTGTTCAATGACAAACAGGC 2543

QY 2699 CTCGTTCAATTTATGTTGATGACACCTAGTAGAAGCAGTGGTCTATGCACTAGTAGACA 2758

Db 2544 CTTACTCGTCTCAGTTTATCTCCTAGCAGACCTGGCTTGTCTATGCTCCAGCGGAAT 2603

QY 2759 AAGAAGAAGAAGAAGAA 2778
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Db 2604 GAGAACACCAAGAGGCAGCA 2623

Search completed: July 5, 2003, 13:51:51
Job time : 674.636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:31:27 ; Search time 137.619 Seconds
(without alignments)
7032.959 Million cell updates/sec

Title: US-10-056-454a-18_COPY_45_3200
Perfect score: 3156
Sequence: 1 AAAACCTCCCTCACTCAGT.....TGCCTGATCAATGATGTTT 3156

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2.6/ptodata/1/ina/PCUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2955.2	93.6	3074	4	US-09-087-277-1 Sequence 1, Appli
2	2955.2	93.6	3074	4	US-09-087-277-1 Sequence 1, Appli
3	1372.2	43.5	1393	4	US-09-087-277-3 Sequence 3, Appli
4	1372.2	43.5	1393	4	US-09-087-277-3 Sequence 3, Appli
5	1200.4	38.0	2665	4	US-09-257-894-1 Sequence 1, Appli
6	1200.4	38.0	2725	3	US-08-941-445A-14 Sequence 14, Appli
7	1049.8	33.3	2087	4	US-09-257-894-9 Sequence 9, Appli
8	1048.2	33.2	2165	4	US-09-257-894-8 Sequence 8, Appli
9	637.4	20.2	2128	3	US-08-716-449-1 Sequence 1, Appli
10	632.4	20.0	2487	4	US-09-257-894-19 Sequence 19, Appli
11	632.4	20.0	2565	4	US-09-257-894-24 Sequence 24, Appli
12	632.4	20.0	2763	3	US-08-941-445A-16 Sequence 16, Appli
13	632.4	20.0	2772	4	US-09-257-894-12 Sequence 12, Appli
14	623.2	19.7	2909	4	US-08-104-158-1 Sequence 1, Appli
15	546	17.3	1809	4	US-09-257-894-25 Sequence 25, Appli
16	546	17.3	1865	4	US-09-257-894-20 Sequence 20, Appli
17	371.6	11.8	11478	3	US-08-381-803-29 Sequence 29, Appli
18	371.6	11.8	11478	4	US-08-381-803-29 Sequence 29, Appli
19	358.2	11.3	5402	4	US-09-221-017B-194 Sequence 194, App
20	107	3.4	414	4	US-09-257-894-2 Sequence 2, Appli
21	70.6	2.2	2426	4	US-08-528-0260-3 Sequence 3, Appli
22	63.2	2.0	4403765	4	US-09-103-840A-2 Sequence 2, Appli
23	63.2	2.0	4411529	4	US-09-103-840A-1 Sequence 1, Appli
24	56.8	1.8	7218	1	US-08-232-463-14 Sequence 14, Appli
25	54.6	1.7	571	4	US-09-257-894-16 Sequence 16, Appli
26	53.8	1.7	16442	3	US-08-781-891-208 Sequence 208, App
27	51.4	1.6	5394	3	US-08-688-376-1 Sequence 1, Appli

C 28	49.4	1.6	188	1	US-08-115-497-21	Sequence 21, Appli
C 29	49.4	1.6	188	1	US-08-466-670-21	Sequence 21, Appli
C 30	49.4	1.6	188	2	US-08-291-011-1	Sequence 1, Appli
C 31	49.4	1.6	188	4	US-09-266-065-1	Sequence 1, Appli
C 32	49.4	1.6	405	2	US-08-299-074A-1	Sequence 1, Appli
C 33	49.4	1.6	405	4	US-09-399-773-1	Sequence 1, Appli
C 34	46.8	1.5	252	2	US-08-623-906A-1	Sequence 1, Appli
C 35	46.6	1.5	661	3	US-08-961-083-77	Sequence 77, Appli
C 36	46.6	1.5	11384	4	US-08-961-527-45	Sequence 45, Appli
C 37	46.4	1.5	6701	4	US-09-004-838-107	Sequence 107, App
C 38	46.4	1.5	43795	3	US-08-742-185-101	Sequence 101, App
C 39	45.8	1.5	2100	1	US-07-927-316A-1	Sequence 1, Appli
C 40	45.2	1.4	3211	2	US-08-574-959A-8	Sequence 8, Appli
C 41	45.2	1.4	3211	4	US-09-357-014-8	Sequence 8, Appli
C 42	45.2	1.4	3901	2	US-08-574-959A-6	Sequence 6, Appli
C 43	45.2	1.4	3901	4	US-09-357-014-6	Sequence 6, Appli
C 44	45	1.4	2691	4	US-09-298-924-5	Sequence 5, Appli
C 45	43.2	1.4	3337	1	US-08-072-610-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-087-277-1
Sequence 1, Application US/09087277B

Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bell gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189)...(2825)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189)...(332)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)...(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)...(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)...(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:

see recent 3, ver 1
Vire date

PO
LATE

QY	774	GTATTTCAGTACAAAGAAAATCAGGAGGCAATTGACAAGTATGAGGTGGTTTGAAGC	8333
Db	779	GTATTTCAGTACAAAGAAAATCAGGAGGCAATTGACAAGTATGAGGTGGTTTGAAGC	838
QY	834	TTTWTTCGTGGTTANGAAAAAANGGGTTTCACCTCGTAGTCTACAGGTATCATTACCG	893
Db	839	TTTWTTCGTGGTTANGAAAAAANGGGTTTCACCTCGTAGTCTACAGGTATCATTACCG	898
QY	894	TGAGTGGGCTCCTGGTGCCCACTCAGCTGCTCTCATTTGGAGATTTTCAACAATTGGAGCGC	953
Db	899	TGAGTGGGCTCCTGGTGCCCACTCAGCTGCTCTCATTTGGAGATTTTCAACAATTGGAGCGC	958
QY	954	AAATGCTGACATTAATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAATAAA	1013
Db	959	AAATGCTGACATTAATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAATAAA	1018
QY	1014	TGTCGATGGTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACCGATGGACATTC	1073
Db	1019	TGTCGATGGTCTCCTGCAATTCCTCATGGGTCCAGAGTGAAGATACCGATGGACATTC	1078
QY	1074	ATCAGGTGTTAAGGATTCCTTCCTGCTGGATCAACTACCTCTTTACAGCTTCCTGATGA	1133
Db	1079	ATCAGGTGTTAAGGATTCCTTCCTGCTGGATCAACTACCTCTTTACAGCTTCCTGATGA	1138
QY	1134	AAATCCATATAATGGAATATAATTAATGATCCACCGAGAGAGAGGTAATGCTTCCCAACA	1193
Db	1139	AAATCCATATAATGGAATATAATTAATGATCCACCGAGAGAGAGGTAATGCTTCCCAACA	1198
QY	1194	CCCACGGCCAAAGAAAACCAAGTCGCTCAGATAATATGAATCTCATATTTGGAATGAGTAG	1253
Db	1199	CCCACGGCCAAAGAAAACCAAGTCGCTCAGATAATATGAATCTCATATTTGGAATGAGTAG	1258
QY	1254	TCCGGAGGCTTAAATTAATCTCATACGTGAATTTTAGAGATGAAGTCTTCTCTCGATAAAA	1313
Db	1259	TCCGGAGGCTTAAATTAATCTCATACGTGAATTTTAGAGATGAAGTCTTCTCTCGATAAAA	1318
QY	1314	AAACCTTTGGGTACAAATCGGGTGCAAAATTTATGGCTATTCAACAGCATCTTATATGCTAG	1373
Db	1319	AAACCTTTGGGTACAAATCGGGTGCAAAATTTATGGCTATTCAACAGCATCTTATATGCTAG	1378
QY	1374	TTTWTGGTTATCATGTCAAAATTTTWTGACCAAGCAGCCGTTTGTGAAGCCCGCAGGA	1433
Db	1379	TTTWTGGTTATCATGTCAAAATTTTWTGACCAAGCAGCCGTTTGTGAAGCCCGCAGGA	1438
QY	1434	CCTTAAGCTTTTGATTCGATAAAGCTCATGAGTAGGATTTGTTGTTCTCATGGAGATTTG	1493
Db	1439	CCTTAAGCTTTTGATTCGATAAAGCTCATGAGTAGGATTTGTTGTTCTCATGGAGATTTG	1498
QY	1494	TCACAGCCATGCATCAAAATAATCTTTAGATGGACTGAACATGTTTGACGGCACAGATAG	1553
Db	1499	TCACAGCCATGCATCAAAATAATCTTTAGATGGACTGAACATGTTTGACGGCACAGATAG	1558
QY	1554	TTGTTACTTTTCACTCTGGAGCTCGTGTTTATCATTTGGATTTGGGATTTCCCGCCTCTTTAA	1613
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QY	1614	CTATGGAACCTGGGAGTACTTAGGTATCTTCTCTCAAAATCGGAGATGGTGGTGGATGA	1673
Db	1619	CTATGGAACCTGGGAGTACTTAGGTATCTTCTCTCAAAATCGGAGATGGTGGTGGATGA	1678
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Db	1679	GTCCAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGATTACTCACCACGG	1738
QY	1734	ATTATCGGTGGGATTCACCTGGGAACACTACGAGGAATACTTTTGGACTCGCAACTCATGTRGA	1793
Db	1739	ATTATCGGTGGGATTCACCTGGGAACACTACGAGGAATACTTTTGGACTCGCAACTCATGTRGA	1798
QY	1794	TGCTGGCGGTATCTGATGCTGGCCAAAGATCTTATTCATFGGGCTTTTCCAGATGCAAT	1853
Db	1799	TGCTGGTGTGTATCTGATGCTGGTCAACGATCTTATTCATFGGGCTTTTCCAGATGCAAT	1858

QY 1854 TACCATTCGCTGAAGATGTTACGGGAATGCCGACATTTTGTATTCCTGTTCAAGATGGGG 1913
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QY 1914 TGTGGCTTTGACATATCGCTGCTATATGCAATTCCTGATAAATGGATTGAGTTCTCTCAA 1973
DB 1919 TGTGGCTTTGACATATCGCTGCTATATGCAATTCCTGATAAATGGATTGAGTTCTCTCAA 1978
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DB 2219 ATTAGAGGAGAGGTTACCTAAATTTTCATGGGAATGAATTCGGCCACCCCTGAGTGGAT 2278
QY 2274 TGATTTCCCTAGGGCTGAACACACCTCTCTGATGGCTCAGTAATTCCTGGGAACCAAT 2333
DB 2279 TGATTTCCCTAGGGCTGAACACACCTCTCTGATGGCTCAGTAATTCCTGGGAACCAAT 2338
QY 2334 CAGTTATGATAATGCAGCGGAGATTTGACCTGGGAGATGCAGATAATTTAAGATACGG 2393
DB 2339 CAGTTATGATAATGCAGCGGAGATTTGACCTGGGAGATGCAGATAATTTAAGATACGG 2398
QY 2394 TGGGTTGCAAGATTTGACCGGGCTATGCAGTATCTTGAAGATAATATGATTTATGAC 2453
DB 2399 TGGGTTGCAAGATTTGACCGGGCTATGCAGTATCTTGAAGATAATATGATTTATGAC 2458
QY 2454 TTCAGAACACCAAGTTTCATATCAGAAAGGATGAAGGATAGGATGATTGATTGAAAA 2513
DB 2459 TTCAGAACACCAAGTTTCATATCAGAAAGGATGAAGGATAGGATGATTGATTGAAAA 2518
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DB 2519 AGGAACCTAGTTTGTCTTTAATTTTCTACCTGGACAAAAGCTATTCAGACTATCGCAT 2578
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DB 2579 AGGCTGGCTGAAGCTGGAAAAATACAAGTTGCTTGGACTCAGATGATCCACTTTTGG 2638
QY 2634 TGGCTTCGGGAGAAATGATCAATAGCCGAATGTTTCACTTTGAAGGATGTTATGATGA 2693
DB 2639 TGGCTTCGGGAGAAATGATCAATAGCCGAATGTTTCACTTTGAAGGATGTTATGATGA 2698
QY 2694 TGGCTTCGTTCAATATGTTGATGACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2753
DB 2699 TGGCTTCGTTCAATATGTTGATGACCTAGTAGAACAGCAGTGGTCTATGCACTAGT 2758
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DB 2759 AGACAAGAGAGAGAGAGAGAGAGAGAGTAGTAGTAGAGAGAGTAGTAGTAGAAGA 2818
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DB 2819 AGAATGAAGCAACTTGTGTCGGTTGAAAGATTTGAAGCTACATAGAGCTTCTTGACG 2878
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DB 2879 TATCTGGCAATATGCAATCAGTCTTGGCGGAATTTCAATGACAAAGGTTTCAATCT 2938
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DB 2939 TTCCACTATATAGTAGTGCACAGGATATACCGCAGAGATGAAGTGTGACAAACATATGTAA 2998
QY 2991 AATCGATGAATTTATGTCGAATTCCTGGGACGGCTTCACGAGTTTTCCTAGTGTTC 3050
DB 2999 AATCGATGAATTTATGTCGAATTCCTGGGACGGCTTCACGAGTTTTCCTAGTGTTC 3058
QY 3051 TGTAAATTCATCTC 3066
DB 3059 TGTAAATTCATCTC 3074

RESULT 2
US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: beii gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

[illegible][illegible]

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Db 2159 AACATCATTAATAGATCGTGGATAGCATTCACAAAGATGATTAGGCTTGTAACATATGGG 2218
QY 2214 ATTAGGAGGAAGGTCACCTTAATTTCTATGGGAATGAATTCGCGCCACCTTGATGGAT 2273
Db 2219 ATTAGGAGGAAGGTCACCTTAATTTCTATGGGAATGAATTCGCGCCACCTTGATGGAT 2278
QY 2274 TGATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTCGCGGAACCAAT 2333
Db 2279 TGATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTCGCGGAACCAAT 2338
QY 2334 CAGTTATGATAAATGCAGCGGAGATTTGACCTGGGAGATGAGATAATTTTAAGATACGG 2393
Db 2339 CAGTTATGATAAATGCAGCGGAGATTTGACCTGGGAGATGAGATAATTTTAAGATACGG 2398
QY 2394 TGGGTTGCAAGNAATTTGACCGGCTATGCGATATCTTGAAGATAAATATGATTTATGAC 2453
Db 2399 TGGGTTGCAAGNAATTTGACCGGCTATGCGATATCTTGAAGATAAATATGATTTATGAC 2458
QY 2454 TTCAGAACACCATGTTTCATATCACGAAAGGATGAAGAGATAGATGATTTGTAATAA 2513
Db 2459 TTCAGAACACCATGTTTCATATCACGAAAGGATGAAGAGATAGATGATTTGTAATAA 2518
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QY 2634 TGGCTTCGGGAGATTTGATCAATATCCGAAATGTTTCACTTTGAAGGATGATGATGA 2693
Db 2639 TGGCTTCGGGAGATTTGATCAATATCCGAAATGTTTCACTTTGAAGGATGATGATGA 2698
QY 2694 TGGTCTCGTTCAATATGTTGATGACCTAGTAGACAGCAGTGGCTATGACCTAGT 2753
Db 2699 TGGTCTCGTTCAATATGTTGATGACCTAGTAGACAGCAGTGGCTATGACCTAGT 2758
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QY 2811 AGAATGAACGAACCTTGTGATCGCTTGAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
Db 2819 AGAATGAACGAACCTTGTGATCGCTTGAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878
QY 2871 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTGACAAAAGGTTTGCATTTCT 2930
Db 2879 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTGACAAAAGGTTTGCATTTCT 2938
QY 2931 TTCCACTATTAGTAGTGAACCATATACGACAGATGAAGTGTGACAAACAAATATGTAA 2990
Db 2939 TTCCACTATTAGTAGTGAACCATATACGACAGATGAAGTGTGACAAACAAATATGTAA 2998
QY 2991 AATCGATGAATTTATGCGAATGCTGGGACGGGCTTACGAGGTTTGTCTAGTAGGTTTC 3050
Db 2999 AATCGATGAATTTATGCGAATGCTGGGACGGGCTTACGAGGTTTGTCTAGTAGGTTTC 3058
QY 3051 TGTAAATTTGTCATC 3066
Db 3059 TGTAAATTTGTCATC 3074
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RESULT 3

US-09-087-277-3

; Sequence 3, Application US/09087277B

; Patent No. 6169226

; GENERAL INFORMATION:

; APPLICANT: EK, BO

```
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Cläs-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-09-087-277-3
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Query Match

43.5%; Score 1372.2; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

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QY 1122 GCTTCCTGATGAATTTCCATATATATGAATATATATGATCCACCGAGAGAGGTA 1181
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Db 841 CCCAGATGCAATTTACATTTGTTGAAGATGTTAGCGGAATGCGACATTTTGTATCCCGT 900
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Db 901 TCAAGATGGGTGTTGGCTTTGACTATCGGCTGCATATGSCAAATGCTGATAAATGGAT 960
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Db 961 TGAGTGTCTCAAGAACGGATGAGGATGAGATGAGATGAGTGGTATATTTGCATACACTGAC 2021
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QY 2202 TGTAACTATGGATTAGGAGAGAAGGTACCTAAATTTTCATGGGAAATGAATTCGGCCA 2261
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QY 2262 CCCGAGTGGATTCATTTCCCTAGGCTGACACACACCTCTCTGATGCTCAGTAATTC 2321
Db 1261 CCCGAGTGGATTCATTTCCCTAGGCTGACACACACCTCTCTGATGCTCAGTAATTC 1320
QY 2322 CGGAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGATA 2381
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Db 1381 TTTAAGTACCGT 1393

RESULT 4

US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; NAME/KEY: misc.feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc.feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc.feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc.feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

Query Match 43.5%; Score 1372.2; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1002 TCTGCCAAATAATGTGGATGTTCTCTGCAATTCCTCATGCGTCCAGATGAAGATACG 1061
Db 1 TCTGCCAAATAATGTGGATGTTCTCTGCAATTCCTCATGCGTCCAGATGAAGATACG 60
QY 1062 CATGACACTTCATCAGGIGITTAAGATTCCTGCTGGATCACTACTCTTTACA 1121
Db 61 TATGGACATTCATCAGGIGITTAAGATTCCTGCTGGATCACTACTCTTTACA 120
QY 1122 GCTTCTGATGAAATTCATATAATGGAATATATGATCATCCCGAGAGAGAGTA 1181
Db 121 GCTTCTGATGAAATTCATATAATGGAATATATGATCATCCCGAGAGAGAGTA 180
QY 1182 TGTCTTCCACACCCACCGCCAAAGAACCCAAAGTCCGTGAGATATATGATCTCATAT 1241
Db 181 TATCTTCCACACCCACCGCCAAAGAACCCAAAGTCCGTGAGATATATGATCTCATAT 240
QY 1242 TGGATGAGTACTCCGGAGCCCTAAATTAACATCACTACGTGATTTAGATGAAGTCTCT 1301

Db 241 TGGAAATGAGTATCGCGAGCCAAAATTAACATACAGGAAATTTAGAGATGAAGTTCT 300
QY 1302 TCCTCGCAATAAAACCTTGGGTACAAATCGCGTGCAGAAATATGGTATTCACAGAGCATTC 1361
Db 301 TCCTCGCAATAAAAGCTTGGGTACAAATCGCGTGCAGAAATATGGTATTCACAGAGCATTC 360
QY 1362 TTATTATGCTAGTTTGGTTATCATGTGCACAAATTTTTTGGCAACAGAGCCGTTTGG 1421
Db 361 TTATTATGCTAGTTTGGTTATCATGTGCACAAATTTTTTGGCAACAGAGCCGTTTGA 420
QY 1422 AACGCCGACGACCTTAAGTCTTTGATGATAAGCTCATGAGTAAATTTGCTTCT 1481
Db 421 AACNCCGACGACCTTAAGTCTTTGATGATAAGCTCATGAGTAAATTTGCTTCT 480
QY 1482 CATGGACATTTGTTACAGCATCATCAATTAATCTTTAGTGGACTGAACATGTTTGA 1541
Db 481 CATGGACATTTGTTACAGCATCATCAATTAATCTTTAGTGGACTGAACATGTTTGA 540
QY 1542 CGGCACAGATAGTTTACTTCTCTGGAGCTCGTGGTTATCATGATGATGGGATTC 1601
Db 541 CGGCACAGATAGTTTACTTCTCTGGAGCTCGTGGTTATCATGATGATGGGATTC 600
QY 1602 CGGCTCTTTAACTATGAACTGGAGCTACTTAGGTATCTTCTCAAAATGCGAGATG 1661
Db 601 CGGCTCTTTAACTATGAACTGGAGCTACTTAGGTATCTTCTCAAAATGCGAGATG 660
QY 1662 GTGGTTGGATGAGTGCAAATTTGRTGGATTTAGATTTGATGTTGACATCAATGATGA 1721
Db 661 GTGGTTGGATGAGTGCAAATTTGATGATTTAGATTTGATGTTGACATCAATGATGA 720
QY 1722 TACTCACCAGCATATCGTGGGATTCCTCTGGAGTACAGGAAATATCTTTGGACTCGC 1781
Db 721 TACTCACCAGCATATCGTGGGATTCCTCTGGAGTACAGGAAATATCTTTGGACTCGC 780
QY 1782 AACTGATGPRGATGCTGCGTGTATCTGATGCTGGCCACAGATCTTATTCATGGGCTTT 1841
Db 781 AACTGATGPRGATGCTGCTGTGTAICTGATGCTGGTCAAGATCTTATTCATGGGCTTT 840
QY 1842 CCAGATGCAATACCAATTTGGTGAAGATTTAGCGGAATCGCGACATTTGTTATCCCGT 1901
Db 841 CCAGATGCAATACCAATTTGGTGAAGATTTAGCGGAATCGCGACATTTGTTATCCCGT 900
QY 1902 TCAAGATGGGTTGGCTTTGACTATCGGCTGCATATGGCAATTCCTGATAAATGGAT 1961
Db 901 TCAAGATGGGTTGGCTTTGACTATCGGCTGCATATGGCAATTCCTGATAAATGGAT 960
QY 1962 TGAGTTGCTCAAGAAACGGGATGAGGATGGAGTGGGTGATTTGTTCAATACACTGAC 2021
Db 961 TGAGTTGCTCAAGAAACGGGATGAGGATGGAGTGGGTGATTTGTTCAATACACTGAC 1020
QY 2022 AAATGAGATGGTGGGAAAGTGTTCATACGCTGAAAGTCATGATCAAGCTTAGT 2081
Db 1021 AAATGAGATGGTGGGAAAGTGTTCATACGCTGAAAGTCATGATCAAGCTTAGT 1080
QY 2082 CGGTGATAAACTATAGCTTCTGGCTGATGACAGGATGATGATGATTTATGCTTT 2141
Db 1081 CGGTGATAAACTATAGCTTCTGGCTGATGACAGGATGATGATGATTTATGCTTT 1140
QY 2142 GGATGACCGCTCAACATCATTAATAGATCGTGGGATAGCATTCGCAAGATGATAGGCT 2201
Db 1141 GGATGACCGCTCAACATCATTAATAGATCGTGGGATAGCATTCGCAAGATGATAGGCT 1200
QY 2202 TGTAACTATGGGATAGGAGGAGAGGTACCTTAATTTCAATGGGAAATGAATTCGGCCA 2261
Db 1201 TGTAACTATGGGATAGGAGGAGAGGTACCTTAATTTCAATGGGAAATGAATTCGGCCA 1260
QY 2262 CCTGAGTGGATGATTTCCCTAGGCTGACACACACCTCTCTGATGGCTCAGTAATTC 2321
Db 1261 CCTGAGTGGATGATTTCCCTAGGCTGACACACACCTCTCTGATGGCTCAGTAATTC 1320
QY 2322 CGGAAACCAATTCAGTTATGATAAATGCGACAGGATTTGACCTGGGAGATCAGAATA 2381

Db 1321 CGGAACCAATTCAGTTATGATAAATGCGACAGGATTTGACCTGGGAGATCAGAATA 1380
QY 2382 TTTAAGATACCGT 2394
Db 1381 TTTAAGATACCGT 1393
RESULT 5
US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: E. I. du Pont de Nemours and Company
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 79..2476
; US-09-257-894-1
Query Match 38.0%; Score 1200.4; DB 4; Length 2665;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 1534; Conservative 2; Mismatches 558; Indels 0; Gaps 0;
QY 663 TGAATGATCTGATAGATGATCAGAGAGGAGGCGATCCCTCCACCTGGACTTGGTCAGAGAT 722
Db 381 TGAATGATCTGATAGATGATCAGAGAGTTCGAGTGGTCCGCCACCAAGCGATGGACAAAAAT 440
QY 723 TTAAGAAATAGACCCCTTTTGACAACTATCGTCACACCTTGTGATTACAGGTATTCACA 782
Db 441 ATTCCAGATTGACCCCATGTTGCAAGCTATAAGTACCATCTTGGATGATCGTACAGCCT 500
QY 783 GTACAGAAATAGAGGAGGCAATTCAGAGTATGAGGGTGGTGGTGGAGCTTTTTCG 842
Db 501 CTATAGAGATCCGTTACACATGTATGACATGAGGAGGCTTGGAGCCCTTCTCCG 560

QY	843	TGTTATGAAAAATGGTTTTCAC	TCTAGTGTACAGGTATCAC	TTTACCGTGA	TGGCGG	902	
Db	561	TAGTTATGAGAAGTTTGGATTT	AATGCGACGGGAAGGTAT	CACATATCG	AAATGGCG	620	
QY	903	TCCTGTTGCCACGACGTCTC	ATTCATTTGAGATTTCAACA	AAATTTGGACGCAAA	TCTGA	962	
Db	621	TCCTGGAGCATTTTCTCG	ACGATTTGGTGGTACTTC	ACACAC	TGGGATCCAA	680	
QY	963	CATTATGACTCGGGAATGA	ATTTGGTCTCGGAGATTTT	CTGCCAAAT	AATGTGATGG	1022	
Db	681	TCGTATGAGCAAAAATG	ATTTGGTGTTTGGAAAT	TTTTCTG	CTTAACAATGC	740	
QY	1023	TTCTCTTGCAATTCCTCAT	GGGTCCAGAGTGAAGATAC	GCATGGACACTT	CTATCAGTGT	1082	
Db	741	TACATCACCATTTCTCAT	GGATCTCGTGTAAAGGTG	AGAAATGGATCT	CCATCAGGAT	800	
QY	1083	TAGGATTCCTACTCTCTT	GGATCAACTACTCTTTAC	AGTTCCTCATGAAAT	TCACATA	1142	
Db	801	AAAGGATTCATCCAC	CTGGATCAAGTACTCAG	TCAGCGCCCGCAG	AGAAATACCAT	860	
QY	1143	TANTGGAAATATATGAT	CCACCCGAGAGAGAGGT	ATGTCTTCCAA	CACCCACGGCC	1202	
Db	861	TGATGGGATTTATGAT	CTCTGTAAGAGGTAAG	TATGTGTTCAGG	CATGCGCAACC	920	
QY	1203	AAAGAAACCAAGTCGTG	AGATATATGATCTCAT	ATTGGAAATGAGT	AGTTCGGAGCC	1262	
Db	921	TAAACGACCAAAATCAT	TGGGATATATGAACACA	CAATGTCGAA	TGAGTACGCCGGAACC	980	
QY	1263	TAAAAATTAACCTAC	GTGAATTTAGAGATGA	AGTTTCTCTCGCAT	ATAAAAACCTTG	1322	
Db	981	GAAGATAAACACATAT	GTAACTTTAGGATGA	AGTCTCC	CCAGAAATATAAA	1040	
QY	1323	GTACATGCGGTGCA	AAATATGCTATTC	CAAGACATTTAT	TATCTAGTTTGGTTA	1382	
Db	1041	ATACAATGTCAGTGC	AAAATATGGAATCC	CAAGACACTAT	TATGGAAGCTTTGGATA	1100	
QY	1383	TCATGTCACAAATTTTT	TGCACCAAGCACGCG	CTTTGGACGCGG	CAGACCTTAAGTC	1442	
Db	1101	CCAATGAACATAA	TTTTTTCGCCAGTAG	CTGTTTGGTACCC	CCAGAAATTTGAAGTC	1160	
QY	1443	TTTGATGTAPAAAG	CTCATGAGCTAG	GAATTTGTCTCATG	ACAATTTTCCACAGCCA	1502	
Db	1161	TTTGATGTATAGAC	ACATGAGCTTGG	TTTCTAGTTC	TCATGSAATGCTGTTCCATAGTCA	1220	
QY	1503	TGCAATCAAAATAA	ACTTTAGATGCACTG	ACAATGTTT	GAGGCGACAGATAGTTGTTACTT	1562	
Db	1221	TGCGTCAAGTAATAC	TCTGGAATGGTGTGA	TGTTTGTATG	GTGTACAGATACACATTA	1280	
QY	1563	TCACTCTGGAGCTG	TGTTATCATTTGGAT	TGGGATTC	CGGCTCTTTAACTATGAAA	1622	
Db	1281	TCAGTGGTCCAGT	GGCCATCACATG	GAATGCGGAT	CTCGGCTATTTAACTATGGGAA	1340	
QY	1623	CTGGGAGGTACTT	AGTATCTTCTC	CAATGCGAGATG	GTGTTGATGGAATGAGTGC	1682	
Db	1341	CTGGGAAGTTTAA	GATTTCTCTC	CCAATGCTAG	ATGSGTGCCTGAGGAAATTAAGTT	1400	
QY	1683	TGRTGATTTAGATTT	TGATGCTGTGACAT	CAATGATG	TATATCWCACACAGGATATCGGT	1742	
Db	1401	TGATGTTTCCGTTT	TGATGCTGTACCT	CCATGATGTAC	ACTATC	ACACGAGTACAA	1460
QY	1743	GGCATTCAC	TGGAACTAC	TTCGAC	TGCGCAACTGATG	ATGCTGCCGT	1802
Db	1461	ARCAATTTACGGG	AACTTCAATG	AGATTTTGGCTT	TGGCCAGGATGATG	CACTGTT	1520
QY	1803	GTAATCATG	CTGGCCAAAGAT	CTTATCATG	GGCTTTTCCAGATG	CAATACCATTTG	1862
Db	1521	TTACTTGATG	CTGGTAAATGAT	CTAATCAT	GAGCTTTATCTG	TGAGGCTGTAA	1580
QY	1863	TGAAGATGTTAG	CGGAATGCCACAT	TTTTGTAT	TCCGTTCAAGAT	GGGGGTGTTGGCTT	1922
Db	1581	TGAAGATGTTAG	TGGAATGCTACAT	TTTTGCCCTCTG	TTCAGATG	GGTGGGATGTTT	1640

QY	1923	TGACTATCGCGTGCATATGGCAATTGCTGATAAATGGAATGAGTTGCTCAGAACAACGGGA	1982
Db	1641	TGACTATCGGATGATATGGCTGTGGGTGACAAATGGATTTACCTTCTCAAGCAAAAGTGA	1700
QY	1983	TGAGGATTTGGAGATGGGTGATATGTTCTATACACTCACAAATAGAGATGGTCGGAAAA	2042
Db	1701	TGAACCTTGGGAAGATGGTGATATGTGACACACTGACAAATAGGAGGTGGTTAGAGAA	1760
QY	2043	GTGTGTTTCATACGCTCAAACTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCAATT	2102
Db	1761	GTGTGTAACCTTATGCTCAAACTCATGATCAAGCANTAGTCGGGCACAAGACTATTGGGTT	1820
QY	2103	CTGCGTGATGGACAAGAPATGATGATTTTATGCGTTTGGCTTGGATAGACCGTCAACATCAATT	2162
Db	1821	TTGTGTATGGACAAGGATATGTAATGATTTTCATGGCCCTCGATAGACCTTCAACTCCTAC	1880
QY	2163	AATAGATCGTGGGATAGCAATGCAACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGG	2222
Db	1881	CATTGATCGTGGGATAGCAATACATAGATGATTAGACTTATCACATGGGTTTAGAGG	1940
QY	2223	AGAAGGATACCTAAATTTTCATGGGAAATGAATTCGGCCACCCAGTGGGATTGATTTCC	2282
Db	1941	AGAGGGCTATCTTAATTTTCATGGGAAATGAGTTTGGACATCTCTGAATGGATGATTTTC	2000
QY	2283	TAGGSCGTGAACAACACCTCTCTGATGCTCAGTAAATTTCCCGGAAACCAATTCAGTTATGA	2342
Db	2001	AAGAGGTCCGAAAGACTTCCAAGTGTGATGTTATTTCCAGGGAATTAACACAGTTATGA	2060
QY	2343	TAAATGCAGACGGAGATTTCACCTGGGAGATGCAGAAATATTAAAGATACCGTGGGTGCA	2402
Db	2061	CAAAATGCTCGAAGATTTCACCTGGGTGATGCAGACTATCTTAGGTATCATGGTATGCA	2120
QY	2403	AGAATTTGACCGGGCTATGCAGTATCTTTGTAAGATATAAATGAGTTTATGACTTTCAGTA	2462
Db	2121	AGATTTTGTATCAGGCAATGCAACATCTWTGASCAAAATATGAATTCATGACATCTGATCA	2180
QY	2463	CCAGTTCATATCAGAAAGGATGAAGGAGATAGGATGATGTTATTTGAAAAAGGAACCT	2522
Db	2181	CCAGTATATTCCCGGAACATGAGGAGGATAGGTGATGTGTGTTCTCGAAAAGGGAGATT	2240
QY	2523	AGTTTTGTCTTTAAATTTTCACTGGACAAAAGCTATTCAGACTATCGCATAGGCTGGCT	2582
Db	2241	GGTATTTGTCTCAACTTCCACTGCAACAACAGCTATTTTGACTACGGTATTTGGTTGTGG	2300
QY	2583	GAAGCCCTGGAAATACAAAGTTGCTTGGACTCAGATGATCCACTTTTTTGGTGGCTTCGG	2642
Db	2301	AAAGCCCTGGGTGTATAAAGTGTGCTTTGGACTCCGACGCTGGACTATTTTGGTGGATTAG	2360
QY	2643	GAGAATTTGATCAATATGCCGAATGTTTCACTTTGAAGGATGGTATGATCATCGTCTCG	2702
Db	2361	CAGGATCCATCAGCAGCCGAGCACITTCACCGCCGACTGTTCGCAATGATAATAGGCCATA	2420
QY	2703	TTCAATTTATGGTGTATGCACCTAGTAGACACAGACAGATGGTCTATGCACACTAGTAGA	2756
Db	2421	TTCACTCTCGGTTTATACACAAGACAGACATGTGCTCTATGTCTCCAGTGGGA	2474

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RESULT 6
US-08-941-445A-14
: Sequence 14, Application US/08941445A
: Patent No. 6107060
: GENERAL INFORMATION:
: APPLICANT: Keeling, Peter
: APPLICANT: Guan, Haining
: TITLE OF INVENTION: Starch Encapsulation
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: Greenlee, Winner and Sullivan
: STREET: 5370 Manhattan Circle
: CITY: Boulder
: STATE: CO
: COUNTRY: US
: ZIP: 80303

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P.
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOPHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 38.0%; Score 1200.4; DB 3; Length 2725;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 1534; Conservative 2; Mismatches 558; Indels 0; Gaps 0;

QY	663	TGATGAATCTGATAGATCAGACAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAGAT	722
DB	393	TGATGTCAGCCCTTGAACAGAGTTCGAGTGGTCCCGCCACCAAGCGATGACAAAAAT	452
QY	723	TTATGAATAGACCCCTTTTGACAACTATCGTCAACACTTGATACAGGTATTCCACA	782
DB	453	ATTCCAGATTGACCCCATGTTGCAAGGCTATAGTACCATCTTGAGTATCGGTACAGCCT	512
QY	783	GTACAAAGAAATGAGGAGGCAATGACAAAGTATGAGGGTGTGGAGCTTTTCTCG	842
DB	513	CTATAGAAGAAATCCGTTACACATATGATGAACATGAAGGAGGCTTGAAGCCCTTC	572
QY	843	TGGTATGAAGAAATGGTTTCTACTCGTAGTGTACAGGTATCACCTACCGTGGTGGC	902
DB	573	TAGTTATGAGAAATTTGGATTTAATGCCGCGGAGGATACACATATCGAATGGGC	632
QY	903	TCTGGTGGCCAGTCAGCTCTCTCAATTGGAGATTTCAACAATTTGGACGCAATGCTGA	962
DB	633	TCTGGAGCATTTCTGCAGCATTTGGTGGTGAGCTCAACACTGGGATCCAAATGCGA	692
QY	963	CATTGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATATATGGTGG	1022
DB	693	TCGTATGAGCAAAATGAGTTGGTGTTCGGAAATTTTCTGCCTAACAAATCCAGATGG	752
QY	1023	TTCTCTGCAATTCCTCATCGGTCCAGAGTGAAGATACCGATGACACATTCATCAGGTG	1082
DB	753	TACATCACCTATTCTCTCATGGATCTCGTGAAGGTGAGAATGGATACCTCCATCAGGAT	812
QY	1083	TAGGATTCCATTCCTGCTTGGATCACTACTCTTTACAGCTTCTTGATGAAATTCATA	1142

DB	813	AAAGGATTCATTCAGCCCTGGATCAAGTACTCAGTCAGGCCGCCAGAGAGAAATACATA	872
QY	1143	TAATGAATATATATGATCCACCGAAGAGGAGGTATGTCTTCAACACCCACCGGCC	1202
DB	873	TGATGGATTTTATGATCTCTCTGAAGAGGTAAGATATGTGTTCAGGCATCGCAACC	932
QY	1203	AAAGAACCAAGTCGCTGAGATATATGATATCATATTTGGAATGATGATCGGAGCC	1262
DB	933	TAAACGACCAAAATCATTTGGGATATATGAACACATGTCGGAATGATGATCGCGAAC	992
QY	1263	TAAATTAACATCATACGTGAATTTAGAGATGAAGTCTTCTCCGCGCATAAACACCTGG	1322
DB	993	GAAGATTAACACATATGTAACATTTAGGATGAAGTCTCCCAAGAAATAAACAACTGG	1052
QY	1323	GTACATCGGTGCAAAATATGCTATTCAAGAGCATTTCTTATATGATCTAGTTGTGA	1382
DB	1053	ATCAATGCAGTGCAAAATATGCAATCCAAAGAGCACTATATATGAAAGCTTGGATA	1112
QY	1383	TCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAGCCGCCACGACCTTAAGTC	1442
DB	1113	CCATGTAACATAATTTTTTGGCCAGTAGTCGTTTTGGTACCCCGAAGATTTGAAGTC	1172
QY	1443	TTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTCTCATGAGCATTTGTTACAGCCA	1502
DB	1173	TTTGATTGATAGACCAATGAGCTGGTTGCTAGTTCTCATGATGGTTCATAGTCA	1232
QY	1503	TGCATCAAAATAACTTTTAGATGAGTGAACATGTTTGAAGGCAAGATAGTTGTTACTT	1562
DB	1233	TGGTCAAGTAATACTCTGAGTGGTGAATGTTTGTATGGTACAGATACACATTAATT	1292
QY	1563	TCACTCTGGAGCTCGTGGTTATCATTTGGATGCGGATTCGCGCTCTTTTACTATGAAA	1622
DB	1293	TCACAGTGGTCCAGTGGCCATCACTGGATGCGGATTCGCGCTATTTTACTATGGAA	1352
QY	1623	CTGGAGGTACTTAGGTATCTTCTCAAAATGCGAGATGGTGGTGGATGAGTCAAAAT	1682
DB	1353	CTGGAGATTTTAAAGATTTCTTCTCAATGCTAGATGGTGGTTCGAGGATATAAGTT	1412
QY	1583	TGRTGATTTAGATTTGATGGTGTGACATCAATGATGATATACACACCGGATTTACGTT	1742
DB	1413	TGATGGTTTCGTTTTGATGTGTGACCTCCATCATGATACACTCACCAGGATTTACAAGT	1472
QY	1743	GGATTCACCTGGGAACTACAGGAAATCTTTGGACTCGCAACTGATGATGATGCTGGCT	1802
DB	1473	AACATTTACGGGAACTCAATGATTTTGGCTTTTGGCCACCGATGTAGATGAGTGGT	1532
QY	1803	GTATCTCATGTGGCCCAACGATCTTATTCATGGGCTTTTCCAGATCAATACCATTTGG	1862
DB	1533	TTACTTGTGCTGTAATGATCTAATTCATGGACTTTATCTCGAGCTGTAACCATTTGG	1592
QY	1863	TGAAGATGTTTAGCGGAATGCGGACATTTTGTATTTCCGTTTCAAGATGGGGTGTGGCTT	1922
DB	1593	TGAAGATGTTTAGTGAATGCTACATTTTGCCTTCTCTGTTCAOGATGGTGGGTAGGTTT	1652
QY	1923	TGACTATCGCTGCATATGCAATTTCTGATAAATGATGATGCTGCTCAGAAACCGGA	1982
DB	1653	TGACTATCGATGCATATGCTGTGGCTGCAAAATGATTTGACCTTCTCAAGCAAAATGA	1712
QY	1983	TGAGGATTTGAGAGAGTGGTGTATTTGTTATACACTCACAATAGAGATGGTGGGAAA	2042
DB	1713	TGAACATTTGAAGATGGTGTATTTGTCACACTCACAATAGAGAGTGGTGTAGAGAA	1772
QY	2043	GTCTGTTTCACTACGCTGAAAGTTCATGATCAAGCTCTAGTCGGTGTATAAACTATAGCAT	2102
DB	1773	GTGTGTAACCTTATCTCTGAAAGTTCATGATCAAGCATTTAGTCGGCGCAAGCATTTGCTT	1832
QY	2103	CTGCTCATGAGCAAGGATATGATGATTTTATGCTTTTGGATGAGCCGTCACATCATTT	2162
DB	1833	TTGTTGATGACAAAGGATATGATGATTTTATGCTGCTGATGATGATGATGATGATGAT	1892
QY	2163	AATAGATCTGGGATAGCATTTGCACAGATGATTTAGCTTGTACTACTGATGATGAGG	2222

Db 1893 CATGTATCGTGGGATAGCAATACATAGATGATTAGACTTATCACAAATGGTTTAGGAGG 1952
QY 2223 AGAAGGTTACCTAAATTCATGGAAATGAATTCGGCCACCCCTGAGTGGATTGATTTCC 2282
Db 1953 AGAGGCTATCTTAATTCATGGAAATGAGTTGGACATCCCTGAATGGATGATTTCC 2012
QY 2283 TAGGCTGTAACACACTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTATGA 2342
Db 2013 AAGAGTCCGCAAGACTCCAAAGTGTAAAGTTTATTCAGGGAATGAACACAGTTATGA 2072
QY 2343 TAAATCAGACGAGGATTTGACCTGGGAGATGAGCAATATTTAAGATACCGTGGTTGCA 2402
Db 2073 CAAATGCTCGAAGATTTGACCTGGGATGAGCAATATTTAAGATACCGTGGTTGCA 2132
QY 2403 AGAATTTGACCGGCTATCAGTATCTTGAAGATAAATATGACTTTATGACTTCAGACA 2462
Db 2133 AGAGTTGATCAGGCAATGCAATCTTGAAGATAAATATGACTTTATGACTTCAGACA 2192
QY 2463 CCAGTTTATATCAACGAAGATGAAGGATGATGATGATGATGATGATGATGATGATGAT 2522
Db 2193 CCAGTATATTCGCGAAACATCAGGAGGATAGGTTGATGATGATGATGATGATGATGAT 2252
QY 2523 ACTTTTGTCTTAATTTTCACTGGACAAAGACTATTCAGACTATTCGATAGGCTGGCT 2582
Db 2253 GGTATTTGTCTTAATTTTCACTGGACAAAGACTATTCAGACTATTCGATAGGCTGGCT 2312
QY 2583 GAAGCTCGGAAATCAAGTTGCTGCTGACTCAGATGATGATGATGATGATGATGATGAT 2642
Db 2313 AAAGCTGGGCTGATAGGTTGCTGCTGACTCAGATGATGATGATGATGATGATGATGAT 2372
QY 2643 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2702
Db 2373 CAGGATCCATCAGCAGCGGAGCACTTCACGCGGACTGTTGCTGATGATGATGATGATGAT 2432
QY 2703 TTCAATTTAGTGTATGACCTAGTAGACAGCAGTGGTCTATGACTAGTAGA 2756
Db 2433 TTCAATTCGTTTATACCAAGCAGACATGTCGCTATGCTCCAGTGA 2486

RESULT 7

US-09-257-894-9

: Sequence 9, Application US/09257894

: Patent No. 6376749

: GENERAL INFORMATION:

: APPLICANT: Broglie, Karen E.

: APPLICANT: Klein, Theodore M.

: APPLICANT: Hubbard, Natalie L.

: APPLICANT: Lightner, Jonathan E.

: TITLE OF INVENTION: No. 6376749el Starches via Modification of

: TITLE OF INVENTION: Expression of Starch Biosynthesis

: NUMBER OF SEQUENCES: 25

: CORRESPONDENCE ADDRESS:

: ADDRESS: E. I. du Pont de Nemours and Company

: CITY: Wilmington

: STATE: Delaware

: COUNTRY: USA

: ZIP: 19898

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: OPERATING SYSTEM: Microsoft Windows 95

: SOFTWARE: Version 7.0A

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/257,894

: FILING DATE:

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 09/091,052

: FILING DATE: JUNE 10, 1998

: ATTORNEY/AGENT INFORMATION:

: NAME: Majarian, William R.

: REGISTRATION NUMBER: 41,173
: REFERENCE/DOCKET NUMBER: BB-1066-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 302-992-4926
: TELEFAX: 302-773-0164
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2087 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-257-894-9

Query Match 33.3%; Score 1049.8; DB 4; Length 2087;

Best Local Similarity 74.2%; Pred. No. 4.3e-308;

Matches 1324; Conservative 2; Mismatches 459; Indels 0; Gaps 0;

QY 663 TGATGATCTGATAGGATCAGAGAGGGGCATCCCTCCACCTGGGACTTGTGTCAGAGAT 722
Db 303 TGATGCTCAAGCCTTGNACAGAGTTCGAGTGGTCCCCCACCACAGCGATGACAAAAAT 362
QY 723 TTATGAATAGACCCCTTTTGACAAACTATCGTCAACACCTTTGATTACAGGATTCACA 782
Db 363 ATTCCAGATTGACCCCATGTTGCAAGGCTATAAGTACCATCTTGGTATCGGTACAGCCT 422
QY 783 GTACAAGAAATCAGGAGGACCAATTGACAAGTATGAGGGTGGTTTGAAGCTTTTCTCG 842
Db 423 CTATAGAAGAAATCCGTTACAGACATTTGATGAACATGAAGSAGGCTTGAAGCCTTCTCCCG 482
QY 843 TGGTTATGAAAAAATGGGTTTCACTCGTAGTGTACAGGTATCACTTACCCTGAGTGGC 902
Db 483 TAGTTATGAGAAATTTGGATTTAATGCCAGCGGAGGATACATATCGAATGAGGCG 542
QY 903 TCTGTGTCACCTAGCTGCTCTCATTTGAGATTTTCAACAATTTGGGACCAAAATGCTGA 962
Db 543 TCTGTGAGCAATTTTCTGCAGCATTTGTTGGGTGACTTCAACAACCTGGGATCCAAATGCGA 602
QY 963 CATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAAATTAATGATGG 1022
Db 603 TCGFATGAGCAAAAAATGAGTTTGGTGTGGGAAATTTTCTGCCTAACATCCAGATGG 662
QY 1023 TCTCCTGTCAATTCCTCATGGGTCACAGAGTGAAGATACGCAATGACACCTTCATCAGGTGT 1082
Db 663 TACATCACCTATTTCCTCATGGAATCTCGTGTAAAGGTGAGAATGATACTCCATCAGGAT 722
QY 1083 TANGGATTCACCTCTCTTGGATCACTACTCTTTACAGCTTCTTCCATGAATAATCCATA 1142
Db 723 AAAGGATTCAAATTCAGCCCTGGATCAAGTACTCAGTCCAGGCCCCCAGGAGAAATACCAT 782
QY 1143 TATGGAATATATTATGATCCACCGAAGAGAGAGGTATGTCTTCCATGCAATAAAACCTGG 1202
Db 783 TGAATGGATTTATTAATGATCCTCTGAGAGGTAAAGTATGTTTTCAGGATCGGCAACC 842
QY 1203 AAAGAAACCAACTCGCTGAGATATATGAAATCTCATATTGGAAATGAGTATCGGAGCC 1262
Db 843 TAAACGACCAAAATCATTCGGATATATGAACACATGTCGGAATGAGTAGAGCCGGAACC 902
QY 1263 TAAATTAATCACTCATAGTGAATTTAGAGATGAAGTCTTCTCCATGCAATAAAACCTGG 1322
Db 903 GAAGATAACACATATGTAACCTTTAGGGATGAAGTCTTCCCAAGAAATAAAAAATTTGG 962
QY 1323 GTACATGGGGTGCAAAATATGCTATTCAAGAGCATTTCTTATGATGATGATGATGATGAT 1382
Db 963 ATACATGTCAGTGAATATGCAATATGCAATCCAGAGCACTCATATATGAGAGCTTTGGATA 1022
QY 1383 TCATGTCACAAATTTTGGACCAAGCAGCCGTTTGGACAGCCCGCCGACGCTTAAGTC 1442
Db 1023 CCATGTAACATAATTTTGGCGCAAGTAGTCTGTTGGTGTACCCAGAGAGATTGAAGTC 1082
QY 1443 TTTGATTGATAAGCTCATGAGTGAAGTGTGTTCTCATGAGCACTTTGTTTCACAGCCA 1502
Db 1083 TTTGATTGATAGACACATGAGCTTGGTTGCTAGTGTCTCATGAGTGTGTTTCATAGTCA 1142

QY	1503	TGCATCAAAATAACTTTAGATGAGCATGCAACATGTTTGACGGCACAGATAGTTGTACTT	1561
Db	1143	TGCGTCAAGTAACTCTGGATGGGTTGAATGGTTTATGGTTACAGATACACATTACTT	1202
QY	1563	TCACTCTGGAGCTGCTGGTTATCATTTGGATGTGGGATTCGGCCTCTTTAACTATGAAA	1622
Db	1203	TCACATGTGTCACGTGGCCATCACTGGATGTGGGATTCGGCTATTTAACTATGGAA	1262
QY	1623	CTGGGAGGTACTTAGGTATCTCTCAAAATGGAGATGGTGGTTGGATGAGTGCAAAT	1682
Db	1263	CTGGGAAGTTTAAAGATTTCTCTCCTCAAGTGTAGATGGTGTGGAGATATAAATT	1322
QY	1683	TGRTGGATTTAGATTTTCATGTGTGATCAATATGATATATACACACGAGATATACGGT	1742
Db	1323	TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACACGGAATTACAAGT	1382
QY	1743	GGGATTCACATGGGAACACTACGAGGAATACITTTGSACTCGCAACTGTATGTGATGCTGCGGT	1802
Db	1383	AACATTTACGGGAACTTCAATGAGTATTTTGCTTTGCCACCGATGTAGATGCACTGGT	1442
QY	1803	GTATCTGATCTGGCCAAACGATCTTATCATGGCTTTTCCACAGATGCAATTACCAATGG	1862
Db	1443	TTACTTGAAGCTGCTAAATGATCTAATCTAGCACTTTATCTGAGGCTGTACCAATGG	1502
QY	1863	TGAAGATGTTAGCGGAATGCCGACATTTGTATTCCGCTCAAGATGGGGTGTGGCTT	1922
Db	1503	TGAAGATGTTAGTGGAAATGCTTACATTTGCCCTTCTGTTACAGATGGTGGGCTAGGTTT	1562
QY	1923	TGACTATCGGCTGCATATGCCAATTCGCTGATTAATGGATAGTTGCTCAAGAAACGGGA	1982
Db	1563	TGACTATCGGATGCATATGGCTGTGGCTGCACAAATGATGACCTTCTCAAGCAAAAGTGA	1622
QY	1983	TGAGGATGTGAGAGTGGGTGATATGTTCTATACACTGCACAAATAGAAAGATGGTCGAAAA	2042
Db	1623	TGAACCTTGAAGATGGGTGATATTGTCACACACTGCACAAATAGGAGGTGGTTAGAGAA	1682
QY	2043	GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCATT	2102
Db	1683	GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGGGTT	1742
QY	2103	CTGGCTGATGGCAAGGATATGATGATTTATGGCTTTGGATAGACCGTCAACATCATTT	2162
Db	1743	TTGGTTGATGGCAAGGATATGATGATTTATGTCGCTCGATAGACCTTCAACTCTCTAC	1802
QY	2163	AATAGATCGTGGGATAGCATTGCACAAAGATGATTAGGCTTGTAACATATGGGATTAGGAGG	2222
Db	1803	CAITGATCTGGGATAGCATTACATAGATGATTAAGCTTATCACAATGGGTTTAGAGG	1862
QY	2223	AGAAGGTACTTAATTTCAATGGGAATGAATTCGGCCACCTCGAGTGGATGATTTCCTCC	2282
Db	1863	AGAGGGCTATCTTAATTTCAATGGGAATGAGTTTGGACATCCCTGAATGGATATTTCC	1922
QY	2283	TAGGGCTGAACAACACCTCTCTGATGCTCAGTAATTCGGGAAACCAATTCAGTTATGA	2342
Db	1923	AGAGGTCCGAAGACTTCCAAGTGGTAAGTTTATTCCAGGGAATTAACACAGTTATGA	1982
QY	2343	TAAATCAGACCGGAGATTTGACCTGGGAGATGCAGAAATATTTAAGATACCGTGGGTTGCA	2402
Db	1983	CAAAATGCTGCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATCGTATGCA	2042
QY	2403	AGAAATTCACCGGGCTATGCAGTATCTTGAAGATAAATATGAGTT	2447
Db	2043	AGATTTTATGACGCAATGCAATCTTGACGCAAAATATCAATT	2087

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1  APPLICANT: Hubbard, Natalie L.
2  APPLICANT: Lightner, Jonathan E.
3  TITLE OF INVENTION: No. 6376749e1 Starches via Mod
4  TITLE OF INVENTION: Expression of Starch Biosynth
5  TITLE OF INVENTION: Enzyme Genes
6  NUMBER OF SEQUENCES: 25
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: E. I. du Pont de Nemours and Company
9  STREET: 1007 Market Street
10 CITY: Wilmington
11 STATE: Delaware
12 COUNTRY: USA
13 ZIP: 19898
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC Compatible
17 OPERATING SYSTEM: Microsoft Windows 95
18 SOFTWARE: Version 7.0A
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/257,894
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 09/091,052
25 FILING DATE: JUNE 10, 1998
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Majarian, William R.
28 REGISTRATION NUMBER: 41,173
29 REFERENCE/DOCKET NUMBER: BB-1066-A
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 302-992-4326
32 TELEFAX: 302-773-0164
33 INFORMATION FOR SEQ ID NO: 8:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 2165 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: DNA (genomic)
40 US-09-257-894--8

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Query Match	33.2%	Score 1048.2	DB 4	Length 2165
Best Local Similarity	74.1%	Pred. No. 1.4e-307		
Matches 1323	Conservative 2	Mismatches 460	Indels 0	Gaps 0
Qy	663	TGATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTCGACTTGGTCAGAGAAT	722	
Db	1785	TGATGCTCAAGCCTTGAACAGAGTTCAGATGGTCCCCCACCACCATGGACAAAAAT	1726	
Qy	723	TTATGAATATGACCCCCCTTTTGGACAACTATPCGTTCACACCTTGATTCACAGGTATTCACA	782	
Db	1725	AITCCAGATTGACCCCATGTTGCAAGGCTATAAGTAGCATCTTGAGTATCGGTACAGCCT	1666	
Qy	783	GTACAAAGAAATATGAGGGAGGCAATTGACAGTATGAGGGTGGTTTGGAACTTTTCTCG	842	
Db	1665	CTATAGAGAAATCCGTTTCAGACATGATGACATGAAGAGGCGTTGGAAGCCTTCCTCCG	1606	
Qy	843	TGTTATCAAAAAATGGGTTTCTACTCGTAGTGTCTACAGGTATCACTTACCCTGAGTGGC	902	
Db	1605	TAGTTATGAGAAGTTTGGATTTAATGCCAGCGCGAAGTATACATATCGAAGTGGC	1546	
Qy	903	TCTCGTGGCCAGTCAGCTCTCATTTGGAGATTTCAACAATTTGGACCAATGCTGA	962	
Db	1545	TCCTGGAGCATTTTCTCGACATTGGTGGGTGAGCTCAACACCTGGGATCCAATGCAGA	1486	
Qy	963	CATTATGACTCGGAAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATTAATGTGATGG	1022	
Db	1485	TCGTTATGAGCAAAAATGATGGTTTGGTGTGGGAAATTTTCTGCCTAACATGCAGATGG	1426	
Qy	1023	TTCTCCGCAATTCCTCATGGGTCAGATGCAAGATACGATGACACTTTCATCAGGTGT	1082	
Db	1425	TACATCACCATTTCCTCATGATCTCGTGTAAAGGTGAGATGATCTCTCATCAGGAT	1366	

RESULT 8
US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.

1083 TAAGGATTCATCTCCCTGCTGGATCAACTACTCTTTACAGCTTCCTGATGAATAATCCATA 1142
1365 AAAGGATTAATTCAGCTGGATCAAGTACTCAGTGCAGGCCAGGAGAAATACCA 1306
1143 TAATGAATATATATATGATCCACCCGAGAGAGAGATGCTTCCACACACCCAGGCC 1202
1305 TGAAGGATTAATATGATCCCTGCTGAGAGGTAAGATGCTTCCAGGATCGGCAACC 1246
1203 AAGAAACCAAGTCTGCTGAGATATATGAATCTCATATTTGGAATGAGTAGTCCGGAGCC 1262
1245 TAAACGACCAAAATCATTCGGGATATATGAACACATGTCGGAATGAGTAGCCGCAACC 1186
1263 TAAATTAATCATATGCTGAATTTAGAGATGAAGTCTTCCCTGCGATATAAAACCTTGG 1322
1185 GAAGATTAACACATATGTAACCTTTAGGATGAAGTCTCCCAAGATATAAAACCTTGG 1126
1323 GTACAATGGGTGCAAAATATGCTATTCAGAGCATCTTATATGCTAGTTTGGTTA 1382
1125 ATACAATGAGTGCAGAAATATGGAATCCAGAGCACTCATATATGGAAGCTTTGGATA 1066
1383 TCAATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTGGAACCCGCGACACCTTAAGTC 1442
1065 CCATGTAACATAATTTTTTGGCCAGTAGTCTGTTTTGTACCCAGAGATTTAGTC 1006
1443 TTGATGATGAAGTCACTAGCTAGGATTTGTTGTCATGAGCAATGTTCCACAGCCA 1502
1005 TTGATGATGAGACACATGAGCTGGTTGTTGCTAGTCTCATGATGTTGTTATAGTCA 946
1503 TGCATCAATAATATCTTTAGATGAGCTGAACATGTTTACGGGACAGATAGTTGTTACTT 1562
945 TCCGTCACGATATCTCTGGATGGTGTGATGGTTTGAATGTTGATGATGATGATGATGAT 886
1563 TCACCTCTGAGCTCGTGGTTATCATGATGAGTGGGATCCCGCTCTTTAACTATGAAA 1622
885 TCACAGTGTCCACGTCGACCTACTGGATGTTGGATTTCTGCGCTATTTAACTATGGAA 826
1623 CTGGAGGTAATCTAGTATCTCTCAATCCGAGATGTTGTTGATGAGTGCAGTAAAT 1682
825 CTGGAGGATTTAAGATTTCTCTCCAACTGATAGTGGTCTGAGGATATAGTT 766
1683 TGTGATTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
765 TGATGTTTCCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706
1743 GGGATCTAGGACTAGGAGATATCTTTGAGTTCGCACTGCACTGATGATGATGATGATGAT 1802
705 AACATTTACGGGAACTTCAATGATGATTTTGGCTTTCGACCGATGATGATGATGATGAT 646
1803 GTATCTGATGCTGCGCAAGATCTTATTCATGCTGCTTTCCAGATGCAATTACCATGG 1862
645 TTACTTGATGCTGGTAATGATCTAATTCATGCACTTTATCTGAGGCTGTAACCATGG 586
1863 TGAAGATTTAGCGGAATCCGACATTTTGTATTCCTGCTCAAGATGGGGTGTGGCTT 1922
585 TGAAGATTTAGTGAATGCTTACATTTGCCCTTCTGTTACGATGGTGGGTAGTTT 526
1923 TGACTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
525 TGACTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 466
1983 TGAGCATTTGAGAGTGGTGTATTTTCATGCACTGCAATAGAGATGATGATGATGATGATGAT 2042
465 TGAACCTTGGAGATGGTGTATTTGTCACACTGACAAATAGAGGATGATGATGATGATGAT 406
2043 GTGTGTTTATACGCTGAAGTCAATGATCAAGCTAGTCGCTGATAAACTATAGCAAT 2102
405 GTGTGTAATGCTGAAGTCAATGATCAAGCTAGTCGCTGATAAACTATAGCAAT 346
2103 CTGGCTGATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
345 TTGGTTGATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 286
2163 AATAGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222

285 CATGATCGTGGATAGCAATACATAAGATGATAGACTTATCAATGGTTTGGAGG 226
2223 AGAAGGTACTATAATTTTCAATGAGGAATGAATTCGGCCACCCTGAGTGGATGATTTCCC 2282
225 AGAGGGCTATCTTAATTTTCAATGAGGAATGAATTTGGACATCTCTGAATGGATGATTTCC 166
2283 TAGGGTGAACAACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTATGA 2342
165 AAGAGTCCCAAGACTTCCAAGTGTAGTTTATTCAGGGGATGACACAGTTATGA 106
2343 TAAATCAGACGAGATTTGACCTGGGAGATGAGAGATATTTAAGATACCGTGGGTTGCA 2402
105 CAAATGCTGCTGAAGATTTCACTGGGTGATGACACTATCTTAGTATCATGATGATGCA 46
2403 AGAATTTGACCGGCTGATGAGTATCTTGAAGATAAATAGATT 2447
45 AGAGTTGATCAGGCAATGCAACATCTTGAGCAAAATATGAAT 1

RESULT 9

US-08-716-449-1

; Sequence 1, Application US/08716449
; Patent No. 6103893
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment
; APPLICANT: Holding Corporation
; TITLE OF INVENTION: Method for Producing Altered Starch
; TITLE OF INVENTION: Method for Producing Altered Starch
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott & Aylen
; STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
; CITY: Toronto
; STATE: Canada M5K 1H6
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IMB 1.44 MB High Density Diskette
; COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 7.0 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,449
; FILING DATE: FILED CONCURRENTLY HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00634
; FILING DATE: 22.03.95
; ATTORNEY/AGENT INFORMATION:
; NAME: Anita E. Nador
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1552
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 368-2400
; TELEFAX: (416) 363-7246
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA encoding starch branching enzyme
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE: clone 1.2.1 and E2
; ORGANISM: Solanum tuberosum
; STRAIN: cv desiree
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE: mature tuber
; HAPLOTYPE:
; TISSUE TYPE:


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QY 1966 TIGCTCAAGAAACGGGATGA--GGATTGGAGATGGGTGATATGTTTCATACACTGACA 2022
Db 867 TACCTGAAGAATAAAGATGACTCTGAGTGGTCGATGGGTGAATAGCCGATACCTTTGACT 808
QY 2023 AATAGAAGATGGTGGAAAGTGTTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTC 2082
Db 807 AACAGGAGATATCTGAAATAATGATCCGATATGCTGAGAGCCATGATCAGTCTATTGTT 748
QY 2083 GGTGATAAACTATAGCAATTCCTGGTGTATGACACAGGATATGATGATTTTANGCCTTTG 2142
Db 747 GGCACAAACTATATGCAATTCCTGCTGATGACACAGGAAATGTACACTGGATGTGCAGAC 688
QY 2143 GATAGACCGTCAACATCATTAATAGATCGTGGATAGCATGTGCAAGATGATTAGGCTT 2202
Db 687 TTGACGCTGCTTACCTACATTAATGATGATGAGGATGACCTCCAAAGATGATTCACATTC 628
QY 2203 GTAATATGATAGGAGGAGAGGATGACCTTAAATTTTCATGGGAAATGAATTCGGCCAC 2262
Db 627 ATCAATATGGCCCTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTTTGGTCAC 568
QY 2263 CCTGAGTGGAUTGATTTCCCTAGGCTGATGACACACCTCTCTGATGGCTCAGTAATCC 2322
Db 567 CCAGATGGATGATGACTTTCCAAAGAA-----541
QY 2323 GGAACCAATTCAGTTATGATAAATGACAGAGGAGATTGACCTGGGAGATGCAAAATAT 2382
Db 540 GGGACAACTGGAGCTATGATAAATGACAGACAGCTGGAGCTTCTGGACACTGATCAC 481
QY 2383 TTAAGATACCGTGGTTCGACAGAAATTTGACCGGGCTATGACATPCTTGAAGATAAATAT 2442
Db 480 TTGCGGTACAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATT 421
QY 2443 GAGTTTATGACTTCAGACACACCTTATATATCACCAGGATGAAGAGATAGGATGATT 2502
Db 420 TCCCTCTTTCGTCTGAACAGCATGCTCAGCAGCATGACGATGAGGAAAGGTTTATT 361
QY 2503 GTATTGAAAAGGAAACCTAGTTTTTGTCTTTTAAATTTTCACTGGACAAAGAGCTATTCA 2562
Db 360 GTCITTTGAACGTGGAGATTTAGTTTGTCTTTTCAATTTCCATCCCAAGAAACTTACGAG 301
QY 2563 GACTATCCATAGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2622
Db 300 GGCTACAAAGTGGGATGCGATTGCGTGGGAAATACAGAGTAGCCCTGAGCTCTGATGCT 241
QY 2623 CCACCTTTTGGTGGCTTCGGGAGATTTGATCATAATGCGGAATGTTTCACCT 2674
Db 240 CTGGTCTTCGTGGACATGGAGAGACTTGGCCACGACGATGGATCACTTCACTG 189
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RESULT 11

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US-09-257-894-24
; Sequence 24, Application us/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
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; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/091,052
; APPLICATION NUMBER:
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-257-894-24
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Query Match 20.0%; Score 632.4; DB 4; Length 2565;
Best Local Similarity 59.7%; Pred. No. 2.1e-181;
Matches 1178; Conservative 2; Mismatches 738; Indels 54; Gaps 5;
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QY 721 ATTATGAATAGACCCCTTTTGTACAAACTATCTCAACACCTTGTATACAGGTATTCGA 780
Db 253 ATATAGGACCTGGACCCCAAGCTGGAGATATCAAGGACCAATTCAGGTACCGGATGAAA 312
QY 781 CAGTACAGAAATAGAGGAGGCAATTTGACAACTATGAGGTGTTGGAGGCTTTTCT 840
Db 313 AGATTCTAGACAGCAAGAGGATCAATTTGAAGAAATGAGGAGTCTTGAATCTTTTCT 372
QY 841 CGTGTGTATGAAAATAGGTTTTCATCTGCTAGTGTCTACAGGTATCACTTACGTTAGTGG 900
Db 373 AAAGCTATTTGAAATTTGGGATTAACAATAGGATGGAACGTATATCTGTAATGG 432
QY 901 GTCCTGTGTGCCAGTCTGCTCTCAATTTGAGATTTCAACAATTTGGGACCAATATGCT 960
Db 433 GCACCTGTGTGCGAGGAGGAGGAGCTTATTTGCTGACTTCAATGACTGGAATGTTGCAAC 492
QY 961 GACATTATCACTCGGAATCAATTTGCTGCTGGAGATTTTCTGCCAATATATGAT 1020
Db 493 CATAGATGAGGAGGATTAATTTGGTGTGTTGCTGATCAAAAAT---TGACCATGTCAAA 549
QY 1021 GGTTCCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACACTTCAATCAGCT 1080
Db 550 GGGAAACCTGCCATCCCTCACAATTTCCAAGGTTAATTTTCGCTTCTACATGTTGAGTA 609
QY 1081 GTTAAGGATTCATCTCTGCTGGATTCAACTACTCTTTACAGCTTCTCTGATGAAAT--- 1136
Db 610 TGGGTGTGCTGATTTCCAGCAATTTGCTTATGCTGATGCTGTTGATGCCCTCAATTTTGA 669
QY 1137 --TCCATATAATGGAATATATTTATGATCCACCCGAGAGGAGGATGATCTTTCAACAC 1194
Db 670 GCTCCTATGATGGTGTTCATTTGGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
QY 1195 CCACGGCCAAAGAAACCAAAAGTCGCTGAGAATATATGATCTCATATTGGAATGATGATG 1254
Db 730 CCTCGGCTTCAAGGCTGCTGCTCCACGTATCTATGAAGCCCATGTTAGGTATGATGTT 789
QY 1255 CCGGAGCCTTAAATTAACCTCATACGTTGAATTTTAGAGATGAAGTTCTTCTCGCATAAA 1314
Db 790 GAAAAGCCAGCAGTAAAGACATATAGGGAATTTGAGACAAATGTTGTCACGCAATACGA 849
QY 1315 AACCTTGGTACAATGCGGTGCAAAATATGCGTATTTCAAGAGCAATCTTTATATGCTAGT 1374
Db 850 GCAATAAATACACACAGATTCAGTTGATGGAGTATGAGGATTCGCTACTTCTTCT 909
QY 1375 TTGTGTTATCATGTCACAAAATTTTGTGACCAAGCAGCCGTTTGTGACGCGCCGACGAC 1434
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Db 910 TTGGGTACATGTGACAAATTTCTTTGGGGTAGCAGCAGATCAGGCACACACAGAGGAC 969
QY 1435 CTTAAGTCTTTGATTGATTAAGCTCATGAGCTAGGAAATTTGTTCTCTCATGGACATGTT 1494
Db 970 CTCAAATATCTTGTTGATTAAGCAGACATTTGGGGTTTGGAGTTCTGTGATGGATGTGC 1029
QY 1495 CACAGCCATGATCAATAATATCTTTAGATGAGTCAAGCATGTTTGACG-----GC 1545
Db 1030 CATAGCCATGCAAGTAATAATCTCACAGATGGTTTAAATGGCTATGATGTTGACAAAGC 1089
QY 1546 ACAGATAGTTGTTACTTCACTCTGAGCTCGGGTTATCATCATGATGGGATTCGCGC 1605
Db 1090 ACCCAAGAGTCTTATTTTCATCGGGAGATAGAGTTATCAATAAATTTGGGATACGCG 1149
QY 1606 CTCTTAACTATGGAACGAGGAGTACTTAGTATCTCTCTCAATCGGAGATGGTG 1665
Db 1150 CTGTTCACTATGCTAACTGGGAGGTATTAAGTTTCTTCTAACTGAGATATGG 1209
QY 1666 TTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGTTGATGTTGACATCAATGATGAT 1725
Db 1210 TTGGATGAATTCATGTTTTCATGCTTCGATTTGATGGAGTTACATCAATGCTGTATCAT 1269
QY 1726 CACCGAGATTCGTTGGATTCATGAGTCACTGAGTACGAGATACATTTGACATCGCACT 1785
Db 1270 CACCATGGTATCAATGTGGGGTTTACTGGAACCTACCGAGATATTTTCACTTTGGACACA 1329
QY 1786 GATGRTGATGCTGCCGTGATCTGATGCTGGCCCAACGATCTTATTCATGGCTTTTCCCA 1845
Db 1330 GCTGTGGAGCAGTTGTTTACATGATGCTTGAACCATTTAATGACACAACTCTTGCCA 1389
QY 1846 GATGCAATACCATTTGGTGAAGATTTAGCGGAATGCCGACATTTTGTATTCOCGTTCAA 1905
Db 1390 GAAGCAACTGTTGTCTGAAGATGTTTTCAGGCATGCCGTGCTTTGCCGCCAGTTGAT 1449
QY 1906 GATGGGGTGGCTTTGACTATCGCTGCATGCTGCAATGCGCAATGCTGATTAATGGATGAG 1965
Db 1450 GAAGTGGGGTGGCTTTGACTATCCCTGCAATGGCTATCCCTGATAGATGGATGATGAC 1509
QY 1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGTGGGTGATATTTTTCATACACTGACA 2022
Db 1510 TACCTGAAGATAAAGATGACTCTGAGTGTGCTGATGGTGAATAGCGCATCTTTGACT 1569
QY 2023 ATAGAAGATGTCGGAAGTGTGTTTCACTGATGCTGAAGTGAAGTCAATCAAGCTGATGC 2082
Db 1570 AACAGGAGATATACCTGAAATATGATGCTGATGCTGAGAGCATGATCAGTCTATGTT 1629
QY 2083 GGTGATAAACTATAGCATCTGCTGATGAGCAAGGATATGATGATTTTATGGCTTTG 2142
Db 1630 GCGCACAAACTATTTGCAATTTCTCTGATGGAAGGAATGATGATGCTGCAATGTCAGAC 1689
QY 2143 GATAGCCGTCACATCATTAATAGATGCTGGGATAGCATTTGCACAAAGATGATTAGGCTT 2202
Db 1690 TTGCAGCCTGCTTCACTACATTTGATCGAGGATGCTCACTCCAAAGATGATTCATCTC 1749
QY 2203 GTAACTATGGATTAGGAGGAGGAGGATGCTTCACTGATGCTGAAGTGAAGTGAATTCGCGCAC 2262
Db 1750 ATCAATATGGCCCTGGAGGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1809
QY 2263 CCGTATGATGATTTCCCTAGAGGCTGAACAAACCTCTCTGATGGCTCAGTAATTCOC 2322
Db 1810 CCAGATGATGATTTCCAGAGAA----- 1836
QY 2323 GGAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAATAT 2382
Db 1837 GGAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAATAT 1896
QY 2383 TTAAGATACCGTGGTTCAGAAATTTGACCGGCTATGCTGATGCTGATGCTGATGCTGATGCT 2442
Db 1897 TTGGGTACAGTACATGATGCTGTTTGAACCAAGCGATGATGCTGATGCTGATGCTGATGCT 1956
QY 2443 GAGTTTATGACTTCAGAACACCGATTCATATCACGAAAGGATGAAGGAGATAGGATGAT 2502

RESULT 12

US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060

GENERAL INFORMATION:
APPLICANT: Keeling, Peter

APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941,445A

FILING DATE: 30-SEP-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Winner, Ellen P.

REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2763 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ORGANISM: Zea mays

FEATURE:

NAME/KEY: transit_peptide

LOCATION: 2..190

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 191..2467

FEATURE:

NAME/KEY: CDS

LOCATION: 2..2470

US-08-941-445A-16

Query Match

Best Local Similarity

20.0%; Score 632.4; DB 3; Length 2763;

59.7%; Pred. No. 2.2e-181;

;; TITLE OF INVENTION: Enzyme Genes
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: E. I. du Pont de Nemours and Company
;; STREET: 1007 Market Street
;; CITY: Wilmington
;; STATE: Delaware
;; COUNTRY: USA
;; ZIP: 19898
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Microsoft Windows 95
;; SOFTWARE: Version 7.0A
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/257,894
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/091,052
;; FILING DATE: JUNE 10, 1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Majarian, William R.
;; REGISTRATION NUMBER: 41,173
;; REFERENCE/DOCKET NUMBER: BB-1066-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4926
;; TELEFAX: 302-773-0164
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2772 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 49..2580
;; US-09-257-894-12

Query Match 20.0%; Score 632.4; DB 4; Length 2772;
Best Local Similarity 59.7%; Pred. No. 2.2e-181;
Matches 1178; Conservative 2; Mismatches 738; Indels 54; Gaps 5;
QY 721 ATTATGAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATACAGGTATCA 780
DB 364 ATATAGACCTGGACCCCAAGCTGGAGATATCAAGGACCATTTGAGGTACCGGATCAA 423
QY 781 CAGTACAAGAAATGAGGAGGCAATGACAGTATGAGGTGTTGGAGCTTTTCT 840
DB 424 AGATTCTAGAGCAGAAAGATCAATGAAGAAATGAGGAAAGTCTTGAATCTTTTCT 483
QY 841 CGTGGTATGAAATGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTGAGTGG 900
DB 484 AAGGCTATTGAAATTTGGGATTAATACAAATGAGGATGGAAGTATATCGTGAATGG 543
QY 901 GTCCTCGGCGCCAGTCAGCTGCTCATTTGAGATTTCAACAAATGGGACGCAAAATGCT 960
DB 544 GCACCTGCTGGCAGGAGGACAGCTTATGGTGACTTCAATGACTGGATGGTCAAC 603
QY 961 GACATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTTCGCCAATAATGAGAT 1020
DB 604 CATAAGATGAGAAGGATTAATTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 660
QY 1021 GPTTCPCWCAATTCCTCATGGTCCAGAGTCAAGATAGCGATGGACATTCATCAGGT 1080
DB 661 GGGAAACCGCCATCCCTCACAATTCAGGTTAAATTTCCGTTCTACATGGTGAGTA 720
QY 1081 GTTAAGGATTCCTCTGCTGGATCAACTACTTTTACAGCTTCTCTGATGAAT--- 1136
DB 721 TGGGTTGATCGTATTCAGCATTTGATCGTATGAGTGTGATGCTGCTGCTGCTGCTGCT 780
QY 1137 --TCCATATAATGGAATATATATGATCCACCCAGAGAGGATGATGCTTCCACAC 1194

DB 781 GCTCCCTATGATGTTGTTTCATTTGGATCCCTCTCTCTGAAAGGTACACATTTAAGCAT 840
QY 1195 CCACGGCCAAAGAAACCAAGTCTGAGATATATGAAATCTATATGAAATGAGT 1254
DB 841 CCTCGGCTTCAAAAGCTGCTGCTCCAGTATCTATGAAGCCCATGATGAGTGGT 900
QY 1255 CCGAGCTAAATTAATCTCATAGTGAATTTAGAGATGAAGTCTCTCTCGCATAAAA 1314
DB 901 GAAAGCCAGCAGTAAAGCAATATGAGGAATTTGACAGCAATGTTTCCACGATACGA 960
QY 1315 AACCTTGGGTACAAATGGGTGCAAAATATGCTATTCAGAGCATTTCTTATGCTAGT 1374
DB 961 GCAAATAACTACAAACACAGTTCAGTTGATGGCAGTTATGAGCATTCGTACTGCTCT 1020
QY 1375 TTGGTTATCATGTCACAAATTTTTCACCAAGCAGCCGTTTGGAAAGCCCGCAGAC 1434
DB 1021 TTCGGTACCATGTGACAAATTTCTTTGCGGTAGCAGCAGATGAGCAGCAGCAGAG 1080
QY 1435 CTTAAGTCTTTGATTTGATAAAGCTCATGAGTAGGAATGTTGTTCTCATCGGACATGTT 1494
DB 1081 CTCAAATATCTTGTGATAGGCACACAGTTGGTTTGGAGTTCATGATGATGTTGTC 1140
QY 1495 CACAGCATGCATCAATAATATCTTTAGTGGACTGAACATGTTTGACG-----GC 1545
DB 1141 CATAGCCATGCAAGTAAATATGTCACAGATGGTTTAAATGGCTATGATGTTGCAAAAG 1200
QY 1546 ACAGATAGTTGTTACTTTTCTACTCTGAGCTCGTGGTTATCATTTGATGATGTTCCGC 1605
DB 1201 ACCAGAGTCTTATTTTCAITGGGGAGATAGAGTTATCATAACTTTGGGATGATCGG 1260
QY 1606 CTCTTTAACTATGAAACTGGAGTACTTAGTATCTCTCTCAAAATGAGAGATGTTGG 1665
DB 1261 CTGTTCAACTATGCTACTGGAGTATTAAGTTTCTTCTTCTTAACCTGAGATATGG 1320
QY 1666 TTGGATGAGTGCAAATTTGRTGGATTTAGATGTTGATGGTGTGACATCAATGATGAT 1725
DB 1321 TTGGATGATTCATGTTGATGGCTTCCGATTTGATGGATTTACATCAATGCTGTATCAT 1380
QY 1726 CACACGGAATATCGGTGGGATTCACCTGGGAACTACAGGAATATCTTTGGACCTGCAACT 1785
DB 1381 CACCTGGTATCAATGTTGGGTTTACTGGAACTTACCAGGAATATTTTCAAGTTGGACACA 1440
QY 1786 GATGTGATGCTGCCGTGATCTGATCTGCCCAACGATCTTATATGATGGCTTTTCCCA 1845
DB 1441 GCTGTGATGCAGTTGTTTACATGATGCTTTGCAAAACCATTTAATGCAAACTCTTGG 1500
QY 1846 GATGCAATTACCATTTGTTGAGATGTTAGCGGAATGCCGACATTTGATTTCCGTTCAA 1905
DB 1501 GAAGCAACTGTTGTTGCTGAAGATGTTTTCAGGCAATGCCGTCTTTCGCCGCCAGTTGAT 1560
QY 1906 GATGGGGTCTTGGCTTTGACTATCGCTGCATATGCAATGCTGATTAATGATGATGAG 1965
DB 1561 GAAGTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1620
QY 1966 TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGGTGATATTTGTTATACACTGACA 2022
DB 1621 TACCTGAAGAATAAAGATGACTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1680
QY 2023 AATAGAAGTGGTGGGAAAGTGGTTCATACGCTGAAAGTCAATGATGATGATGATGATG 2082
DB 1681 AACAGGAGATATCTGAAATGCAATGCTATGCTGAGAGGATGATGATGATGATGATGAT 1740
QY 2083 GGTGAVAAAACTATGATCTTGGCTCATGGAAGGATATGATGATGATGATGATGATGATG 2142
DB 1741 GGGGACAAACTATGCTATTTCTCTGATGGAAGGAATGATGATGATGATGATGATGATG 1800
QY 2143 GATAGACCGTCAACATCAATTAATGATGCTGGGATGATGATGATGATGATGATGATGATG 2202
DB 1801 TTGAGGCTGCTTCAACCTACAAATGATGAGGAGTTCATCTCCAAAAGATGATGATGATG 1860
QY 2203 GTAACATGGATGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 2262

Db 1861 ATCAATAGCCCTTGGAGTGATGGCTACTTGAATTTTATGGAAATGAGTTGGTGCAC 1920
QY 2263 CTTGAGTGGATTGATTCCTAGGGCTGACACACACTCTCTGATGGCTCAGTAATCCC 2322
Db 1921 CCAGATGGATTGACTTTCCAGAGAA----- 1947
QY 2323 GGAACCAATTCAGTTATGATAATGACAGCGAGATTTGACCTGGGAGATGAGATAT 2382
Db 1948 GGAACCACTGGAGCTATGATAATGACAGCGAGATTTGAGCTGACATGATCAC 2007
QY 2383 TTAAGATACCGTGGTGGTGAAGAAATTTGACCGGCTATGAGTATCTTGAAGATAAATAT 2442
Db 2008 TTGCGGTACAAATGATGATGATGCTTGAACCAAGCATGAATGCGCTCGATGAGATTT 2067
QY 2443 GAGTTATGACTTCAGAACACCATGATATATACAGGAAGATGAAGAGATAGATGATT 2502
Db 2068 TCGTCTTCTTGGTGGTGAAGCAAGCATGCTGACGACATGACGATGAGGAAAGGATTT 2127
QY 2503 GATTTGAAAAGAAACCTAGTTTGTCTTTAAATTTTCACTGGACAAAAGCTATTC 2562
Db 2128 GTCTTGAAGTGGAGATTTAGTTTGTCTTTTCAATTTCAATCCAGAAACTTACGAG 2187
QY 2563 GACTATCGCATAGCTGGCTGAGCGCTGGAAATACAAAGTTGCTTGGACTCAGATGAT 2622
Db 2188 GGTACAAAGTGGATGCGATTTGCTGCGGAAATACAGATAGCCCTGGACTCTGATGCT 2247
QY 2623 CCACCTTTTGGTGGCTTGGGAGAAATGATGATGATGATGATGATGATGATGATGAT 2674
Db 2248 CTGGTCTTGGTGGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGAT 2299

RESULT 14

US-08-104-158-1
Sequence 1, Application US/08104158
Patent No. 6215042
GENERAL INFORMATION:
APPLICANT: Willmitzer, Lothar
APPLICANT: Sonnewald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Franciscus
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
CAUSE CHANGES IN THE CARBOHYDRATE COMPOSITION AND THE
CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
CONTAINING THESE PLASMIDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,158
FILING DATE: 13-AUG-1993
CLASSIFICATION: B00
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Solanum tuberosum cv. Desiree

STRAIN: Desiree

DEVELOPMENTAL STAGE: growing tuber

TISSUE TYPE: tuber

CELL TYPE: total tuber

IMMEDIATE SOURCE:

LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)

FEATURE:

NAME/KEY: CDS

LOCATION: 2..1699

OTHER INFORMATION: /note= "for Branching enzyme I

OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to

OTHER INFORMATION: active potato branching enzyme"

US-08-104-158-1

Query Match

Best Local Similarity 19.78; Score 623.2; DB 4; Length 2909;
Matches 1188; Conservative 1; Mismatches 729; Indels 58; Gaps 7;
QY 731 TAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGTATTCACAGTACAGA 790
Db 165 TGGATCCAACTTTGGAACCTTATCTAGATCATTACACACAGAAATGAGATATG 224
QY 791 AAATGAGGAGCAATGACAAAGTATGAGGTTGTTGGAAGCTTTTCTCGTGGTATG 850
Db 225 ATCAGAAATGCTCAATGAAAAATATGAGGACCCCTTGAGGAATTTGCTCAAGTTAT 284
QY 851 AAAAATGGTTTCACTCGTAGTGTACAGTATCATCTACCTGAGTGGCTGCTGGT 910
Db 285 TAAATTTGGATTACACAGGAAGATGTTGCAATGCTATCTGTAATGAGTGGCTGCTG 344
QY 911 CCAGTACGCTGCTCATTTGGAGATTTCAACAAATGGGACGCAAAATGCTGACATTA 970
Db 345 CACAGGAGCAGAAATTTGGGATTTCAATGTTAGGAGGAGGTTCTAACCATGATG 404
QY 971 CTCGGAATGATTTGGTGTCTGGAGATTTTCTGCCAAATAATGTTGGTGTCTGCTG 1030
Db 405 AGAAGACCAAGTTGGTGTGTTGGAGTATAGAAATTC---TGATGTTGACAGTAAG 461
QY 1031 CAATTCCTCATGGTCCAGATGAAGATGACGATGACATTCATCAGGTGTTAAG---G 1087
Db 462 TCATTCACACAACTCCAGATTAAAGTTTCTGTTTCAACATGTTAAGTGGTGGTAG 521
QY 1088 ATTCCATTCCTGCTGGATCACTACTCTTTACAGTTC---TGATGAATTCAT 1141
Db 522 ATCGTATCCTGCTGGATAAAGTATGCCACTCCAGACGCCAAGATTTGACAGCAAT 581
QY 1142 ATATGATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1201
Db 582 ATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 641
QY 1202 CAAAGAAACCAAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1261
Db 642 CTCCTCAACCCGAGCCCAAGTATGATGATGATGATGATGATGATGATGATGATG 701
QY 1262 CTAAATTAACATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1321
Db 702 CAGGTAAATTCGTAATCGTATGATGATGATGATGATGATGATGATGATGATGAT 761

Db	253	ATATACGACCTGGACCCCAAGCTGGAGATATTCAGGACCAATTCAGGTACCGGATGAAA	1312	Db	1330	GCCTGTGATCAGTGTGTTTACATGAUCGTTTGCAAAACCAATTAATGCAAAACTCTTGCCA	1389
QY	781	CAGTCAAGAAATAGGAGGCAATTCAGAAATATGAGGTGGTTTGAAGCTTTTCT	840	QY	1846	GATGCAATTACCAATTTGTTGAAGATGTTAGCGGAATGCCACATTTTCTGATTTCCCGTCAA	1905
Db	313	AGATTCTAGACGAGAAGGATCAATGGAAGAAATGAGGAAGTCTTGAATCTTTCT	372	Db	1390	GAAGCAACTGTTGTTGCTGAAGATGTTTCAAGCATGCCGCTCTTTCCCGGCAAGTTGAT	1449
QY	841	CGTGGTATGAAAAATGGTTTCACTCGTAGTCTACAGGATACACTTACCGTGAGTG	900	QY	1906	GATGGGGTCTTGGCTTGTACTATCGCTGCAATATGCGCAATTTGCTGATAAATGATGAG	1965
Db	373	AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAATGTATATCGTAATG	432	Db	1450	GAAGGTGGGCTTGGTTGACTATCGCTGGCAATGCTATCCCTGATAGATGATGAC	1509
QY	901	GCTCTGTGTCAGTACGCTGCTCAATGAGATTTCAACAATTTGGAGCGCAATGCT	960	QY	1966	TTGCTCAAGAAACGGGATGA---GGATTGAGAGTGGGTGATATTTTCACTACACTGACA	2022
Db	433	GCACCTGCTGCGCAGGAGCAGACTTATGTTGACTTCAUGACTGGAATGTTGCAAC	492	Db	1510	TACCTGAAGAAATAAGAACTGCTGAGTGGTGGTGAATAGGCACTATTGACT	1569
QY	961	GACATTATGACTCGGAAATGAAATTTGGTGTCTGGAGATTTTTCGCAAAATATGTTGAT	1020	QY	2023	AATAGAAGATGGTGGGAAAAAGTGTGTTTCACTGCTGAAAGTCATGATCAAGCTCTAGTC	2082
Db	493	CATAAGATGAGAAGGATAAATTTGGTGTGTCGATCAAAAT---TGACCATGTCAA	549	Db	1570	AACAGGAGATATCTGAAATAATGCAATGCTGAGAGCCATGATCACTCTATTGTT	1629
QY	1021	GGTCTCCGCAATTCCTCATGGTCCAGAGTCAAGATACGATGACACTTCATCAGGT	1080	QY	2083	GGTATAAATACTATAGCAATTTCTGGCTGATGACAAAGATATGATGATTTTATGGCTTG	2142
Db	550	GGGAACCTGCCATCCCTCACAATCCCAAGGTAAATTTCCGCTTCTACATGGTGGAGTA	609	Db	1630	GGCGACAAACTATTGCTATTTCTCTGATGGCAAGGAAATGTACACTGGCATGTGACAC	1689
QY	1081	GTTAAGATTCATCTCTGCTGGATCAACTACTCTTTACAGCTTCTCTGATCAAAAT---	1136	QY	2143	GATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTCACACAGATGATAGCTT	2202
Db	610	TGGGTTGATCGTATCCAGCATGATTCGTATGCGACTGTTGATGCCCTTAAATTTGGA	669	Db	1690	TTCCAGCCCTGCTTACCTACATTTGATCGAGGATTTGCACTCCAAAGATGATTCATTC	1749
QY	1137	---TCCATATAATGGAATATATATGATCCACCGAGAGGAGGATGCTTTCCAAACAC	1194	QY	2203	GTAACATATGGGATTAGGAGGAGGAGGATGCTAAATTTCAATGGAAATGAATTCGGCCAC	2262
Db	670	GCTCCCTATGATGGTGTTCATGTTGGATCTCTGCTCTGAAAGGTACACATTTAAGCAT	729	Db	1750	ATCACAATGGCCCTTGGAGGTGATGCTACTTCAATTTTATGGAAATGATTTGGTTCAC	1809
QY	1195	CCACGGCCAAAGCAACAAAGTCGCTGAGAATATATGAATCTCATATTTGGAATGATG	1254				
Db	730	CTCTGGCCTTCAGAGCTGCTGCTCCACATATCTATGAAGCCCATGTAGGTATGATG	789				
QY	1255	CCGGAGCTTAAATTAACCTCATACGTGAATTTAGAGATGAAGTCTCTCTGCTGCAATAA	1314				
Db	790	GAAGAGCCAGCAGTAAAGACATATAGGGAATTTGAGACAAATGTTGCCAGCATACGA	849				
QY	1315	RACCTTGGGTACAATGCGGTGCAATATATGGCTATTCAGAGCAATTTTATATGCTAGT	1374				
Db	850	GCAATAACTACACACAGTTCAGTTGATGGAGTATGAGCAATTCGTAATGCTTCT	909				
QY	1375	TTTGTATTATGTCACAAATTTTTCACCAAGCAGCGGTTTGGACGCCCGCAGAC	1434				
Db	910	ITCGGATACCAATGACAAATTTCTTTGCGGTTAGCAGCAGATCAGGCACAGAGGAC	969				
QY	1435	CTTAAGCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGGACATTTGT	1494				
Db	970	CTCAAAATATCTTTGATAAGSCACACAGTTTGGGTTTGGGTTCTGATGATGTTGTC	1029				
QY	1495	CACAGCCATGCATCAATAATTAATTTAGAGCTGACATGCTTTGACG-----GC	1545				
Db	1030	CAIAGCCATGAAGTAATATGTCACATGTTTAAATGGCTATGATGTTGGACAAAGC	1089				
QY	1546	ACAGATGTTGTTTACCTTCACTCTGAGCTGCTGCTGTTATCATTTGGATGGGATTC	1605				
Db	1090	ACCAAGAGTCTTATTTCACTCGGAGATAGAGGTTATCAATACTTTGGGATAGTCGG	1149				
QY	1606	CTCTTTAATAGGAACTGGAGGAGTACTTATGATCTCTCTCAAAATCGGAGATGGTGG	1665				
Db	1150	CTGTTCAACTATGCTAACTGGGAGTATTAAGGTTTCTTCTTCAACCTGAGATATGG	1209				
QY	1666	TTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGGTGGATCAATCAATGATATCT	1725				
Db	1210	TTGGATGAATTAATGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1269				
QY	1726	CACACGATATCGTGGGATTCAGTGGAGTACGAGGATACATTTGGACTCCCACT	1785				
Db	1270	CACCAAGTATCAATGTTGGGTTTACTGGAACTACAGGAATATTTCACTTTGGACACA	1329				
QY	1786	GATGTRGATGCTGCGTGTATCTGATGCTGGCCAAAGCATCTTATTCATGGGCTTTTCCA	1845				

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Job time : 160.619 secs

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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:51:57 ; Search time 486.292 Seconds
(without alignments)
10130.730 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200

Perfect score: 3156

Sequence: 1 AAAAAGCTCTCCACTCACT.....TGCTGATCTAATGATCTTTT 3156

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2955.2	93.6	3074	9	US-10-254-534-1
2	1372.2	43.5	1393	9	US-10-254-534-3
3	1323	41.9	2418	9	US-09-938-842A-872
4	1296	41.1	2577	9	US-09-938-842A-337
5	1185.6	37.6	3039	10	US-09-792-127-3
6	1185	37.5	2559	10	US-09-792-127-1
7	598.2	19.0	2994	9	US-10-084-817-92
8	596.6	18.9	2955	9	US-09-918-624B-30
9	596.6	18.9	2955	10	US-09-880-107-2148
10	257.8	8.2	602	10	US-09-770-143-955
11	139.6	4.4	604	10	US-09-925-300-453
12	114.6	3.6	441	10	US-09-770-444-893
13	108	3.4	601	9	US-10-025-380-304
14	108	3.4	601	10	US-09-922-217-304
15	108	3.4	601	10	US-09-833-263-304
16	88.2	2.8	1877	10	US-09-974-300-653
17	87.2	2.8	204	10	US-09-878-574-12567
18	85.4	2.7	1830121	9	US-10-329-960-1
19	81.4	2.6	2193	9	US-09-738-626-1354

c	20	81.4	2.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
c	21	79.4	2.5	310	9	US-10-102-524-1616	Sequence 1616, Ap
c	22	69.8	2.2	543	10	US-09-815-343-373	Sequence 373, App
c	23	68.8	2.2	576	10	US-09-815-343-924	Sequence 924, App
c	24	59	1.9	261	10	US-09-864-761-19524	Sequence 19524, A
c	25	59	1.9	261	10	US-09-864-761-25517	Sequence 25517, A
c	26	59	1.9	448	10	US-09-864-761-557	Sequence 557, App
c	27	59	1.9	513	10	US-09-864-761-8851	Sequence 8851, Ap
c	28	55.4	1.8	255883	9	US-10-175-523-57	Sequence 57, Appli
c	29	54.6	1.7	381	10	US-09-864-761-21610	Sequence 21610, A
c	30	54.6	1.7	90650	9	US-10-175-523-80	Sequence 80, Appli
c	31	54.2	1.7	419	10	US-09-864-761-6432	Sequence 6432, Ap
c	32	53.8	1.7	8895	9	US-10-091-438-250	Sequence 250, App
c	33	53.8	1.7	8895	9	US-10-091-438-256	Sequence 256, App
c	34	53.8	1.7	8895	10	US-09-764-853-887	Sequence 887, App
c	35	53.8	1.7	8895	10	US-09-764-853-937	Sequence 937, App
c	36	53.8	1.7	9656	9	US-10-091-438-246	Sequence 246, App
c	37	53.8	1.7	9656	9	US-10-091-438-255	Sequence 255, App
c	38	53.8	1.7	9656	10	US-09-764-853-886	Sequence 886, App
c	39	53.8	1.7	9656	10	US-09-764-853-933	Sequence 933, App
c	40	53.4	1.7	1282	9	US-10-002-344A-89	Sequence 89, Appli
c	41	53.4	1.7	16299	9	US-10-175-523-64	Sequence 64, Appli
c	42	53.4	1.7	1691139	9	US-10-067-514-1	Sequence 1, Appli
c	43	53	1.7	312	10	US-09-864-761-22972	Sequence 22972, A
c	44	52.6	1.7	483	10	US-09-864-761-1384	Sequence 1384, A
c	45	52.4	1.7	288	9	US-09-728-444-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:

Db 1679 GTTCAAAATTTGATGGATTTAGATTTGATGTTGACATCAATGATGTAHACTCACCACGG 1738
QY 1734 ATTATCGGTGGGATTTACTCGGGAACATGAGAGAAATCTTTGGACTCGCAACTGAGTGRGA 1793
Db 1739 ATTATCGGTGGGATTTACTCGGGAACATGAGAGAAATCTTTGGACTCGCAACTGAGTGRGA 1798
QY 1794 TGTCTGCGGTGATCTGATGTCGCGCAACGATCTTATTCATGCGGCTTTTCCACAGTCAAT 1853
Db 1799 TGTCTGTTGATCTGATGTCGCGCAACGATCTTATTCATGCGGCTTTTCCACAGTCAAT 1858
QY 1854 TACCATTGTTGAGATGTTAGCGGAATGCGGCAATTTTGTATTCCTTCAAGATGGGG 1913
Db 1859 TACCATTGTTGAGATGTTAGCGGAATGCGGCAATTTTGTATTCCTTCAAGATGGGG 1918
QY 1914 TGTGCTTTGACATCTGCGCTGATGCGCAATGCGCAATGCGCAATGCGCAATGCGCAAT 1973
Db 1919 TGTGCTTTGACATCTGCGCTGATGCGCAATGCGCAATGCGCAATGCGCAATGCGCAAT 1978
QY 1974 GAAACGGGATGAGATTTGGAGATGGGTGATATTTGTTTCATACACTGACAAATGAGATG 2033
Db 1979 GAAACGGGATGAGATTTGGAGATGGGTGATATTTGTTTCATACACTGACAAATGAGATG 2038
QY 2034 GTCGGAAGATGTTTTCATACCTGAAAGTCAATGATCAAGCTCTAGTCGCTGATAAAC 2093
Db 2039 GTCGGAAGATGTTTTCATACCTGAAAGTCAATGATCAAGCTCTAGTCGCTGATAAAC 2098
QY 2094 TATAGCATCTGCTGATGACAGAGATATGATATTTATGCTTTGCTTTGATAGACCGTC 2153
Db 2099 TATAGCATCTGCTGATGACAGAGATATGATATTTATGCTTTGCTTTGATAGACCGTC 2158
QY 2154 AACATCAATTAATAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2213
Db 2159 AACATCAATTAATAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATG 2218
QY 2214 ATTAGAGAGAGAGGTACTAAATTTTCATGGAATGATGATGATGATGATGATGATGATG 2273
Db 2219 ATTAGAGAGAGAGGTACTAAATTTTCATGGAATGATGATGATGATGATGATGATGATG 2278
QY 2274 TGATTTCCCTAGGCTGACACACCTCTGATGCTGATGATGATGATGATGATGATGATGATG 2333
Db 2279 TGATTTCCCTAGGCTGACACACCTCTGATGCTGATGATGATGATGATGATGATGATGATG 2338
QY 2334 CAGTTATGATAATGACAGCGGAGATTTGACCTGGGAGATGACAGATGATGATGATGATGATG 2393
Db 2339 CAGTTATGATAATGACAGCGGAGATTTGACCTGGGAGATGACAGATGATGATGATGATGATG 2398
QY 2394 TGGTTGCAAGAAATTTGACCGGCTATGCGAGTATCTTGAAGATAAATATGAGTTATGAC 2453
Db 2399 TGGTTGCAAGAAATTTGACCGGCTATGCGAGTATCTTGAAGATAAATATGAGTTATGAC 2458
QY 2454 TTCAGAACACCGATTCATATCAGGAAGATGAGGATGATGATGATGATGATGATGATGATG 2513
Db 2459 TTCAGAACACCGATTCATATCAGGAAGATGAGGATGATGATGATGATGATGATGATGATG 2518
QY 2514 AGSAAACCTAGTTTTCCTTTTAAATTTTCACTGACAAAAGCTATTCAGACTATGCGAT 2573
Db 2519 AGSAAACCTAGTTTTCCTTTTAAATTTTCACTGACAAAAGCTATTCAGACTATGCGAT 2578
QY 2574 AGCTGGCTGAGCCCTGGAATAATACAGGTTCCTTGGACTCAGATGATGATGATGATGATG 2633
Db 2579 AGCTGGCTGAGCCCTGGAATAATACAGGTTCCTTGGACTCAGATGATGATGATGATGATG 2638
QY 2634 TGGCTTCGGGAGAAATGATCAATATCCGAAATTTTCCCTTTGAAGGATGGTATGATGA 2693
Db 2639 TGGCTTCGGGAGAAATGATCAATATCCGAAATTTTCCCTTTGAAGGATGGTATGATGA 2698
QY 2694 TGTCTCTGTTCAATTAATGTTGATGACCTTAGTAGAAGAGTGGTCTATGCTACCTAGT 2753
Db 2699 TGTCTCTGTTCAATTAATGTTGATGACCTTAGTAGAAGAGTGGTCTATGCTACCTAGT 2758
QY 2754 AGACA---AGAGAGAGAGAGAGAGAGTACGATGATGATGATGATGATGATGATGATGATG 2810
Db 2759 AGACAAGAGAGAGAGAGAGAGAGTACGATGATGATGATGATGATGATGATGATGATGATG 2818

QY 2811 AGAATGAACAACTTTGTCATCGCTTGAACGATTTGAACGCTACATAGAGCTTCTTGACG 2870
Db 2819 AGAATGAACAACTTTGTCATCGCTTGAACGATTTGAACGCTACATAGAGCTTCTTGACG 2878
QY 2871 TAICTGCAATATTGTCATCAGTCTTGGCGGAATTTTCATGTCACAAAAGGTTTGCAATTCT 2930
Db 2879 TAICTGCAATATTGTCATCAGTCTTGGCGGAATTTTCATGTCACAAAAGGTTTGCAATTCT 2938
QY 2931 TTCCACTATTAGTAGTCAACGATATACGACAGATGAAGTGTGACAAACATATGTAA 2990
Db 2939 TTCCACTATTAGTAGTCAACGATATACGACAGATGAAGTGTGACAAACATATGTAA 2998
QY 2991 AATCGATGAATTTAATGTCGAATGCTGGAGCGGCTTCAGCAGGTTTTCCTTAGTGAGTTC 3050
Db 2999 AATCGATGAATTTAATGTCGAATGCTGGAGCGGCTTCAGCAGGTTTTCCTTAGTGAGTTC 3058
QY 3051 TGTAATTTGTCATCTC 3066
Db 3059 TGTAATTTGTCATCTC 3074

RESULT 2

US-10-554-534-3

; Sequence 3, Application US/10254534

; Publication No. US20030046730A1

; GENERAL INFORMATION:

; APPLICANT: EK, BO

; APPLICANT: KHOSNOODI, Jamshid

; APPLICANT: LARSSON, Clas-Tomas

; APPLICANT: LARSSON, Hakan

; APPLICANT: RASK, Lars

; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

; FILE REFERENCE: 003300-486

; CURRENT APPLICATION NUMBER: US/10/254,534

; CURRENT FILING DATE: 2002-09-26

; PRIOR APPLICATION NUMBER: US/09/087,277

; PRIOR FILING DATE: 1998-05-29

; PRIOR APPLICATION NUMBER: PCT/SE96/01558

; PRIOR FILING DATE: 1996-11-28

; PRIOR APPLICATION NUMBER: SE 9504272-7

; PRIOR FILING DATE: 1995-11-29

; PRIOR APPLICATION NUMBER: SE 9601506-0

; PRIOR FILING DATE: 1996-04-19

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1393

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment

; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

; OTHER INFORMATION: (potato)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(1393)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (424)..(1150)

; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,

; OTHER INFORMATION: C, G or T.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (422)..(424)

; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (890)..(892)

; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys

; OTHER INFORMATION: or Phe.

; FEATURE:

; NAME/KEY: misc_feature

QY 1962 TGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGTGATATTGTTTCATACACTGAC 2021

[illegible]

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QY 797 GGGAGGCAAT TGGCAAGTATGAGGGTGGT TTTGGTGGTATGAAAAA 830

Db 449 GTGAGGAATATAGCAAGTATGAGGTGGTCTTGGGCAATCTCTCGTGGCTATGAAAAAGT 508
QY TGGGTTTACATCGTAGTCTACAGTATCACTTACCGTGACTGGGCTCCTCGTGCCAGT 916
Db TGGTATTTCCGCGAGTATGCGCGTATPACTTATAGAGATGGGCGCTCGAGCTAAGG 568
QY 917 CAGCTGCTCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGACATTTAGCTCGGA 976
Db 569 CTGCATCATTTATCGGAGATTTCAACAATTTGGGACGCAAAATGCTGACATTTAGCTCGGA 628
QY 977 ATGAATTTGGTCTGGGAGATTTTTCGCGCAAAATGCTGAGTGGTCTCCTGCAATTC 1036
Db 629 ATGAATTTGGTCTGGGAGATTTTTCGCGCAAAATGCTGAGTGGTCTCCTGCAATTC 688
QY 1037 CTCATGGGTCAGAGTGAAGATACGATGGACATCTCATCAGGTGTTAAAGATTCATTC 1096
Db 689 CTCATGGGTCAGGTGAAGATTCGATGGATCTCCATCTGGCATTAAGACATCAATTC 748
QY 1097 CTGCTTGGATCAACTCTTTACAGCTTCTCTGATGAAATTTCCATATAATGGAATATAT 1156
Db 749 CTGCTTGGATCAAGTCTCGGTGCAAGCTCCAGCTGAAATCCCATTCATGGCATATACT 808
QY 1157 ATGATCCACCGAAGAGAGAGTATGCTTCCAAACCCAGGCGCAAAAGT 1216
Db 809 ATGATCCACCGAAGAGAGAGTATGCTTCCAAACCCAGGCGCAAAAGT 868
QY 1217 CGCTGAGATATATGAATCTCATATTTGGAATGAGTGTCCGAGGCTTAATTAATCAT 1276
Db 869 CGCTGAGATATATGAATCTCATATTTGGAATGAGTGTCCGAGGCTTAATTAATCAT 928
QY 1277 ACGTGAATTTAGAGATGAAGTCTTCTCCGATFAAAAAACCTTGGGTACAATCGGTGC 1336
Db 929 ATGCTAACTTTAGAGATGATGTTCTTCCCGCATCAAAAAGCTTGGATATATCTGTC 988
QY 1337 AATATGAGTATTTCAAGACATCTTATATGCTAGTCTTTGGTATCATGTCACAAT 1396
Db 989 AATATGAGTATTTCAAGACATCTTATATGCTAGTCTTTGGTATCATGTCACAAT 1048
QY 1397 TTTTTCACCAAGCAGCGCTTTTGGAGCGCCGAGGACCTTAAGTCTTTGATTCATTAAG 1456
Db 1049 TTTTTCACCAAGCAGCGCTTTTGGAGCGCCGAGGACCTTAAGTCTTTGATTCATTAAG 1108
QY 1457 CTCATGAGCTAGGAATTTGTTCTCATGGACATTTTCACAGCATGCTATCAAAATATA 1516
Db 1109 CTCACAGTATGAGGCTGCTGATGCTGATGATGCTTATAGGCTTCAAAAACA 1168
QY 1517 CTTTATGATGACTGACATGTTTTCACGCGACAGATGTTGTTACTTTCACTCTGGAGCTC 1576
Db 1169 CATTGATGACTGACATGTTTTCACGCGACAGATGTTGTTACTTTCACTCTGGAGCTC 1228
QY 1577 GTGGTTATCATTTGGATTTCCGCTCTTTAACTATGAAACTGGGAGTACTTA 1636
Db 1229 GGGATACCATTTGGATTTGGATTTCCAGCTTTTCAATTAAGGAGCTGGAGATTAAC 1288
QY 1637 GGTATCTCTCTCAATGCGAGATGTTGGTGGATGAGTGCATAATTTGRTGATTTAGAT 1696
Db 1289 GATAATCTCTCTCAATGCGAGTGGTGGCTAGAGAAATACAGTTTATGATTTAGAT 1348
QY 1697 TTGATGCTGATCATCAATGATGATCTACCTACAGGATTTATCGGTGGGATTCAGTGGGA 1756
Db 1349 TTGATGCTGATCATCAATGATGATCTACCTACAGGATTTATCGGTGGGATTTACTGGGA 1408
QY 1757 ACTACAGGAAATCTTTGGGACTCGCAACTGATGATGCTGCGGTATCTGATCTGCTGG 1816
Db 1409 ACTACAGGAAATCTTTGGGACTCGCAACTGATGATGCTGCGGTATCTGATCTGCTGG 1468
QY 1817 CCAACGATCTTATTCATGGGCTTTTCCAGATGCAATTAACATTTGTTGAAGATTTAGCG 1876
Db 1469 TTAATGATGATGATTTGATGCTGCTACCTGACCGATTAACGTTGGTGAAGATTTAGTG 1528
QY 1877 GATGCGGACATTTTGTATTCCTGCTCAGATGGGCTGTTGCTTTGATGATCTGCTGCTG 1936
Db 1529 GATGCGGACATTTTGTATTCCTGCTCAGATGGGCTGTTGCTTTGATGATCTGCTGCTG 1588

QY 1937 ATATGGCAATTTGCTCATTAATTTGGATTTGAGTTGCTCTCAAGAAACGGGATGAGATTTGAGAG 1996
Db 1589 ACATGGCATAGCTGATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1648
QY 1997 TGGGATGATTTGCTCATACACTGACAAATAGAGATGTTGCGAAAGTGTGTTTTCATAGC 2056
Db 1649 TGGGCGCATCATTTTACACACTTACCAACAGAGGTGGTTCAGAGAAGTGTATCTCTTATG 1708
QY 2057 CTGAAGATCATGATCAAGCTCTAGTCTGATGATAAAACTATAGCATTTGCGCTGATGGACA 2116
Db 1709 CTGAAGATCATGATCAAGCTCTTGTGTTGATGATAAAACTTGCCTTCTGTTTAAAGTGA 1768
QY 2117 AGGATATGATGATTTTATGCTTTGGATGATGATGATGATGATGATGATGATGATGATGAT 2176
Db 1769 AGGATATGATGATTTTATGCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1828
QY 2177 TAGCATTCACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2236
Db 1829 TAGCTTTCACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1888
QY 2237 ATTTATGCGGAAATGATTTGCGGCACTTCTGATGATGATGATGATGATGATGATGATGATGAT 2296
Db 1889 ATTTATGCGGAAATGATTTGCGGCACTTCTGATGATGATGATGATGATGATGATGATGATGAT 1948
QY 2297 ACCCTCTGATGCTCAGTAAATTTCCGGAACCAATTCAGTTATGATGATGATGATGATGATGAT 2356
Db 1949 GTCCTTCTGATGCTCAGTAAATTTCCGGAACCAATTCAGTTATGATGATGATGATGATGATGAT 2008
QY 2357 GATTTGACTCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2416
Db 2009 GATTTGACTCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2068
QY 2417 CTATGCTAGTCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2476
Db 2069 CAATGCTAGTCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2128
QY 2477 GAAAGATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2536
Db 2129 GAAAGATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2188
QY 2537 ATTTTCTACTGACAAAAGCTTATTCAGACTATCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2596
Db 2189 ACTTTTCTACTGACAAAAGCTTATTCAGACTATCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2248
QY 2597 ACAAGTGTGCTTTGAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2656
Db 2249 ATAAGATGCTATTTGAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2308
QY 2657 ATGCGGATGCTTTTACCTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2716
Db 2309 AGGAGATGCTTTTACCTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2368
QY 2717 ATGCACTAGTAGAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2762
Db 2369 ATGCACTAGTAGAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2414

RESULT 4

US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-337

Query Match      41.1%; Score 1296; DB 9; Length 2577;
Best Local Similarity 76.2%; Pred. No. 0;
Matches 1593; Conservative 1; Mismatches 496; Indels 0; Gaps 0;

QY 686 AGAGGGGCAATCCCTCCACCTGGACTTGGTCAGAGAAATATGAAATAGACCCCTTTTGA 745
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Db 443 AGAGGAAGATTCACCTCCCTGGAGATGGGAAGAGATATATGACATTTGATCCTATGTTGA 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 746 CAAACTATCGTCAACACCTTGATTACAGGTATTTCACAGTACAAAGAAATCAGGAGGCAA 805
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 503 ACAGTCACTGATATCATCTTGATTCAGATATCGGAGTACAGAAACTCCGTGAAGAAA 562
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 806 TTGACAAGTATGAGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGTTTCA 865
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 563 TTGACAAGAATGAAGTGGTTTGGAGGCAATTTCTCGTGGTTATGAAATATTTGGCTTCA 622
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 866 CTCGTAGTGTACAGGTATCACTTACGTCAGTGGCTCTCGTGGCCAGTCAGCTGCTC 925
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 623 CTCGAAGCGCACTGATATCACTTACCGGAATGGGCACCGGAGCTTAAGGCAGCATCAC 682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 926 TCATTGGAGATTTCAACAATTTGGACGCAAAATCTGACATTATGACTCGGAATCAATTTG 985
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 683 TGATCGGAGATTTTAACTACTGGAATCGGAAATCTGATGTAATGGCHCGGAACGACTTTG 742
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 986 GTGCTCTGGGAGATTTTCTCCAAATAATGTTGGATGGTTCTCTCGCAATTCCTCATGGGT 1045
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 743 GTGTGTGGGAATATTTCTGCCAAATAATCTGATGGCTCACACGCAATTCCTCATGGGT 802
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1046 CCAGATGAAGATACGATCGACACTTCATCAGGTGTTAAGGATTCATTCCTCTGTTGA 1105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 803 CCCGTGTGAAGATCCGATGGATACCCCATCTGGTATTAAAGACTCCATTCACGCTTGA 862
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1106 TCAACTACTCTTTACAGCTTCCTGATGAAATTCATATATGGAATATATATGATGCCAC 1165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 TCAAGTATCTGTGACGACCACTGGCGAGATCCCATATATGAGGATATATGACCCCTC 922
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1166 CCGAAGAGGAGATGTTCTTCCACACCCAGCGCCAAAGAACCAAAAGTCGCTGAGAA 1225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 923 CTGAGGAGGATAAATATGCGTTCAACATCTCTGCCAAAGAACCCACATCCGCTGGGTA 982
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1226 TATATGAATCTCATATTTGGAATGAGTACGTCGAGCGCTAAATTAACCTCATAGTGAAT 1285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 983 TATATGAATCACATGTTGGAATGAGTACGTCGAGCGCTAAATTAACCTCATAGTGAAT 1042
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1286 TTAGAGATGAAGTTCTTCCCTCGGATAAAAACCTTGGGTCAATFCGCGGTCAAAATATGG 1345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1043 TTAGAGATGATGATCTCCCGTATATAAAGCTAGGCTATATGCTGTGACATATGG 1102
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1346 CTATTCAGAGCATCTTATATGCTAGTTTGGTTATCATGTGCACAAATTTTTTTCAC 1405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1103 CCAATTCAGAGCATGCTTACTATGCCAGCTTGGGTATCATGTGCACAAATTTTTTTCGAC 1162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1406 CAAGCACCGCTTTTGGACCGCCGACGACCTTAAGTCTTGTGATTGATAAGCTCATGAGC 1465
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1163 CTAGACGCGCTTTTGGACACGCTCATGACCTTAATCTTTGATAGACAAAGCTCATGAGC 1222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1466 TAGGAATGTTGTTCTCATGACATTTGTTTCACAGCCATGTCATCAATAAATTAATTTAGAT 1525
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1223 TAGTCTGTTGTTCTGATGATATTTGTCACAGCCATGTCATCAAAACACACACTGGATG 1282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1526 GACTGAACATGTTTGACGGGCACAGATAGTTCTTACTCTGGAGCTCGTGGTTATC 1585
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Db      2363  TTATTGGACTCTGATAAATCTTTATTATTGGAGGCTTCAACCGCTAGATGACTCCGGGAGT  2422
QY      2666  GTTTCACCTTTGAAGGATGGTATGATGTCGTCTCTCGTTCAATTAATGGTGTATGCACCTA  2725
Db      2423  TTTTCACCTCTGATGGTAGGACGACCATAGGCGCTTCTCCTCATGTTGTATGCACCGT  2482
QY      2726  GTAGACAGCAGTGGTCTATCCACTAGTAGACAAAGAAAGAAAGAAAGAA  2775
Db      2483  GCAGAACCGGTGTAGTTACGCTGCATAGATGATGATGATGAA  2532

RESULT 5
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IiB
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-09-792-127-3

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QY	1204	AGAAACC	AAAGTCG	TGAGATAT	ATATGAATCT	CAATTAT	TGGAAATC	AGTAGTCCG	GAGCCT	1263	
DB	1014	AAACGACCA	AAAATCAIT	TGCGGATAT	ATATGAACACAT	GTGGCAT	GTAGTAGCGG	GAACCA	1073		
QY	1264	AAAATTAACT	CACTACGTGAAAT	TTTAGATAG	AGAGTTCT	CTTCGCGAT	AAAAAACT	TTGGG	1323		
DB	1074	AAGATCAAC	ACACATATGCAAACT	TCAGGAT	AGGTGCTT	CCAGAAGAT	TTAAAGACT	TTGGA	1133		
QY	1324	TACAATGCGGT	GCAAAATATGCGT	ATTAACAGAG	CAITCTTAT	TATPCTAGT	TTTGGTTAT	1383			
DB	1134	TACAATGCGAGT	GCAAAATATGCGAAT	TCCAAAGC	ACTCATATCT	ATGGAAGCT	TTGGGTAC	1193			
QY	1384	CATGTCACAA	ATTTTTTTGACCA	AGCAGCGCT	TTTGGAA	CGCCGAG	CGACCTTAA	GTC	1443		
DB	1194	CATGTTACCA	ATTTCTTTGCACCA	AGTAGCCGTT	TTTGGTCCC	CAGAAGAT	TTTAAATCT	1253			
QY	1444	TTGATTTGAT	ATAAGCTCATGAGCT	ATAGGAAT	TTGTTCT	CTCATGSG	ACATTTGTT	CACAGCAT	1503		
DB	1254	TTGATTTGAT	ATAGAGCTTCAGGAGCT	TGGCTTGGCT	TTGCTCAT	GTGATGTTGTT	TCACAGT	TCAC	1313		
QY	1504	GCATCAAA	ATAATACTTTAGAT	TGGACTGCA	CACTGTTGAC	GCACAGAT	TAGTGT	TACTTT	1563		
DB	1314	GGCTCAAT	ATATACCTTGAC	CGGTTGAATGGTTT	TATG	ATGCGAC	AGGATACACAT	TACTT	1373		
QY	1564	CACCTG	GAGCTCGTGGTTAT	CAITGGAATG	TGGGATCCG	CCCTCTTAACT	ATGGAAC	1623			
DB	1374	CATGCGCT	TCACGGGCCATCACT	TGGATGTGGAT	TCGCTGTTTAACT	ATGGAAT	1433				
QY	1624	TGGGAGT	TACTTAGTATCT	CTCAATGCG	AGATGGTGGT	TGGATGAGT	AGTCAAA	TTT	1683		
DB	1434	AGGAAGT	ATTAAGGTTTCTACT	TTCCAACT	CAAGATGGTGGCT	TAGAGG	AGTATAAGTT	1493			
QY	1684	RTGATTTAG	ATTTGATGGTGCACAT	CAATGATGTAT	ACTCAC	ACGGAATAT	CGGTG	1743			
DB	1494	GATGTTTCC	GAATCGATGGCGG	CCCTCCATGAT	GTATACCAT	GATGTTAC	CAATGTTAC	AA	1553		
QY	1744	GAATCACT	TGGAACTACGAGGAAT	ACTTTGGGACT	CGCAACTGAT	GTGATGCTG	CCGCTG	1803			
DB	1554	ACCTTTAC	AGGAAGCTACCAT	GAATATTTTGGCT	TTGCCACTGAT	GTAGATGCG	TCGTT	1613			
QY	1804	TATCTGAT	GCHGGCCACGATCT	TATTCAT	TGGGCTTTCC	CAGATCAAT	TACCAT	TGGT	1863		
DB	1614	TACTTTGAT	GCTGTGATGATCT	AAATCAT	TGGGTTTATCT	CTCAAGCCG	TAACTAC	TCGT	1673		
QY	1864	GAAGATGTT	TAGCGGAATCGCG	ACATTTGAT	TCCGCTTCA	AGATGGGGT	GTGCG	TTT	1923		
DB	1674	GAAGATGTT	AGATGGCATATTTG	CTATTTG	CCCTTCTCTTCA	AGTTGGTGGG	TTGGTTT	1733			
QY	1924	GACTAT	CGGCTGCATATG	GCAAATGCTGAT	PAATGGAT	TGCTGCTCA	AGAAACGGAT	1983			
DB	1734	GACTAT	CGCTTACATATG	CGCTGTTGCG	GACAAATGAT	TGAATCT	CAAGGAACCGAT	1793			
QY	1984	GAGGAT	TGGAGATGGGT	GTATTTGTTAT	CACTGACAAAT	TAGAGAT	TGTCGGA	AAAG	2043		
DB	1794	GAGCTTTGG	GAGATGGGTATAT	TGTGSC	ACACTAACAA	CAGAAAGGT	TGGTGA	AAAG	1853		
QY	2044	TGTGTTT	CATACGCTGAA	AGCTCATGAT	CAAGCTCTAGT	CGGTGATA	AAACAT	TAGCAT	2103		
DB	1854	TGTTTACT	ATCTGAAAGT	CAGATCAAG	CACTTGT	TGGAGACA	AGCATATTG	CAATC	1913		
QY	2104	TGCTGAT	GGACAGGATATG	TATGATTTTAT	TGGCTTTGGAT	PAGACCTTCA	CAATCATTA	2163			
DB	1914	TGTTGAT	GGACAAGGATATG	TATGATTTTAT	TGGCTTCA	GGGCTTCA	GGGCTTCA	GGCCTTAT	1973		
QY	2164	ATAGAT	TCGTGGGATAC	CAATTCAC	AAAGATGAT	TAGGCTTGA	CTTAAC	TATG	GGGAT	2223	
DB	1974	ATTGAT	TCGTGGAAATAG	CACTGCA	TAAATGATT	TAGACTTAT	CA	AAU	GGGCT	2033	
QY	2224	GAAGG	TACTAAATTTTCA	TGGAATG	NAATTCG	CCACCTG	AGTGA	TGAT	TCCT	2283	
DB	2034	GAGG	TTATCTTA	CTTATG	GGAATG	AGTTCG	GGCATCT	GAATG	AGAT	TTCCA	2093


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Db 1225 TTCCTGTTCAAGTTGGTGGGTTGGTTTGGATCTATCGCTTACATATGGCTGTGCGGACA 1284
QY 1955 AATGATTCAGTGTCTCAAGAAACGGGATGGAGATTGGAGAGTGGGTGATATGTTGATA 2014
Db 1285 AATGATTCAGTGTCTCAAGAAACGGGATGGAGATTGGAGAGTGGGTGATATGTTGATA 1344
QY 2015 CACTGACAAATAGAGATGGTGGGAAAAGTGTGTTTCATAGCTGAAAGTCATGATCAAG 2074
Db 1345 CACTAACAAACAGAGGTGGCTGGAAAAGTGTGTTTACTATGCTGAAAGTCACGATCAAG 1404
QY 2075 CTCATGTCGGTGTAAATACTATAGCATCTCTGGCTGATGAGCAAGGATATGATATTTA 2134
Db 1405 CACTGTTGGAGACAGACTATGCTATCTGGTTGATGGACAAAGGATATGATATTCA 1464
QY 2135 TGGCTTTGGATAGACCTCAACATCAATTAATAGATCGTGGGATAGCATTGACATGGAATGA 2194
Db 1465 TGGCGCTGAACGGACCTTCGACGCTTAATATGATGCTGGAATAGCATTGACATGGAATGA 1524
QY 2195 ITAGGCTTGAACCTATGGGATAGGAGGAGAGGATACCTAAATTTTCATGGAATGAAT 2254
Db 1525 TTAGCATATCACAATGGGCTTAGGAGGAGAGGTTTATCTTAACCTTTATGGAATGAGT 1584
QY 2255 TCGGCCACCTGAGTGATTGATTTCCCTAGGCTGACACACCTCTCTGATGGCTAG 2314
Db 1585 TCGGGCATCTGATGATAGATGATTTCCAGAGGCCCAAGTACTTCCAAGTGGTAAGT 1644
QY 2315 TAATCCCGGAACCAATTCAGTTATGATAAATCGACAGCGAGATTTGACCTGGAGATG 2374
Db 1645 TCATCCCGGAACCAACACAGTTACGACAAATGCCCTCGAAGTTGACCTGGGTGATG 1704
QY 2375 CAGAAATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGGCTATGACATGTTGGAAG 2434
Db 1705 CAGAAATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGGCTATGACATGTTGGAAG 1764
QY 2435 ATAAATGAGTTTATGATTCAGATCAGAACACCTGATATCATACCAAGAGGATGAGGAGATA 2494
Db 1765 AAAAAATGTTTATGATCAGATCAGAACACCTGATATCATACCAAGAGGATGAGGAGATA 1824
QY 2495 GGATGATGTTATTTGAAAAGGAACCTAGTTTGTCTTAAATTTTCACTGGACAAAAA 2554
Db 1825 AGTGATGCTGTTTGAAGAGGGGACTTGTATTGTGTTCACTTCCACTGGAGTAGTA 1884
QY 2555 GCTATTACAGACTATCCATAGCTGCTGAGGCTGGAATAACAAAGTTGCCCTGGACT 2614
Db 1885 GCTATTACAGACTATCCATAGCTGCTGAGGCTGGAATAACAAAGTTGCCCTGGACT 1944
QY 2615 CAGATGATCCACTTTTGGTGGCTTCGGGAGATTCATCATATGCGGATGTTTCACT 2674
Db 1945 CGGACGCTGGACTTTTGGTGGCTTCGGGAGATTCATCATATGCGGATGTTTCACT 2004
QY 2675 TTGAAGATGGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2734
Db 2005 CTGATGCTCAACATGACACAGCGCCCAATTCATCTCAGTGTACACTCCTAGCAGACCT 2064
QY 2735 CAGTGGCTATGCTAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2794
Db 2065 GTGTGCTATGCTCCATGAACTAACAGCAAGTGCAGCATACGCTGCGGCTGTJGT 2124
QY 2795 AAGTAGTAGTAGAGAA 2811
Db 2125 TCCTAGTAGCAGAGAA 2141
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RESULT 7
US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

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; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 92  
; LENGTH: 2994  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc_feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CBI  
US-10-084-817-92  
  
Query Match 19.0%; Score 598.2; DB 9; Length 2994;  
Best Local Similarity 58.0%; Pred. No. 2.5e-158;  
Matches 1175; Conservative 2; Mismatches 800; Indels 48; Gaps 5;  
  
QY 727 GAAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786  
Db 215 GAGATCGACCCGTACTTCAAGCCCTACCCGTGGACTCCAGCGAGGTATAAGCAGTTT 274  
QY 787 AAGAAATGAGGGAGGCAATTCACAAGTATGAGGGTGGTTTGGAGCTTTTCTCGTGT 846  
Db 275 AGCCAAATTTTGAAGAACATTTGAGAAATCAAGGTGCTATGATAAGTTTCCAGAGCC 334  
QY 847 TATCAAAATGAGGGTTCACATCTAGTCTGACAGTATGAGGTATTCACCTTACCGT 903  
Db 335 TATGAAATTTTGGGCTCCACAGATGCTGATGGTGGTTTATCTACTGCAAGAAATGGGCC 394  
QY 904 CCTGGTCCCGAGTCAGTCTCTCATTTGGAGATTTCAACATTTGGAGCGCAATGCTGAC 963  
Db 395 CCGGAGCAGAGAGTCTTCTTACTGGAGATTTTATGGTTGGAATTCATTTTCGTAC 454  
QY 964 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAAATATATGTTGATGGT 1023  
Db 455 CCATACAAAATCGGATTTATGGAATTTGGAGCTGATATCCCAACCAAGCAATATAA 514  
QY 1024 TCTCTCAATTTCTCATGGTCCAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1081  
Db 515 TCTGTACTCGTCTCATGGATCCAAATTAAGGTAGTTTATTTACTAGTAAAGCGGAGAG 574  
QY 1082 -TTAAGATTTCCATTTCTGCTGGATCACTACTCTTTACAGCTTCTCTGATGAAATFCCA 1140  
Db 575 ATCTTGTATGCTATTTACCGTGGCAAGTATGCTGCTGAGGTGATATGTAAT 634  
QY 1141 TATAATGGATATATATGATCCACCGGAGAGAGAGTATGCTTCTTCCAAACCCACGG 1200  
Db 635 TATGATTTGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCATTCAGA 688  
QY 1201 CCAAGAAACCAAGTCCGTGAGAATATATGATCTCATATTTGGAATGAGTATGAGTATGAGT 1260  
Db 689 CCNAGAAACCGGAGTCTAGAAATTTATGAACTCATGTGGGAATTTCTTCCCATGAA 748  
QY 1261 CTTAAATTAACCTATACGTGAATTTTAGAGATGAAGTTCTTCTCGCATATAAAACCTT 1320  
Db 749 GGAAGATAGCTTCTTATAAACATTTTACATGCAATGTTACTCCAAAGATCAAGGCTT 808  
QY 1321 GGGTACATGCGGTGCAAAATTAAGCTATTTCAAGAGCATTTCTTATTTAGTCTAGTTTGGT 1380  
Db 809 GGATACAACTGCTATGATGCAATCATGAGCATGCTTACTATGCCAGCTTTGGT 868  
QY 1381 TATCATGTCACAAATTTTTCACCAAGAGCCGTTTGGAAACCCGAGACCTTAAG 1440  
Db 869 TACCAATCAACAAGCTTCTTTCAGCTTCCAGCCGTTTATGGAACACCTTGAAGAGTACAA 928  
QY 1441 TCTTTGATGATAAGCTCATGAGTATGATTTGTTCTCATGAGCATTTGTTACAGC 1500  
Db 929 GAACCTGGTAGACAGCTCATTCCTGAGTATGATGCTTCTTAGATGTGTACACAGC 988  
QY 1501 CATGCATCAATAATACCTTTAGATGGACTGAACATGTTTACGCGCACAGATAGTTGTAC 1560
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2036 ACAGCATTGCCAGGGAAATTCAAAATTGCTAGATTACATCCAGCGGATATGGAGG 2095
2638 TTCCGGAGAAATGATCATATATGCGGAATGTTTCACTTGAAGGATGGTATGATGATCGT 2697
2096 CATCAGAGACTGGACACACAGCAGCTGACTTTTTTCTGAGGCTTTTGAACATAATGGCGT 2155
2698 CCGCTGTTCAATTAATGCTGTAAGCACTGATGAGACAGCAGCTGCTC 2742
2156 CCTATTCTCTTTTGGTGTACATCCCAAGCAGAGTGGCCCTCATC 2200

RESULT 8
US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
; APPLICANT: Sornasse, Xiao Min
; APPLICANT: Sornasse, Thierly
; TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
; FILE REFERENCE: PA-0033 US
; CURRENT APPLICATION NUMBER: US/09/918,624B
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

Query Match 18.9%; Score 596.6; DB 9; Length 2955;
Best Local Similarity 58.0%; Pred. No. 7e-158;
Matches 1174; Conservative 2; Mismatches 801; Indels 48; Gaps 5;

727 GAAATAGACCCCTTTTGACAAACATATCGTCAACACCTTGATTTACAGGTATTCACAGTAC 786
187 GAGATCGACCCGTACTTGAAGCCCTACGCGTGGACTCCAGCGAGGTATAAGCAGTTT 246
787 AAGAAATAGAGGAGGCAATTCACAGTATGAGGCTGTTTGAAGCTTTTCTGCTGT 846
247 AGCCAAATTTTGAGAACATTTGGAGAAATTTGAGGATTTGATTAAGTTTCCAGAGC 306
847 TATGAAATAATGGGTTTTCACCTGCTAGTGTACAGGTATCAGTACCTACCTGCT 903
307 TATGAATCAATTTGGGCTCCACAGATGCTGATGGTGTATCTCCAAAGATGGGCT 366
904 CCTGTGCGCAGTCACTGCTCTCATTTGGAGATTTCAACAATTTGGACCAATGCTGAC 963
367 CCGGAGCAGAGGAGTTTCTTACTGGAGATTTTAAATGTTGAATCCATTTTGTGAC 426
964 ATTATGACTCGGAATCAATTTGGTCTCGGACATTTTCTGCCAAATTAATGTGATGT 1023
427 CCATACAAAATACTGGATTTATGAAATGGAGCTGATATCCCAAGCAGATATA 486
1024 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGACACTTTCACAGGTG 1081
487 TCTGTAATCTGCTGCTGATGCAATTTAAGGTAGTTTATTACTAGTAAAGCGAGAG 546
1082 -TTAAGTAATCCATCTGCTGGATCAACTACTCTTTACAGTTTCTCTGATGAATTC 1140
547 ATCTGTATGATTTTACCGTGGGCAAAAGTATGTTCTGCTGAGGTGATATGTGAT 606
1141 TATAATGAATATATTTATGATCCACCGGAGAGAGGTATGCTTCCAAACACCCACGG 1200
607 TATGATGATGATACCTGGGATCC-----AGAACATCATATAGTTTAAAGTCCAGA 660
1201 CCAAGAAACCAAGTCCGTGAGATATATGATCTCATATTTGAATGATGATGTCGGAG 1260

989 CATGCTTCAAAAATTCACAGATGATGAATATGTTTATGATGGGACAGATTCCTGTTAT 1048
1561 TTCTACTCGAGCTCGTGGTATCATCTGATGATGGAATTCGCGCTCTTTAACTAATGA 1620
1049 TTTCAATTCGGACCTAGAGGACTCATGATCTTTGGATAGCAGATTTGTTGCTACTCC 1108
1621 AACTGGAGGTACTTAGTATCTTCTCTCAATGCGAGATGGTGGTGTAGTGCACA 1680
1109 AGCTGGGAAGTTTAAAGATTCCTTCTGTCACAAATAGATGGTGGTGAAGAAATATCG 1168
1681 TTTGRTGGATTTAGATTTGATGCTGATCAATCATATGATGATATACATCCACGATATCG 1740
1169 TTTGATGGATTTGCTTTTATGATGTTTATGCTCATCTTTATCATCACCAGATGGGT 1228
1741 GTGGATTCCTACTGGGAACACGAGATATCTTTGGACTCGCAACTGATGATGATGCTGC 1800
1229 CAAGGTTTCTCAGCTGATACAGTGAATATTTCCGACTACAAGTAGATGAAGATGCTTG 1288
1801 GTGTATCTGATGCTGCCAACGATCTTATTCATGCGGCTTTTCCAGATGCAATTACCATT 1860
1289 ACTTACCTCAITGTCGAATCATTTGGTTACACGCTGTGTCCGATTCATTAACAATA 1348
1861 GGTGAAGTGTAGCGGAATGCGACATTTTATTCCTGCTCAAGATGGGCTGTGGC 1920
1349 GCTGAGATGATACAGGAATGCCAGCTCTGCTCTCCATTTCCAGGAGGGGTGGT 1408
1921 TTTGACTATCGCTGCATATGGCAATTCGTGATAAATGATGATGATGCTGCTCA----AGAAA 1977
1409 TTTGACTATCGACTAGCCATGGCAATTCAGATAAGTGGATTCAGCTACTTAAGAGTTT 1468
1978 CGGATGAGATGAGGAGCTGGTGTATTTGTTTATATACATCTGACAAATAGAGATGCTG 2037
1469 AAGATGAAGACTGGAACATGGCGGATATAGTATACAGCTCTCAACACAGCGCTACTT 1528
2038 GAAAGTGTGTTTCATCGCTGAAAGTCATGATCAAGCTCTAGTGGTGAATAAATA 2097
1529 GAAAGTGCATGCTTATGACAGAGCCTGATCAGGCTTGGTGGGATAGCTGGCTG 1588
2098 GCATTCGGCTGATGACAGGATATGATGATTTATGCTTTGAGCTTTGGATAGCCGCTACA 2157
1589 GCATTTGGTGTGATGGATGCGGAATGTATACAAACATGATGCTGCTGACTCTTTTACT 1648
2158 TCATTAATAGATCTGCGATAGCATTCGACAGATGATTAAGCTTGTAACTATGGATTA 2217
1649 CCAGTTATGATCGTGAATACAGCTTCATTAATGATTCACATCAATTCAGCTGGCTT 1708
2218 GGAGGAGAAGGCTACCTAAATTTTCATGGGAAATGAATTCGCGCCACCTGAGTGGATGAT 2277
1709 GGTGAGAGGCTATCTCAATTTTCATGGGTAATGAATTTGGCATCTCTGATGCTGATAG 1768
2278 TTCCCTAGGCTGACAAACACCTCTCTGATGCTCAGTAATTCGCGGAACCAATTCAGT 2337
1769 TTCCCAAAAAA-----GGAAATTAATCAGAGT 1795
2338 TATGATAATCAGACGAGATTTGACCTGGGAGATGAGATAATTTAAGATACCGTGGG 2397
1796 TACATTAATGCCAGCGGAGTTTCACTTAAGTACGACGACCTTCTTCGCTACAGTTC 1855
2398 TTGCAAGAATTTGACCGGCTATGCAATGATCTGTAAGATAAATGATGATTTATGACTTCA 2457
1856 CTAAATAATTTTGACGGGATGATGAATAGATTTGGAAGAAAGATATGTTGGCTTGCAGCT 1915
2458 GAACACAGTTCATATCAGAAAGATGAGAGATGAGTATGATGATTTTCAAAAAGA 2517
1916 CCACAGGCTACGTCAGTGAAGAAACATGAAGCAATAGATCATCTGCTTTTGAAGAGCA 1975
2518 AACCTAGTTTGTCTTTTAAATTTTCACTGCAAAAAGCTATTCAGACTATCGCATPAGC 2577
1976 GGTCTCTTTTCACTTTTCACTTCCATCCAGCAGAGCTACACTGACTTACCGAGTTTGA 2035
2578 TGGCTGAAGCCTGGAAAATACAGGTTGCTTGGACTGAGTCACTTCTTGGTGGC 2637

Db 661 CCAAGAGCCAGCGAGTCTAAGAAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
QY 1261 CCTAAATTAACATCACTAGCTGAATTTTAGAGATGAAGTTCTTCTCCGCAATAAAACCTT 1320
Db 721 GGAAGAGTAGCTTCTTATAACATTTTACATGCAATGTACTACCAAGAAATCAAGGCGCTT 780
QY 1321 GGTACAAATGCGGTGCAAAATATGGCTATTTCAAGACATCTTATTAATAGTACTGTTTGGT 1380
Db 781 GGAATCAAGTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCGACGCTTGGT 840
QY 1381 TATCATGTACAAATTTTTCACCAAGCAGCGCTTTGGAAACGCGCGACGACCTTAAG 1440
Db 841 TACCAATCACAGCTTCTTGGAGCTTCAGCGCTTCAGCGCTTATGGAACACCTGAAGAGCTACAA 900
QY 1441 TCTTTGATGATAAGCTCATGAGCTAGGAATGTTGTTCTCTCAAGACATGTTGCACAGC 1500
Db 901 SAACGGGTAGACACAGCTCATTCATGGGTATCATAGTCTCTTAGATGGTACACAGC 960
QY 1501 CATGCATCAAAATTAATCTTTAGATGAGCTGAACATGTTTGAAGGACAGATAGTTGTAC 1560
Db 961 CATGCTTCMAAAATTCAGCAGATGATGAATGATGTTGATGGGACAGATTCCTGTTAT 1020
QY 1561 TTTCACTCTGAGCTCGTGGTTATCATTTGATGGATGCGATTCGCGCTCTTTACTATGA 1620
Db 1021 TTTCACTCTGAGCTCGTGGTTATCATTTGATGGATGCGATTCGCGCTCTTTACTATGA 1680
QY 1621 RACTGGGAGGTACTTAGTATCTCTCAAAATGCGAGATGTTGGTGGATGAGTGAACAA 1680
Db 1081 ASCTGGGAGGTTTAAAGATCTCTCTGTCAAACATAAGATGTTGGTGGAGAAATATCGC 1140
QY 1681 TTTGTGATGATAGATTTGATGGTGTGACATCAATGATGATFACACCACCGAATATCG 1740
Db 1141 TTTGATGATTTGTTTGGTGGTGTACGCTCATGCTTTATCATCAACATGAGTGGT 1200
QY 1741 GTGGATCTACTGGGAACTCAGGAATCTTGTCACTCGCACTGCACTGATGATGATGCTGCC 1800
Db 1201 CAAGGTTCTCAGTGATTAAGTAAATTTTGGATGAGAGATGTTTGGCTACTCC 1080
QY 1801 GTGTATCTGATGTGGGCAAGATCTTATTCATGGCTTTTCCAGATGCAATACCAAT 1860
Db 1261 ACTTACCTCATGTTGGCAATCAATTTGTTTACACAGCTGTGCTCCGATCTTATCAATA 1320
QY 1861 GGTCAAGATGTACGGAATCCGACATTTTGTATTCGCTTCAAGATGGGCTGTGGC 1920
Db 1321 GCTGAGATGATCAGGAATGCCAGCTGTGCTCTCCAAATTTCCAGGAGGAGGCTGT 1380
QY 1921 TTTGATCTCGCTGATGCAATTTGCTGATAAATGGAATGATGATGCTCA---AGAA 1977
Db 1381 TTTGATCTCGCTGATGCAATTTGCTGATAAATGGAATGATGATGCTCA---AGAA 1977
QY 1978 CGGATCAGATGGAGAGTGGTGATATTGTTATACACTGACAAATAGAAGATGCTG 2037
Db 1441 AAAGATGAAGACTGGACATGGCGATATAGTATACAGCTCACAACAGCGCTACTCT 1500
QY 2038 GAAAGTGTCTTTCATACGCTGAACATCATGATCAAGCTTGTGCGGTGATAAACAATA 2097
Db 1501 GAAAGTGTCTTTCATACGCTGAACATCATGATCAAGCTTGTGCGGTGATAAACAATA 2097
QY 2098 GCATTCGCTGATGGACAGGATATCTATGATTTTATGCTTTGGATACACGCTCAACA 2157
Db 1561 GCATTTTGTGATGATGCCGAATGATATCAAAATGATGATGATGATGATGATGATGAT 1620
QY 2158 TCATTAATAGATCGTGGATAGATTCACAAAGATGATGATGATGATGATGATGATGAT 2217
Db 1621 CCAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 2218 GGAGGAGAGGTTACTTAATTTTCAATGGAATGATGATGATGATGATGATGATGATGAT 2277
Db 1681 GGTGAGAGGCTGATCTCAATTTTCAATGGAATGATGATGATGATGATGATGATGATGAT 1740
QY 2278 TTTCCCTAGGCTGAACAACACCTCTCTGATGCTGATGATGATGATGATGATGATGAT 2337
Db 1741 TTTCCCAAGAAA-----GGAAATATGAGAGT 1767

QY 2338 TATGATAAATGACACGAGATTTGACCTGGAGATGCAGATATTTAAGATACCGTGGG 2397
Db 1768 TACCATTTATGCCAGCGCGCTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827
QY 2398 TTGCAAGAATTTGACCGGCTATGACAGTATCTTTGAAGATAAATATGATTTATGACTTCA 2457
Db 1828 CTAATTAATTTTACAGGATATGATAGATTTGAAGAAAGATGTTGGCTTGCAGCT 1887
QY 2458 GAACACAGTTTATATCAGCAAGAGATGAGGAGATGATGATGATTTGAAAAAGGA 2517
Db 1888 CCACAGCCCTACGTGAGTGAACAAATTCAGAGCAATTAAGATCAATGCTTTTGAAGAGCA 1947
QY 2518 AACCTAGTTTCTCTTTTAAATTTTCACTGGCAAAAAGCTATTCAGACTATCCATAGGC 2577
Db 1948 GGTCTTCTTTTTCATTTTCACTTCCATCCCAAGCAAGAGCTACTGACTACCGAGTTGSA 2007
QY 2578 TGCTGAGCTCGGAAATACAGGTTGCTTTGGACTGAGATCCACCTTTTGTGGC 2637
Db 2008 ACAGCATTTGCCAGGAAATTCAAAATTTGCTAGATTCAGATCGACGGAATATGGAGG 2067
QY 2638 TTTGCGGAGAAATTCATTAATGCGGAATTTTCACTGACCAAGAGCTACTGACTACCGAGTTGSA 2697
Db 2068 CATCAGAGACTGGACACAGCTGACTTTTCTGAGGCTTTTGAACATAATGGCGT 2127
QY 2698 CTTGCTCAATTAATGCTGATGACCTAGTAGAACACAGCAGTGGTC 2742
Db 2128 CCTATTCTTTTGTGTACATTCACAGCAGAGTGGCTCATC 2172

RESULT 9

US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2148
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

Query Match 18.9%; Score 596.6; DB 10; Length 2955;
Best Local Similarity 58.0%; Pred. No. 7e-158;
Matches 1174; Conservative 2; Mismatches 801; Indels 48; Gaps 5;

QY 727 GAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGCATACAGGTATTCACAGTAC 786
Db 187 GAGATGACCCGCTACTTGAAGCCCTAGCCGCTGAGCTTCCAGCGAGGTATTAAGCAGTTT 246
QY 787 ACAAATAGGAGGCAATGACAGTATGAGGGTGGTTTGAAGCTTTTCTCGTGGT 846
Db 247 AGCCAATTTGAAGAACATTTGAGAAAATGAAGGTGGTATTGATGAATTTTCCAGAGC 306
QY 847 TATGAAAAATGGTTTCTACTCTGCTAGTGTACAGGTATTCATCTACCGT---GAGTGGGT 903
Db 307 TATGAATCAATTTGGCTTCCACAGATGCTGTGGTGGTTTATATCTCAAGAAATGGGC 366

Db	1441	AAAGATGAACATGGGAACATGGCGATATAGTATACACGCTCACAAACAGGCGCTACGCTT	1500
QY	2038	GAAGAAGTGTTCATACCGTGAAGCTCATGATCAAGCTCTAGTCGGTGTCAAAACTATA	2097
Db	1501	GAAGAAGTGTTCATTCATGACAGAGAGCAATGATCAGGCATTTGGTTGGGATAGTCGCTG	1560
QY	2098	GCATTCGGCTGATGGACAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTCAACA	2157
Db	1561	GCATTTGGTTGATGATGCGCAAAATCTATACAAACATGAGTCTCTGACTCTCTTTTACT	1620
QY	2158	TCATTTATAGATCGTGGGATAGCATTCGCAAGATGATTAGGCTTTGAATATGGGATTA	2217
Db	1621	CCAGTTTATGATCGTGGAAATACAGCTTCATAAATGATTCGACTCAATTACGCATGGCTT	1680
QY	2218	GGAGGAGAAGGTTACCTTAAATTTCAATGGGAAATGAATTCGGCCACCTGAGTGGATGAT	2277
Db	1681	GGTGGAAAGGCTATCTCAATTTTCATGGTAAATGAATTTGGGCATGCTGAATGGTTAGAC	1740
QY	2278	TTCCCTAGGGCTGAAACAACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGT	2337
Db	1741	TTCCCAAGAAAA-----GGAAATATGAGAGT	1767
QY	2338	TATGATAAATGCAGACGAGATTTGACCTGGGAGATGCAGAAATATTAAAGATACCGTGGG	2397
Db	1768	TACCAATATGCCAGGGGCGAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC	1827
QY	2398	TTGCAAGAATTTGACCGGGCTATCGAGTATCTTGAAGATAAATATGAGTTTATGACTTCA	2457
Db	1828	CTAAATAAATTTTGACAGGGATATGAATAGATTTGAAGAAAGATATGGTTGGCTTGCAGCT	1887
QY	2458	GNACACCAAGTTCAATATCACGAAGATGATGAAGGATAGGATGATTTGTTTGAAGAAAGGA	2517
Db	1889	CCACAGGCGCTAGTCAGTGAAGAAACAUGAAGCGAATAGATCAITGCTTTTGAAGAGCA	1947
QY	2518	AACCTAGTTTTTGTCTTTTAAATTTTCACTTGGCAAAAAAGCTATTCAGACTATCCGATAGGC	2577
Db	1948	GGTCTCTTTTCATTTTCAACTTCCATCCCAAGCAAGCTACACTGACTACCGAGTTGGA	2007
QY	2578	TGGCTGAAGCCCTGGAAATACAAAGTTGCCCTTGGNCTCAGATATCCACTTTTGGTGGC	2637
Db	2008	ACAGCATTTGCCAGGGAAATTCAAAATTTGGCTAGATTCAGATGACAGCGGAATATGGAGG	2067
QY	2638	TTCCGGAGAAATGATCAVAATCCCGCAATTTTTCACCTTTGAAGATGGTATGATGATCGT	2697
Db	2068	CATCAGAGACTGGACCAACAGCACTGACCTTTTCTGAGGCTTTTGAACATAATGGCGGT	2127
QY	2698	CCTCGTTCAATATGGTGTATGCACCTAGTAGAACACAGTGGCT	2742
Db	2128	CCCTATCTCTCTTCTGCTGTACATTCGCAAGCAGTGGGCCCTCATC	2172

RESULT 10
US-09-770-149-955/c
Sequence 955, Application US/09770149
Patent No. US2002005963A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.

QY	904	CCTGCTGCCAGTCAGCTGCTCTCATTCGGAGATTTCAACAATTTGGCAGCAAAATGCTGAC	963
DB	367	CCGGAGCAGAGAGAGATTTTCTTACCTGGAGATTTAATGGTTGGAATCCATTTCTGTCAC	426
QY	964	ATTATGCTCGGAATGAATTTGCTGGGAGATTTTTCTGCCAAATATGTGGATGGT	1023
DB	427	CCATACAAAAACCTGGATTATGGAAATGGGAGCTGTATATCCCAACAAACGAGATAAA	486
QY	1024	TCTCTCGCAATTCCTCATGGGTCGAGAGTGAAGATACGCATGGACACTTCATCAGGTC--	1081
DB	487	TCGTGACTCGTGGCCTCATGGATCAAAATTAAGGTAGTTATTAAGTAAAGCGGAGAG	546
QY	1082	TTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGCTTCCTGATGAATATCCA	1140
DB	547	ATCTTGATATCGTAATTCACCTGGGCAAGTATGTGGTTCGTGAAGTGATAATGTGAAT	606
QY	1141	TATAATGGAATATATTATGATCCACCCGAGGAGGAGGTATGTCCTTCCAAACCCACGG	1200
DB	607	TATGATGATACACTGGGATCC-----AGAACACTCATATGATGTTAAGCATTCGAGA	660
QY	1201	CCAAAGAAACCAAGTCGCTGAGATATATGAATCTCATATGGAATGAGTAGTCCGGAG	1260
DB	661	CCAAAGAACCGAGAGCTAAGAATTTATGAATCTCAITGTCGGAAATTTCTCCCATGA	720
QY	1261	CGTAAATTAACATCATACGTGAATTTTAGAGATGAAGTCTTCTCTCGCATAAAAACCTT	1320
DB	721	GGNAAAGTAGCTCTTATAAACATTTTACATGCAATGACTACCAAGAATCAAGGCCCTT	780
QY	1321	GGGTACAATGGCGTGCAAATTTGGGTATTCAGAGCAATCTTATATGCTAGTATTGGT	1380
DB	781	GGATACAACCTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCCAGCTTGGT	840
QY	1381	TATCATCTCACAAATTTTTCACCAACAGCCGTTTGGAAACGCCGACGACCTTAAG	1440
DB	841	TACCAATCACAGCTTCCTTTCGAGCTCCACCGTATGGAACACCTGAAGAGCTACAA	900
QY	1441	TCCTTGATTGATAAGCTCATGAGCTAGGAATTTGTTCTCATGGACATGTTTCCAGC	1500
DB	901	GAACCTGGTACACACGCTCATTCACATGGGTATCATAGTCTCTTAGATGGTACACAGC	960
QY	1501	CATGCATCAAAATAATTAATTTAGATGGACTGACATGTTTGACGGCACAGATGTTTAC	1560
DB	961	CATGCTTCAAAAATTTACGACAGATGGATTTGAATATGTTTGAATGGGACAGATTCCTGTAT	1020
QY	1561	TTTTCATCTCGAGCTCGTGGTTATCATGATGGATTCGGATTCGCGCTCTTAACTATGA	1620
DB	1021	TTTCATTTCTGGACCTAGAGGACTCAATGCTTTGGATAGCAGATTTGTTGCCACTCC	1080
QY	1621	AACTGGGAGTACTTAGTATCTTCTCAATGCCAGATGTTGGTGGATGAGTGCAAA	1680
DB	1081	AGCTGGGAAGTTTAAGATTCCTTCTGTCAACATAAGATGGTGGTGGAAATATCGC	1140
QY	1681	TTTGRTGGAATTTAGATTTGATGGTGCATCAATCAATGATGTATACTCACACGCAATATCG	1740
DB	1141	TTTGATGGAATTCGTTTGAATGTTTACCTCATGCTTTATCATCACAATGAGTGGGT	1200
QY	1741	GTGGGAATTCAGCTGGCAACTACGAGGAATACTTTGGACTCGCAACTGTGATGTGCTCC	1800
DB	1201	CAAGGTTTCTCAGTGATTCAGTGAATATTTCCGACTACAAGTAGATGAAGATGCTTG	1260
QY	1801	GTGTATCTGATCTGGCCAAACGATTTATTCATGGGCTTTTCCAGATGCAATACCATT	1860
DB	1261	ACTTACCTCATTTGGCAATTCATTTGGTTTCACACGCTGTGCCGATTCATTAACAATA	1320
QY	1861	GGTGAAGATGTTACGGNAATCCGACATTTGTATTCCTCCGTTCAAGATGGGCTGTGGC	1920
DB	1321	GCTGAGGATGTATCAGGAATCCAGCTCTGTGCTCTCCAAATTTCCAGGAGGGGTGGT	1380
QY	1921	TTTGACTATCGCTGCATATGGCAATTTGCTGATAAATGGATTTGAGTTGCTCA---AGAAA	1977
DB	1381	TTTGACTATCCACTAGCCATGGCAATCCAGATAAGTGGATTCAGCTTACTTAAAGACTTT	1440
QY	1978	CGGATGAGGATGGAGAGTGGGTGATATGTTTCATACATGCAAAATGAGAGTGGTCG	2037

```

; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-955

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Query Match	8.2%;	Score 257.8;	DB 10;	Length 602;
Best Local Similarity	75.1%;	Pred. No. 2.5e-62;		
Matches 322; Conservative	0;	Mismatches 107;	Indels	Gaps 0;
QY 2334	CAGTTATGATAAAATCGACACGAGATTGGACTCGGGAGATGCAGAAATATTTAAGATACCG	23933		
Dd				
QY 602	CAGTTATGACAATAATGCCGCCAGATTGATCTTGGGATGCAGATTATCTCAGATACCG	543		
Dd				
QY 2394	TGGTTGCAAGAATTTGACC CGGGCTATGTCAGTATCTTGAAGATAAAATATGAGTTTTATGAC	2453		
Dd				
QY 542	CGGACTACAAGAAUUTTGATCAGGCAATGCACATCTTGAAGAGAAUATACGGTTTTATGAC	483		
Dd				
QY 2454	TTCCAGAACCCAGTTTCATATCACAAAAGGATGAAGAGATAGGATGATTGTATTTGAAAA	2513		
Dd				
QY 482	TTCCGAGACCAATTCATATACGAAAAGACGAGCAGATAGACTAATCGTATTCGAAG	423		
Dd				
QY 2514	AGAAACCTAGTTTTTCTTTAAUUTTCTACTGSAACAAAGCTATTTCAGCATATCGCAT	2573		
Dd				
QY 422	AGTGTACTCGTCTTGCTTTAACTTCTACTGGACCAGCAGCTACTTTGATTACCGCAT	363		
Dd				
QY 2574	AGSGTGCTGAAGCCTGGAAAAATACAAGTTGCGCTTGGACTCAGATGATCCACTTTTGG	2633		
Dd				
QY 362	TGTTTGCTCCAGCCTGGAAAAATATAAGATCGATTGGACTCGGACGATCCTCTCTTTGG	303		
Dd				
QY 2634	TGGCTTGGGAGAAUATGATCAATCCGAATGTTTCACTTTGAGGATGGTATCATGA	2693		
Dd				
QY 302	TGGATTCAATAGCTCGATGCGCAAGGCAGAGTACTTCACTTAITATGGCTTTATACACGA	243		
Dd				
QY 2694	TCGTCTCGTTCAAUATATGGTGTATGCACCTAGTAGACAGCAGTGGTCTATGCATAGT	2753		
Dd				
QY 242	ACGACCTGCTCTTCAITGGTCTATGACCGTGTAGAACCGCGGTATATGCTTTAGC	183		
Dd				
QY 2754	AGACAAGA	2762		
Dd				
QY 182	AAACACGA	174		
Dd				

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RESULT 11
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent NO. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453

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;	LENGTH:	604
;	TYPE:	DNA
;	ORGANISM:	Homo sapiens
;	FEATURE:	
;	NAME/KEY:	misc feature
;	LOCATION:	(12)
;	OTHER INFORMATION:	n equals a,t,g, or c
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;	LOCATION:	(593)
;	OTHER INFORMATION:	n equals a,t,g, or c
;	US-09-925-300-453	

Query Match		
Best Local Similarity 4.4%; Score 139.6; DB 10; Length 604;		
Matches 217; Conservative 1; Mismatches 130; Indels 0; Gaps 0;		

QY	1170	AGAGGAGAGGTATGHTCTCCAACCCACGCCGCCAAAGAACCAAGTCGCTGAGAATA	1229
Db	135	AGAACACTCATATGAGTTTAAGCATTCCAGACCACAAGAGCCACGGAGTCTAAGAATT	184
QY	1230	TGAATCTCATATGGAATGAGTAGTCCGGAGCCCTAAAATTAACTCATACGTGAATTTAG	1289
Db	185	TGATCICATCGTGGGAATTTCTCCCATGAGGAAAGTAGCTTCTTTATAAACATTTTAC	244
QY	1290	AGATGAAGTTCTTCCTCGCATAAAAAACCTTGGTGACAATCGGTGCAAAATTAATGCAT	1349
Db	245	ATGCAATGCTACTACCAAGATCAAGGCCITGGATACAACATGCTTCAGTTGATGCCAT	304
QY	1350	TCAAGAGCATCTTAATTATGCTAGTTTTGGTTATCATGTCAAAATTTTTTGCACCAAG	1409
Db	305	CATGGAGCATGCTTACTATGTCACGCTTGGTTAGTACAAATCACAGCTTCTTTGCAGCTT	364
QY	1410	CAGCCGTTTGGAAACGCCGACGCCCTTAAGTCTTTGATGTATAAGCTCATGAGCTAGS	1469
Db	365	CAGCCGTTATGGAAACACCTGAAGAGCTACAAGAACTGGTAGACACAGCTCATTYCATGG	424
QY	1470	AATGTGTTCTTCAATGACATTTGTTACAGCCATGCAATCAAAATAATAC	1517
Db	425	TATCATAGTCTCTTAGATGTGTACAGSCATGCTTCAAAAATTC	472

RESULTS 12
US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil

APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-893

Query Match 3.6%; Score 114.6; DB 10; Length 441;
Best local Similarity 67.2%; Pred. No. 7.8e-22;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 2535 TAATTTTCACTGGACAAAGCTATTTCAGACTATCGACTAGGCTGGCTGAAGCTGGAAA 2594
Db 1 TAATTTTCCACTGGACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTTCCCGAAA 60
QY 2595 ATACAAGGTTGCTTGGACTCAGATGATCCATTTTGGTGGCTTCGGGAGAAATTGATCA 2654
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QY 2655 TAATGCGGATGTTTACCTTTGAAGATGGTATGATGATCGCTCGTTCAATTATGGT 2714
Db 121 CTCGGGGAGTTTTCACCTCTGATGGAAGGCGAGGATGAGGCTTCTCTTCATGGT 180
QY 2715 GTATGACACTAGTAGACACAGTGGTCTATGACTAGTAGACAAAGAAAGAAAGA 2774
Db 181 GTATGACACTAGTAGACACAGTGGTCTATGACTAGTAGACAAAGAAAGAAAGA 240
QY 2775 A 2775
Db 241 A 241

RESULT 13
US-10-025-380-304/c
; Sequence 304, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaugchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-025-380-304

Query Match 3.4%; Score 108; DB 9; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;
Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;
QY 727 GAAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTACAGTAC 786
Db 590 GAGATCGACCGGTACTTGAAGCCCTACGCGCTGAGCTTCAGCGCAGGTATAGCAGTTT 531
QY 787 AAGAAATAGGGAGGCAATTGACAAGTAGTACGGGTGGTTTGGAGCTTTTCTCGTGGT 846
Db 530 AGCCAAATTTTGAACACATTTGAGAAATGAGGTGGTATTGATAAGTTTCCAGAGGC 471
QY 847 TATGAAAAAATGGGTTTCTACTCGTAGTGTCTACAGGTATCACTTACCGT---GAGTGGCT 903
Db 470 TATGAATCAFTTGGCGTCCACAGATGCTGATGGTGTATTATACTCAAGAATGGGCC 411
QY 904 CTGGTGCCAGTCAGTCTCTCATTTGGAGATTTCACCAATTGGGACGCAAAATGCTGAC 963
Db 410 CCGGGAGCAGAGGAGTTTCTTACTGAGATTTTAATGGTTGGAATCCATTTTCGTAC 351
QY 964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAATAATGTCGATGGT 1023
Db 350 CCATACAAAAACCTGGATTATGGAATGGAGCTGTATATCCACCACCAAGCAGATAAA 291
QY 1024 TCTCCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACACTTCATCAGGTG-- 1081
Db 290 TCTTACTCGTGGCTCATGGATCCAAATTAAGGTAGTTATTACTAGTAAAGCGGAGAG 231
QY 1082 -TTAAGGATTCATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCCTGTGATCAATTCGA 1140
Db 230 AICTTGTATCTGATTTTACCCTGGCAGAGTATGTTGGTTCGTGAAGGTGATAATGTGAAT 171
QY 1141 TATAATGGAATATATTAATGATCCACCGGAGAGAGAGTATGTTCTTCCACACCCACGG 1200
Db 170 TATGATTGGATACACTGGGATCC-----ACAACACTCATATGAGTTTAAAGCAATTCGCGA 117
QY 1201 CCAAGAAACCAAGTCTCGTGAAGATATATGATCTCATATTTGGAATGATGATGTCGGAG 1260
Db 116 CCAAGAAACCGCAGGAGTCTAAGAAATTTATGAATCTCATGTTGGGAATTTCTTCCCATGAA 57
QY 1261 CCTAAATTAACATCATAGTGAATTTTAGAGATGAAGTTCTTCCCTGCGATAAA 1314
Db 56 GGAAGAGTAGTCTTTTAAACATTTTACATCAATGTACTACCAAGAAATCAAA 3

RESULT 14
US-09-922-217-304/c
; Sequence 304, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaugchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601

TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-304

Query Match 3.4%; Score 108; DB 10; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;

Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;

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QY 727 GAAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GAGATCGACCGGTACTTGAGCCCTACGCCGTGGACTCCAGCGCAGGTATTAAGCAGTTT 531

QY 787 AAGAAATGAGGAGGCAATTGACAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 AGCCAAATTTTGAAGAACATTTGAGAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 471

QY 847 TATGAAAAATGGGTTTCACTCGTAGTGTACAGGTATCACTACCGT---GAGTGGGT 903
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 TATGAATCATTTGGCGTCCACAGATGTCTGATGGTGGTGTATGATAAGTTTCCAGAGGC 411

QY 904 CCTGGTCCCGACGTCTCACTGAGATTTCAACAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 411
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 964 ATTATGACTCGGAATGTTGGTCTGGAGATTTTCTGCCAAATTAATGTGGATGT 1023
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Db 350 CCATACAAAAAAGTGGATTTGAGAAATGAGGTGGTGTATATCCCAAGAGCAATAAA 291

QY 1024 TCTCTGCAATTCCTGCTGAGATTTCAACAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 963
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 964 ATTATGACTCGGAATGTTGGTCTGGAGATTTTCTGCCAAATTAATGTGGATGT 1023
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Db 350 CCATACAAAAAAGTGGATTTGAGAAATGAGGTGGTGTATATCCCAAGAGCAATAAA 291

QY 1024 TCTCTGCAATTCCTGCTGAGATTTCAACAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 963
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Db 290 TCTGACTCGTCTGAGATTTTCTGAGATTTTAAAGTGGATCCATTTTCGTAC 351

QY 1082 -TTAAGGATTCATTCCTGCTGAGATTTTCAACAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 963
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 ATCTTGATCGTATTCACCGTGGCAAGTATGTTGTTGGAAGTATTAAGTGGATTAATGTGAAT 171

QY 1141 TATAATGGAATATATATGATCCACCGGAGAGGAGTATGTTCTTCCACACCCAGG 1200
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 TATGATGGATACACTGGATCC-----AGAACACTCATATGAGTTTAAGCATTCGGA 117

QY 1201 CCAAGAAACCAAGTCCCTGAGATATATGATTCATATGGAATGAGTAGTCCGAG 1260
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 CCAAGAAACCAAGTCCCTGAGATATATGATTCATATGGAATGAGTAGTCCGAG 1260

QY 1261 CCTAAAATTAACATCATAGTGAATTTAGAGATGAAGTCTCTCTCCGATATAA 1314
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GGAAGAGTAGCTTCTTATAAACATTTTACAAGCAATGCTACTACCAAGATCAAA 3
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RESULT 15

US-09-833-263-304/c
Sequence 304, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
FILE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 304
LENGTH: 601
TYPE: DNA
ORGANISM: Homo sapien
US-09-833-263-304

Query Match 3.4%; Score 108; DB 10; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;

Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;

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QY 727 GAAATAGACCCCTTTTGACAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
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Db 590 GAGATCGACCGGTACTTGAGCCCTACGCCGTGGACTCCAGCGCAGGTATTAAGCAGTTT 531

QY 787 AAGAAATGAGGAGGCAATTGACAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
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Db 530 AGCCAAATTTTGAAGAACATTTGAGAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 471

QY 847 TATGAAAAATGGGTTTCACTCGTAGTGTACAGGTATCACTACCGT---GAGTGGGT 903
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QY 904 CCTGGTCCCGACGTCTCACTGAGATTTCAACAAATGAGGTGGTGTGGAAGCTTTTCCAGAGGC 411
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Db 230 ATCTTGATCGTATTCACCGTGGCAAGTATGTTGTTGGAAGTATTAAGTGGATTAATGTGAAT 171

QY 1141 TATAATGGAATATATGATCCACCGGAGAGGAGTATGTTCTTCCACACCCAGG 1200
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Db 170 TATGATGGATACACTGGATCC-----AGAACACTCATATGAGTTTAAGCATTCGGA 117

QY 1201 CCAAGAAACCAAGTCCCTGAGATATATGATTCATATGGAATGAGTAGTCCGAG 1260
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Db 116 CCAAGAAACCAAGTCCCTGAGATATATGATTCATATGGAATGAGTAGTCCGAG 1260

QY 1261 CCTAAAATTAACATCATAGTGAATTTAGAGATGAAGTCTCTCTCCGATATAA 1314
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Db 56 GGAAGAGTAGCTTCTTATAAACATTTTACAAGCAATGCTACTACCAAGATCAAA 3
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Job time : 502.292 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:27:32 ; Search time 4280.35 seconds
(without alignments)
11941.316 Million cell updates/sec

Title: US-10-056-454a-18_COPY_45_3200

Perfect score: 3156

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Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estma.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	499.6	15.8	656	9	AI487345
6	488.6	15.5	728	14	BU008463

7	479.4	15.2	713	14	BQ986883
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10	430.6	13.6	678	10	AV939010
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ALIGNMENTS

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ACCESSION	AY109521	CL1245_1	mrna	linear
VERSION	AY109521.1	GI:21213273	mrna	linear
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SOURCE	Zea mays		mrna	linear
ORGANISM	Zea mays		mrna	linear
REFERENCE	1 (bases 1 to 2766)		mrna	linear
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.		mrna	linear
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes		mrna	linear
JOURNAL	Unpublished (2002)		mrna	linear
REFERENCE	2 (bases 1 to 2766)		mrna	linear
AUTHORS	Coe, E.C.		mrna	linear
TITLE	Direct Submission		mrna	linear
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA		mrna	linear
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	/db_xref="taxon:4577"		mrna	linear
	/clone="CL1245_1"		mrna	linear

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BI308555 EST529965
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BE602527 HVSMH009
BM526229 sal38f02.
BU005876 QGG9F08.Y
AW930851 EST356694
BF065047 HV_CEB002
BQ240494 TaE05016F
BG521671 13-3 Stev
BE427534 PSR7153.I
AU238577 AU238577
AW065909 687002609
BG526727 63-11 Ste
BI699680 sal25q09.
AV442128 AV442128
AW244197 687050F06
BI469105 sal07e09.
BI425610 sal07e09.
BM885252 sal97a08.
AW596011 sal96g03.Y
BM309136 sal55b02.
AJ432814 AJ432814
AV913706 AV913706
BU268430 BU268430
BG524041 38-25 Ste
BU008407 QGH7104.Y
BQ253050 sa05e05.Y
BM411030 EST585357
BE402623 CSB009H05
BO608128 BRY_4030
BQ240653 TaE05014F
BJ233506 BJ233506
BG651974 sad72d10.
AJ432886 AJ432886
BQ716536 AGENCOURT
BQ606935 BRY_2812
BI920158 EST540093


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QY 2669 TCACCTTTGAAGGATGATGATGATGCTCTCGTCAATTTATGTTGCTATGCACCTAGTA 2728
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Db 2343 TCACCTGCTGACTGGCGCAIGACACAGCCGCTGTTCTTCTCGGCTATGCAACCCAGCA 2402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2729 GACACAGCTGGTCTATGACAGTAGTAGACAAAGAAAGAAAGAAAGTA 2781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2403 GAACAGCCGCTATATGACCTGCAGGTGCAGAGCAGCAATAGGCGACAGCA 2455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
AY109532
LOCUS AY109532 2732 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays Cl1742_1 mRNA sequence.
ACCESSION AY109532
VERSION AY109532.1 GI:21213287
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 2732)
Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1..2732
/organism="Zea mays"
/db_xref="MaizeDB:630561"
/db_xref="taxon:4577"
/clone="Cl1742_1"
/library="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 659 a 506 c 679 g 710 t 178 others
ORIGIN

Query Match 36.2%; Score 1142.6; DB 11; Length 2732;
Best local Similarity 59.9%; Pred. No. 2.8e-283;
Matches 1463; Conservative 2; Mismatches 629; Indels 0; Gaps 0;

QY 663 TGATGAATCTGATAGATCAGACAGAGGGGCACTCCCTCCACCTGGACTTGGTCAGAAGAT 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 TGATGCTCAAGCCTTGAACAGAGTTCGAGTGGTNNNNNACCAAGCATGACNNNNNT 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 723 TTATGAATATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATACAGGTATTACA 782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 463 ATTCCAGATTGACCCATGTCGAGGCTATAGTACCATCTGTAGTACGTCAGACGCT 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 783 GTACAGAAAATGAGGAGGCAATTGACAAGTATGAGGTGGTTTGAAGCTTTTCTCG 842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 523 CTATAGAAATCCGPTCAGACATTCATGAACATGAGGAGGCTTGAAGCCCTTCGCCG 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 843 TGSTATGAAAATGGGTTTCACTCGTAGTCTACAGGTATCACTTACCGTGAAGTGCG 902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 TAGTTATGAAAGTTTGGATTTAATCGCAGCGGAAAGGTATCACATATCGAAGATGGC 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 903 TCCGTGGTCCCGACGTCAGTGCCTCATTTGGAGATTCAACAATGGGAGCGAAATGCTGA 962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TCCTGGAGCATTTCTCGAGCATTTGGTGGTGACTTCAACAACCTGGGATCCAAATGCAGA 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 963 CATTATGACCTGGAAATGAATTTGCTGTCTGGAGATTTTCTGCCAAATATATGTGGATGG 1022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 TCGTATGAGCANNNNNNIGANNNNNNNNNNNNNNNNNNNNNNCTGCTAACATGCAATGG 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1023 TTTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGCTAGACACTTTCATCAGAGTGT 1082
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 TACATCACCTATTCTCTCATGATCTCGTTAAAGGTGAGATGATCTCCATCAGGGAT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1083 TAAGGATTCCTTCCTGCTGGATCACTACTCTTTACAGCTTCCTGATGAAATTCATTA 1142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 823 AAAGGATCAATTCAGCCTGGATCAAGTACTCAGTGCAGGCCAGGAGAAATACCATA 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1143 TAATGAATATATATGATCCACCGAAGAGGAGGTATGCTTCCACACACCCAGGCC 1202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 883 TGATGGATTTATTAATGATCCCTCGAGAGGTAAAGTATGTTTCAGGCATCGCGAAC 942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1203 AAAGAAACCAAGCTCGCTGAGATATATGAATCTCATATTTGAATCAGTAGTCCGAGCG 1262
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Db 943 TAAACGACCAAAATCATTGGGATATATGAACACACATGTCGGAATGAGTAGCCCGAAC 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1263 TAAATTAATCTCATGCTGAATTTAGACATGAAGTCTTCTCTGCGATATAAAACCTGG 1322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1003 GAAGATAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTGG 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1323 GTACATGCGGTGCAAAATATGCTATTCAAGAGCATCTTATATGCTAGTTTGGTTA 1382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1063 ATACAATGCGTCAAAATATGCGAATCCAAAGCACTCATATATGGAAGCTTTGGATA 1122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1383 TCATGTCACAAATTTTTTGGACCAAGCAGCGCTTTTGAAGCGCCGAGACCTTAAGTC 1442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1123 CCATGTAATAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTGG 1182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1443 TTTGATGATGAAGCTCATGACCTAGGAAATGCTTCTTCATGAGACATGTTTCACAGCCA 1502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1183 TTTGATGATGAGCAGCATGAGCTTGGTTTGTAGTCTCATGAGATGTTTCATGATCA 1242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1503 TGCATCAATAATATCTTTAGATGGACTGAACATGTTTTCAGCGCAGATAGTTGTTCT 1562
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1243 TCGTCAAGTAATACTCTGGATGGTTGAATGGTTTGTATGATACAGATACACATTAAT 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1563 TCATCTGGAGCTCGTGGTTATCATTTGATGGATTCGGGATTCGGCTCTTTAACTATGAAA 1622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1303 TCAGATGGTCCAGGTGGCCATCACTGATGGGATTCGCGCTATTTACTATGGGAA 1362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1623 CTGGAGGACTCTTAGGTATCTCTCAATGCCAGATGGTGGTGGATGAGTGCATAAT 1682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1363 CTGGAAGTTTAAAGATTTCTCTCTCAATGCTAGATGGTGGCTCGAGGAATTAAGTT 1422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1683 TGRTGGATTTAGATTTGATGGTGTGACATCAATGATGATATACACCGCATTAATCGGT 1742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1423 TGATGGTTTCGGTTTCATGGTGTGACCTCCATGATGTACTCACCAGCATTAACAGT 1482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1743 GGAATTCACGTGGGAACCTACGAGGAATATCTTTGGAATCGCAACTGATGTGATGCTGG 1802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1483 AACATTTACGGGGAACCTCAATGATGATTTTGGCTTTGCCACCGCATGTAGATGAGTGT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1803 GTATCTGATGCTGCCCAACGATCTTATCATGAGCTTTTCCAGATGCAATTAACATGG 1862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1543 TTACTTGAATGCTGGTAAATGATTAATCATGAGCTTTTCTCTGAGGTGGGTAGGTTT 1602
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QY 1863 TGAAGATGTTAGCGGAATGCCGACATTTTGTATTCGGTTCAAGATGGGCTGTGGCTT 1922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1603 TGAAGATGTTAGTGGATGCCATTAATTCAGCTTTCTCTGATGAGTGGGTAGGTTT 1662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1923 TGACTATCGGTGCAATATGCAATTCGTGATTAATGATGATGATGCTCAAGAAAGCGGA 1982
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1663 TGACTATCGGTGCAATATGCAATTCGTGATTAATGATGATGATGCTCAAGAAAGCGGA 1722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1983 TGAGGATTCGAGATGGGTGATATGTTTATACACTGACAAATAGAGATGTCGGAATA 2042
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1723 TGAACCTTGGAGATGGGTGATATTTGTCACACACTGACAAATAGAGGTGGTTAGAGA 1782
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1. 3012
/organism="Zea mays"
/db_xref="MaizeDB:633976"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 837 a 628 c 790 g 756 t 1 others
ORIGIN
Query Match 19.6% Score 619.8; DB 11; Length 3012;
Best Local Similarity 59.7%; Pred. No. 1.9e-148;
Matches 1177; Conservative 2; Mismatches 739; Indels 55; Gaps 6;
721 ATTATGAAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGTATCA 780
Db ATATACACCTGGACCCCAAGCTGGAGATATTCAAGGACCAATTTTCAGSTACCGATGAAA 466
781 CAGTACAGAAATAGAGGAGGCAATTCACAAATGATGAGGCTGTTGGAGCTTTTCT 840
Db AGATTCCTAGACGAAAGGATCAATTCAGAAATAGGGAAGTCTTGAATCTTTCT 526
841 CGTGGTATGAAAAATGGGTTTCACCTGATGCTACAGGTATCATCTACCTGAGTGG 900
Db AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACGTATATCGTGAATGG 586
901 GCTCTGTGCCCCAGCTAGCTGCTCTCATTTGAGAGATTTCAACAATGGGAGCAATGCT 960
Db GCACCTGCTGCGAGGAGGAGAGCTTATGCTGACTTCAATGATGGAATGGTGCACAA 646
961 GACATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTCCAAATTAATGAT 1020
Db CATAAGATGGAGAGGATTAATTTGGTGTCTGGTGCATCAAAAT---TGACCATGCTCAA 703
1021 GGTTCCTCGCAATTCCTCATGGGTCCAGAGTGAAGATACCGATGGACATCTCATCAGT 1080
Db GGGAAACCTGCCATCCCTCACAATTCAGAGTTAAATTTGCTTCTACATGCTGGAGTA 763
1081 GTTAAGGATTCATTCCTGCTTGGATCAACTACTCTTTACACCTTCCCTGATCAAAAT--- 1136
Db TGGGTTGATCGTATTCAGCATTTGATTCGTTATGCGACTGTTGATGCGCTCTAAATTTGA 823
1137 --TCCATATATGGAATATATATATGATCCACCGAGAGAGGATGATGCTTCCCAACAC 1194
Db GTCCTCATATGATGGTGTTCATTTGGGATCCCTGCTTCTGCTTGAAGGTACACATTTAAGCAT 883
1195 CCACGCCCAAGAAACCAAGCTCGCTGAGATATATGATCAATTCATATGATGAGATGAT 1254
Db CTTGCGCTTCAAGGCTGCTGCTCCACGATATCTATGAGGCCCATGATGATGATGAT 943
1255 CCGGAGCCCTAAATTAACCTACATGATGATTTTAGAGATCAAGTCTTCTCTCCATATAAA 1314
Db GAAAGCCACGAGTAAAGCATAATATGAGGAAATTTGACAGCAATGTTGTCACCATACGA 1003
1315 AACCTTGGGTACATCGGTGCAAAATTAATGGCTTATGAGGATTTCTTATGATGATGAT 1374
Db GCAATTAACCTACACACAGTTCAGTTGATGGGAGTATGAGGATTCGTTACTGATGAT 1063
1375 TTTGGTTATCATGTCACAAATTTTTCACCAAGCAGCGGTTTTCAGAGCCCGCAGAC 1434
Db TTCGGGTACCATGTGACAAATTTCTTTGGGTTTGGAGGATGATGAGGATGATGATGAT 1123
1435 CTTAAGTCTTTGATGATTAAGCTCATGACGTAGGATTTCTTCTCTCATGAGCATTTGT 1494
Db CTCAAAATATCTTGTGATAGGACACAGTTTGGGTTTGGAGTCTGATGATGATGATGAT 1183
1495 CACAGCCATGCATCAAAATATATCTTTAGATGGAGTGAACATGTTTGACG-----GC 1545

2043 GGTGTTTCATACCGTGAAGATCATGATCAAGCTAGTCTAGTGGTATGAATCAATGAT 2102
Db GTGTGTAATTTATGCTGAAGATCATGATCAAGCTAGTGGTATGAATCAATGATGAT 1842
2103 CTGCGTGTGATGAGGATGATGATGATTTTATGATGATGATGATGATGATGATGAT 2162
Db TTGGTGTGATGAGGATGATGATGATTTTATGATGATGATGATGATGATGATGAT 1902
2163 AATAGATCGTGGATAGCATTCACAGATGATGATGATGATGATGATGATGATGATGAT 2222
Db CATGATCGTGGATAGCATTCACAGATGATGATGATGATGATGATGATGATGATGAT 1962
2223 AGAAGGTTACCTAAATTTTCATGCGCAATGAATTCGCGCAACCTGATGATGATGAT 2282
Db AGAGGCTATCTTAATTTTCATGCGCAATGAATTCGCGCAACCTGATGATGATGATGAT 2022
2283 TAGGCTGTAACACACCTCTCTGATGCTGATGATGATGATGATGATGATGATGATGAT 2342
Db AGAGGCTGTAACACACCTCTCTGATGCTGATGATGATGATGATGATGATGATGATGAT 2082
2343 TAAATGACAGGAGGATTTGACCTGGGAGATGATGATGATGATGATGATGATGATGAT 2402
Db CAAATGCTGCTGAAGATTTGACCTGGGAGATGATGATGATGATGATGATGATGATGAT 2142
2403 AGAATTTGACCGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2462
Db AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2202
2463 CCAATTCATATCAGAAAGGATGAAGGAGATGATGATGATGATGATGATGATGATGAT 2522
Db CCAGTATATTTCCGGAACATGAGGAGATGATGATGATGATGATGATGATGATGATGAT 2262
2523 AGTTTGTCTTTAAATTTTCACTGGCAAAAGATGATGATGATGATGATGATGATGATGAT 2582
Db GGTATTTGTCTTTAAATTTTCACTGGCAAAAGATGATGATGATGATGATGATGATGATGAT 2322
2583 GAACCTCGAAATACAGGTTGCTTGGACTCAGATGATGATGATGATGATGATGATGATGAT 2642
Db AAACCTCGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2382
2643 GAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2702
Db CAGGATCATCAACGAGCGGACCTTCCGCGGAGCTGTTGCGATGATGATGATGATGATGAT 2442
2703 TTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2756
Db TTCGTTCTCGTTTATACCAAGCAGAACATGATGATGATGATGATGATGATGATGATGAT 2496

RESULT 3
AY105679 3012 bp mRNA linear HTC 25-MAY-2002
LOCUS Zea mays PCO072723 mRNA sequence.
DEFINITION Zea mays
ACCESSION AY105679
VERSION AY105679.1 GI:21208757
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3012)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanarey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 3012)
Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers


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Db 1011 ACTGGGAGAGTTTAAAGATTCCTCTCTGCGAATAAGATGCTGTGGAGGAGTACTGC 1070
QY 1681 TTGTGTGATTTAGATTTGATGCTGTGACATCAATGATGTATCTACACACCGATTATCG 1740
Db 1071 TTGTGATGCTTCCGTTTGTGAGGCTGCTACCTCTATGCTCTATCATCACACCGAATGGGT 1130
QY 1741 GTGGGATTCATCGGGAATACGAGGAATACATTTGGGACTCGCAACTGATGTGATGCTGCC 1800
Db 1131 CAAGGTTTTTGGGTGACTATAATGAATATTTGGACACAGTATGAGATGCTTTG 1190
QY 1801 GTGTATCTGATCGCGCAACGAATCTTATTCATGAGGCTTTTCCAGATGCAATTAACCAAT 1860
Db 1191 ATTTATCTCATGTTGGCAATCAATTTGGCTCACAGCTGTACCCAGACTCGATACATA 1250
QY 1861 GGTGAAGATTTAGCGGAATCCGACATTTTGTATTCCTGTTCAAGATGGGGGTGCTGCC 1920
Db 1251 GCAGAGGATGATCAGGAGTCCGCGCTCTGTTCTCCAACTTCCAGGGAGGGGTGGT 1310
QY 1921 TTTCACTATCGGCTGCTATATGGCAATGCTGATAAATGATGATGCTCTCAAGAAA--- 1977
Db 1311 TTTGACTACAGATTAGCAATGGCTATTCAGATTAATGATGATGCTCTCAAGAAA--- 1977
QY 1978 CGGATGAGGATTTGAGAGTGGGTGATGATTTGCTATACATGATGATGCTCTCAAGAAA--- 1977
Db 1371 AAAGATCAAGACTGGAATATGGGCAATATAGTGTATATCTCTCAACATCGACGCTACCTT 1430
QY 2038 GAAAGTGTGTTTCATACGCTGAAAGTCAATGATCAAGCTCTAGTCGCTGATAAACHATA 2097
Db 1431 GAAAAATGTGCTGTTATGAGAGAGTCAATGATCAGCAATGGTGTGATGATGATGATG 1490
QY 2098 GCATTTGCTGCTGATGACAGAGGATATGATGATTTATGCTTTGGATGACCGTCAACA 2157
Db 1491 GCCTTTGCTGCTGATGACAGGCTGATGATGATGATGATGATGATGATGATGATGATG 1550
QY 2158 TCATTAATAGATCGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2217
Db 1551 CCAGTAATTTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1610
QY 2218 GGAGGAGAGGTTACATTAATTTGATGAGAGATGATGATGATGATGATGATGATGATGATG 2277
Db 1611 GGTGAGAGAGGCTATCTCAATTTCAATGAGTATGATGATGATGATGATGATGATGATGATG 1670
QY 2278 TTCCCTAGGCTGACACACACCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2337
Db 1671 TTCCCAAGAAA-----GGAATATGAGAT 1697
QY 2338 TAATGATAATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2397
Db 1698 TACCATTATGCGAGAGGAGCTTTAATTTAACCAGGATGATGATGATGATGATGATGATG 1757
QY 2398 TTGCAAGATTTGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2457
Db 1758 CTAATAATCTTTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1817
QY 2458 GAACACAGCTTATATACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2517
Db 1818 CCACAGGCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1877
QY 2518 AACCTAGTTTGTCTTTTAAATTTTACAGAGATGATGATGATGATGATGATGATGATGATG 2577
Db 1878 GGACTTCTCTTTTAAATTTTACAGAGATGATGATGATGATGATGATGATGATGATGATG 1937
QY 2578 TGGCTGAGCTGGAATAACAGGTTGCTTGGACTGATGATGATGATGATGATGATGATGATG 2637
Db 1938 ACAGCAACACCGAGGAGTCAAAATTTGATGATGATGATGATGATGATGATGATGATGATG 1997
QY 2638 TTGCGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2697
Db 1998 CATCAGAGACTGGACCAACACCACTTCTGCTGAGGCTTTTGAACATAATGGGCGC 2057
QY 2698 CCTGTTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2757
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Db 2058 CCTATTCCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2117
QY 2758 AAGAAGAAGAAGAAGA 2774
Db 2118 CTGCAAACTGAAGAGA 2134

RESULT 5
LOCUS AI487345
DEFINITION EST245667 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
ACCESSION AI487345
VERSION AI487345.1 GI:4382716
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 656)
AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman,
C.L., Niernman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley,
S.D. and Giovannoni, J.
TITLE Generation of ESTs from tomato carpel tissue
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES
Location/Qualifiers
1..656
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/clone="cLED13M4"
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/dev_host="5 days pre-anthesis to 5 days post-anthesis"
/notes="Vector: pBlueScript SK(-); Site: 1: EcoRI; Site: 2:
XhoI; cLED - Tomato Carpel EST Library. Oligo-primed and
directionally cloned cDNA in vector lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 207 a 106 c 149 g 194 t
ORIGIN
Query Match 15.8%; Score 499.6; DB 9; Length 656;
Best Local Similarity 90.7%; Pred. No. 1.2e-117;
Matches 584; Conservative 0; Mismatches 39; Indels 21; Gaps 4;
QY 2428 CTTGAAGATPAATATGAGTTTATGACTTCAGAACACACCTGATATATCAGGAAGATGAA 2487
Db 1 CTTGAAGATPAATATGAGTTTATGACTTCAGAACACACCTGATATATCAGGAAGATGAA 60
QY 2488 GGAGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2547
Db 51 GGAGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 2548 ACAAAGCTATTCAGACTATCGCATAGGCTGCGCTGAGAGCCCTGGAAGATTAACAGTTGCC 2607
Db 121 ACARAATAGCTATTCAGACTATCGCATAGGCTGCGCTGAGAGCCCTGGAAGATTAACAGTTGCC 180
QY 2608 TTGGACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2667
Db 181 TTGGACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 2668 TTCACCTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2727
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KEYWORDS
SOURCE EST
ORGANISM Lactuca sativa.
 Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 1 (bases 1 to 713)
REFERENCE
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
 Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Composite Genome Project
JOURNAL http://compomics.ucdavis.edu/
COMMENT Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmumson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@catc.org [michelmore@vegmil.ucdavis.edu]
 belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
 for details.
FEATURES Plate: QGF10 row: L column: 08.
 Location/Qualifiers
 1..713
 /organism="Lactuca sativa"
 /cultivar="L. serriola"
 /db_xref="taxon:4236"
 /clone="QGF10L08"
 /clone_lib="QG_EFGHJ lettuce serriola"
 /lab_host="E.coli"
 /note="Vector: pBRCDNASfiAB; The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB-QG_EFGHJ lettuce serriola
 TAG_TISSUE=flowers post-fertilized
 TAG_SEQ-TGCCATCGG"
BASE COUNT 221 a 132 c 146 g 214 t
ORIGIN
 Query Match 15.2%; Score 479.4; DB 14; Length 713;
 Best Local Similarity 79.5%; Pred. No. 2e-112;
 Matches 567; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
 QY 859 GGTTCCTACTGCTAGCTACAGGTATCACTACCTGAGTGGCTCTCTGCTGCGGAGTCA 918
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 QY 919 GCTGCTCTCATGTGAGATTTCAACATTTGGACCAATGCTGACATTTATGACTCGGAAT 978
 Db 61 GCTTCACCTTATGGAGATTTCAACAACTGGAATCCAAATGCTGATTAAGACCCGGAAT 120
 QY 979 GAATTTGGTGTCTGGAGATTTTCTGCCAAATATGTTGGATGTTCTCTGCAATTCCT 1038
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 Db 181 CATGGTTCGAGTAAGATTCGTATGATACGCCATCTGCAATTAAGACTCGATTCCT 240
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 QY 1159 GATCCACCCGAAGAGAGAGGTATGTTCTTCCAAACCCACCGGCAAAAGAAAGTGG 1218

Db 301 GATCCCCACAAGAGAGAAAATACGTGTTTCAACATCCAGACCAAGAGCGGAATCT 360
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 Db 361 CTTAGGATTTATFAGGACCATGTGGGAATGAGTAGTACGGAACCAATGATCAACGATAT 420
 QY 1279 GTGAATTTTAGAGATGAAGTTCTTCTCGCATAAAAACCTTGGGTGACAAATCGGTGCA 1338
 Db 421 GCTAACTTTAGAGAGCATGTCTCCTCGCATAAAAAACTCGGTAACTGCAATTCAT 480
 QY 1339 ATTATGGCTATTCAGAGCATCTCTTAATATGCTAGTTTGGTGTATCATGTACAAATTT 1398
 Db 481 ATCATGGCTATTCAGAGCATTCATATATGCTAGCTTTGGTACCATTGACAAATTT 540
 QY 1399 TTTCACCAACAGCAGCGTTTGGACGCCGCCAGACCTTAAGTCTTTGATTGATAAGCT 1458
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 QY 1519 TTAGATGACATGAACATGTTTACGCGCACAGATAGTTTCTTACTTCTACTCTGG 1571
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RESULT 8
BI308555
LOCUS
DEFINITION EST529965 GP0D Medicago truncatula cDNA clone pgPOD-7017 5' end,
 mRNA sequence.
ACCESSION BI308555
VERSION BI308555.1 GI:14982882
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 689)
REFERENCE Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho
 J., and Fraser, C.M.
AUTHORS ESTs from developing reproductive tissues of Medicago truncatula
 Unpublished (2001)
TITLE Contact: Michael A. Grusak
JOURNAL USDA/ARS Children's Nutrition Research Center
COMMENT Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7044
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu
 B395410e

FEATURES TIGR sequence name: MTOA093TK
 More information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA gta gAT CC).
 Location/Qualifiers
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 days after pollination"
 /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Immature pods, ranging in age from 15 to 30 days
 after pollination, were collected from greenhouse-grown
 plants. At harvest, seeds were removed from pods and
 isolated pod walls were collected and immediately frozen

in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 198 a 112 c 165 g 214 t
ORIGIN

Query Match 14.0%; Score 441; DB 13; Length 689;
Best Local Similarity 77.5%; Pred. No. 1.6e-102;
Matches 534; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

2078 TAGTCGGTCATAAACTATAGCATCTCTGGCTGATGACGACAGATATGATGATTTATGG 2137
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2138 CTTTGGATAGACCGTCAACATCAATTAATAGATCGTGGGATGATGATGATGATGATGAT 2197
61 CTTTAGACAGACCATCTACTCCTCTAATGATCGTGGTATGATGATGATGATGATGATGAT 120
2198 GCGTTGTAACATATGGGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2257
121 GCGTTGTAACATATGGGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
2258 GCCACCGTGAAGTATGATTTCCCTAGGCTTGACACACACCTCTGTGATGCTCAGTAA 2317
181 GCCATCCTGATGGATGATTTTCCAAAGGGGTGATCAGCATCTTCCATTAATGGCAGTAG 240
2318 TTCCCGGAACCAATTCAGTTATGATAAATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2377
241 TTCCCGGAATACACAGCTATGATTAATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
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301 AATATCTAGATATCATGGAATGCAAGAAATTTGATCGAGCTATGACGACCTAGAAGAAA 360
2438 AATATGAGTTATGATCTCAGACACAGCTATATATCAGAAAGGATGAGGAGGAGGAGGAGGAG 2497
361 GATATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
2498 TGATTTGATTTGAAAAGGAAAGCTAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2557
421 TTAATATCTTTGAAAGGACAACTGCTCTTTGATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 480
2558 ATTCAGACTATCGCATAGGCTGGCTGAAGCTGGAATATACAGAGTTGCCITGGACACG 2617
481 ATTCAGATTACAAAGTTGGCTGTTAAAGCCAGGGAATATAGATTCTCTTGGATTTCAG 540
2618 ATGATCAGCTTTTGGTGGCTTCGGGAGAAATGATATATGCGGAATGTTTACCTTTG 2677
541 ATGATCAGCTTTTGGTGGCTTCGAATAGGCTCAATATGATGATGATGATGATGATGATGATGAT 600
2678 AAGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2737
601 AAGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
2738 TGGTCTATGCACTAGTAGACAAAGAA 2766
661 TGGTATATGCTCTTGTAGATGAGTTGAA 689

RESULT 9
BE195628 801 bp mRNA linear EST 22-OCT-2001
LOCUS
DEFINITION HVSMH0089P20f Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH0089P20f,
mRNA sequence.
ACCESSION BE195628
VERSION BE195628.2
KEYWORDS Gt:13188305
SOURCE Hordeum vulgare.

ORGANISM

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 801)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Penton
,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library

TITLE

Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:8707823.

JOURNAL

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

COMMENT

Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 408
Seq primer: AATTACCCCTCACTAAAGG
High quality sequence stop: 611.

FEATURES

Location/Qualifiers
1..801
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0089P20f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Penton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 220 a 146 c 198 g 236 t
ORIGIN

Query Match 13.8%; Score 436; DB 10; Length 801;
Best Local Similarity 76.1%; Pred. No. 3.2e-101;
Matches 549; Conservative 0; Mismatches 171; Indels 1; Gaps 1;

QY 1828 APTCATGGCTTTTCCAGATCAATTACCATGGTGAAGATGTAGCGGACG 1887
DB 2 ATTCATGGACTTTATCCGGATGCTGTATCCATGGTGAAGATGTAGCGGACG 61
QY 1888 TTTTGTATTCCTTCAGATGGGCTGTGCTTGTACTATCGCTGCATATGCAAT 1947
DB 62 TTTTGCATCCCTGCCAGATGGTGTGTTGTTTGTACTATCGCTGCATATG 121
QY 1948 GCTGATAAATGGATTGAGTTGCTTCAGAAACGGGATGAGGATGGAGAGTGGGTGATAT 2007

Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 421.

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	/note="vector: pBluescript II SK+; Site.1: EcoRI; Site.2: XhoI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of P1469916. Complementary DNA was synthesized using a primer consisting of a poly(drf) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI- XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."	
169 a	110 c	126 g
		167 t
		1 others
BASE COUNT		
ORIGIN		

	Query Match	13.1%	Score 413.8	DB 13	Length 573
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Db	1	ATTCCATACGCGGAATATCTATGATCCCGGAGAGAGAGGAAAAATATGCTTCARACAT			60

Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akoxl@atgc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig QG_CA_Contig6851, see <http://cgpdb.ucdavis.edu/>
 for details.
 Plate: QGG9. row: F column: 08.

FEATURES	source	BASE COUNT	ORIGIN
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Location/Qualifiers			
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/organism="Lactuca sativa"			
/cultivar="L.serriola"			
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/clone_lib="QG_EFGHJ lettuce serriola"			
/lab_host="E.coli"			
/note="Vector: pBRCdNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/			
TAG_LIB-QG_EFGHJ lettuce serriola			
TAG_TISSUE=germinating seeds			
TAG_SEQ=TCGTGCGGG"			
233 a 122 c 155 g 206 t 1 others			

	Query Match	13.0%	Score 411.8	DB 14	Length 717	
	Best Local Similarity	75.1%	Pred. No. 5.4e-95			
	Matches 526	Conservative 0	Mismatches 173	Indels 1	Gaps 1	
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QY	19	TTCTTTTATTGATTTTCATTAAGAAACTGAAGAAATAGAAAATATTCGATTCTCCTCC	78			
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QY	705	TGGACTTTGGTCAGAGAGATTATGAATATAGACCCCTTTTGACAAAATATCTGTCACACCT	764			
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QY	79	TGAAAAGGGGAGAGAAATATGAAATTCATCCACTTTTAAGCAATTCATCGTGAACATCT	138			
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QY	765	TGATTACAGGTATTCAGATCAAGAAAATGAGGGAGGCAATTGACAAGTATCAGGGTGG	824			
Db						
QY	139	TGAGTATAGATATTACATTTACAGNAGATACGTGAAGCAATTGACAAATATGAAGGTGG	198			
Db						

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